

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (1) APPLICANT: BRUCE C. ROSS et al.
- (2) TITLE: P. GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
- (3) PP 0839
1997-10-12
- (4) PCT/AU98/01023
1998-10-12
- (5) NUMBER OF SEQUENCES: 532
- (6) (A) NIXON & VANDERHYE P.C.
(B) 1100 NORTH GLEBE ROAD, 8TH FLOOR
(C) ARLINGTON
(D) VIRGINIA
(E) USA
(F) 22201
- (7) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: CD ROM
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: WORD 97
- (8) CURRENT APPLICATION DATA:
(A) 09/581,286
(B) June 28, 2000

RECEIVED

MAY 16 2003

TECH CENTER 1600/2900

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

TTCTGTGTCA	TGGCAAAAGT	TATAAAACA	AAAAAAGGCC	TTGCACTTAA	TCTGAAAGGA	60
AAACCGCTGC	CCGAGATGCT	GGCCGAACCG	GCCCAAAGTC	CTACTTACGC	GGTCGTGCCC	120
GACGATTTTG	AAGGTGTAT	CCCCAAGGTG	ACGGCTCGTC	CGGGGGATAA	GGTGCCTGCC	180
GGCTCAGCAC	TGATGCACCA	CAAGGCATAT	CCGGAGATGA	AGTTTACAAG	TCCGGTTAGC	240
GGCGAAGTGA	TCGCGGTGAA	TCGCGGTGCC	AAGCGCAAGG	TGTTGAGCAT	CGAGGTGAAA	300
CCGGACGGAC	TGAACGAATA	CGAGTCATTC	CCTGTGCGGG	ATCCGTCTGC	CCTCTCTGCC	360
GAACAGATCA	AGGAGCTTTT	ACTGTGCGAGC	GGTATGTGGG	GTTTTATTAA	GCAACGTCCT	420
TACGACATAG	TGGCTACACC	GGATATAGCT	CCACGCGACA	TTTATATTAC	TGCCAACTTT	480
ACTGCACCAT	TGGCTCCGGA	CTTCGATTTC	ATCGTTCGAG	GAGAAGAACG	CGCCCTGCAG	540
ACTGCCATCG	ATGCCTTGCC	CAAACTCAGC	ACAGGAAAGG	TGTATGTGGG	CCTGAAGCCG	600
GGTTCATCTC	TGGGCTTGCA	CAATGCAGAA	ATCGTAGAAG	TACACGGACC	TCATCCGGCA	660
GGTAACGTGG	GCGTGCTGAT	CAATCATACG	AAGCCAATCA	ATCGGGGCGA	AACGGTGTGG	720
ACGCTCAAGG	CTACCGACCT	GATCGTGATC	GGACGTTTCC	TGCTTACGGG	CAAAGCCGAT	780
TTTACAGAA	TGATTGCCAT	GACCGGCTCA	GACGCTGCAG	CTCACGGATA	CGTCCGTATT	840
ATGCCGGGTT	GCAATGTCTT	TGCTTCCTTC	CCCGGCCGAC	TGACAATAAA	GGAATCTCAC	900
GAGCGTGTGA	TCGATGGCAA	TGTGCTGACC	GGTAAGAAGC	TCTGCGAGAA	GGAGCCTTTC	960
CTGTACAGCC	GGTGTGACCA	GATCACGGTG	ATCCCCGAAG	GCGACGATGT	GGACGAACTC	1020
TTCCGGTGGG	CTGCACCCCG	TCTCGATCAG	TACAGCATGA	GCAGAGCTTA	TTTCTCTTGG	1080
TTGCAGGGGA	AAAACAAAGA	GTACGTACTC	GATGCCCGGA	TCAAGGGTGG	GCAACGTGCT	1140
ATGATCATGA	GCAACGAGTA	TGACCGCGTT	TTCCCGATGG	ACATCTATCC	GGAGTATTTG	1200
CTCAAGGCTA	TTATAGCATT	CGACATCGAC	AAGATGGAGG	ACTTAGGCAT	ATATGAAGTG	1260

GCTCCGGAGG ACTTTGCCAC TTGCGAATTT GTGGATACAT CCAAGATCGA GCTGCAGCGT 1320
 ATCGTTCGCG AGGGCTTGA TATGCTCTAT AAGGAAATGA AT 1362

(2) INFORMATION FOR SEQ ID NO:2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...603
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

GAAC	TAAGCA	AGTG	TTACAT	GGATAA	AGTG	AGCTAT	GCTC	TGGG	ATTGAG	CATCGG	TAAT	60
AATTT	CAAGT	CTTCG	GGCAT	CGACAG	CGTC	GTTAT	GGATG	ATTTCA	TGCA	AGGTCT	GTCT	120
GATGT	ACTGG	AAGAAA	AAGC	CCCTCA	GCTC	TCGTAT	GACG	AGGCCA	AGCG	CGAAAT	AGAG	180
GCGT	ATTTC	TGGATT	TGCA	GCAGA	AGGCT	GTCAA	ACTGA	ACAAAG	AGGC	CGGAGA	AGAA	240
TTCT	CAAGA	TAAATG	CACA	CAAGGA	AGGT	GTGAC	GACCT	TACCGA	GCGG	CTTGCA	ATAC	300
GAAG	TACAT	AGATGG	GAGA	GGGCCC	GAAA	CCCACC	CCTT	CGGAC	ACGGT	AACCTG	TCA	360
TATCA	CGGTA	CGCTCA	TCAA	CGGTAT	CGTT	TTGAT	AGCT	CTATGG	ACAG	GGGAGA	ACCG	420
GCCAG	TTTCC	CTCTAA	GAGG	AGTTAT	AGCC	GGCTGG	ACGG	AGATTCT	TCA	ATTAAT	GCCT	480
GTAGG	ATCCA	AGTGAA	AGT	AACATA	ACCG	AGCGAT	CTGG	CGTATG	GAGA	TCGTGG	TGCC	540
GGCGA	ACATA	TCAAAC	CGGG	TAGTAC	GCTC	ATTTT	TATAA	TCGAAT	TATT	GAGTAT	CAAC	600
AAA												603

(2) INFORMATION FOR SEQ ID NO:3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...837
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

CAAAAA	AACA	AAGAT	GAAAAA	AGCA	TTACTT	ATTG	GTGCTG	CTCT	TTGGG	AGCA	60	
GTCAGT	TTTG	CAAGTG	CTCA	GTCTTT	GAGC	ACAATC	AAAG	TACAGA	AACA	TTCAGT	ACAG	120
CAACCT	CGTG	AGGAAG	CCAC	TATTCAG	GTT	TGTGG	AGAAT	TGGCAG	AGCA	AGTTGA	CTGC	180
ATTGGG	ACAG	GTAATT	CTGC	AATCAT	AGCC	GCTGC	AGCGA	AATTTG	AAAG	CGATGA	TCTC	240
GAAAGC	TATG	TTGGCT	GGA	GATCAT	GAGT	GTTGAT	TTCT	TCCCTG	GATA	TAAAGC	GTGC	300
AAGTAC	ACAT	CTGCAG	TCTG	GGCTGA	TGAT	ATGACC	ATTT	TGGGCC	AAATC	AGAAGA	TAGT	360
GATCCC	GAAA	TGCAG	ACTAT	CAACA	ATCTT	GCTCT	CAAGA	CTAGTG	TCAA	GATTGA	AGCC	420
GGCAAG	AATT	ACATAG	TTGG	TTATAT	TGCT	AATACC	CGCAG	GTGGAC	ATCC	TATCGG	ATGT	480
GATCAG	GGCC	CTGCCG	TTGA	TGGTAT	TGGA	GATTGG	TTT	CTATAT	CAGA	AGATGG	TGGT	540
GCTACT	TTCC	CTCCGT	TCGA	ATCTCT	TCAT	CAAGCAG	TTT	CTACCT	TAAA	TTACA	ACATC	600
TATGTC	CGTTG	TTCATT	TGAA	GAAGGG	TGAA	GGTGT	TGAGG	CTGTT	CTTAC	CAACGA	CAAG	660
GCTAAT	GTCTT	ATGTT	CAGAA	TGGCGT	TATC	TATGT	AGCCG	GAGCTA	ATGG	TCGTCA	GGTA	720
TCTCTG	TTCG	ACATGA	ACGG	TAAGGT	TGTT	TATACC	GGCG	TTAGCG	AAAC	GATTGC	AGCT	780
CCTCAG	AAGG	GCATG	TATAT	CCTCCG	TGTA	GGTGCT	AAGA	GCATCA	AGCT	GGCTAT	C	837

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

CGTGnATTCC TGCCGGAGAA AGCTCTCTAT ATCGGCTGCC GCGTGGAGAC GCAAGAGGGG	60
CATGCCGTAG GTTTCGGACT GGATGACGGC CTTGCGATGA AAGGCAAGGG CGATCTGGTC	120
GGGAGCTATC TTCCCGGTGC TGCTCCGATG CCTTTTGTCC CGCTTCTGA TATCCGGCT	180
CGTTGATGG ATGCAATTT TTATATCTAT TCTCGTATTT CACTGGGTTC GGGCACGCAG	240
GATGTTCTCC AGCATAGGAT GAAAGTGTAT CCAACCCCTG CCACGACGGA GCTGCATGTG	300
GAAGCCCTGT CCGCATGGGT GGGCGAGCAG GCTGCGGTAT ATGATATGCG TGGTCGTCGG	360
GTATCGGCTC GGACGGTGGA TAGCGAGAAG CTGTGCATCG ACATTGCCTC ACTGCCCGTG	420
GGCGTCTATA TGCTGCGCAT CGGCAGCTAC TCGCCAAGT TCGAGAAGAG A	471

(2) INFORMATION FOR SEQ ID NO:5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

ACAAGAAATG TTCTACTCAT AAAAATGCCA AGAATTATGA AATTAAAAAT TGCACTCAGA	60
CTGCTGCTGG CGACTTTTGC CATAGTTTTA TTAGCCCTC TGGCCAAGGC CCAGATGGAT	120
ATTGGTGGAG ACGATGTATT GATCGAGACG ATGTCCACCC TATCAGGATA TTCAGAGGAT	180
TTTTATTACA AGATGGCTGT GGCAGACAAT GGATGGATCT ATGTGATGTT GGATTTCTCT	240
CGTATTATT TTGATGATGT CAGGCTGTAT CGTCCAAAG ACGGTGGTGC TACTTACCAA	300
AAGTTAGGGT CTTTGGGGTC TTTGGTGCC TATGACTTCG ATGTCTCGCA TTGCGATTTT	360
ATTGTAACGG GAAAGGATGA AGATGATATC AATGTTTGA CAGTCATGAC AGCATTCGAA	420
TATGTAGGTG GTACTATTGG CAATGGCGTT TTGCTGATGC ATCGCCATGA TGCAGATATC	480
AATAATACAG AGTGTGTGTA CAAGAAGGAT TTCCCTAATA ATAGACTGAT GGGTGTAGCC	540
ATCGCCTCCA ACTACCGTGC GCCCTCTCCT TACGGTTTGG GGGGCGATCC TTTTGCTCTC	600
GCTGTGCGCC TTAGTGGCTC CGGAAGCGAT CACAGCTTCT TGGACTATAT TTTTTCGTTA	660
GATGGTGGAG TACACTTTGA GCAAAGCGT ATTTACACAA GACCCCAAAA ACTGACTATC	720
AATAGAGTAG ACCTTTCATT AGGCAGTACA TCTCCTTCTC TTGGATTTAA TACTTGGCCA	780
CTAATGGGAG TCGTATTCGA AATGAATAAG AACCTTGATG GCTTCGACAT TGGTTTCATT	840
TCCAACTTTG TGGACTATGA TCCCGCTAT GCGTGGTCTG AACCGATAAT AATAGAAGAA	900
GACTGTGGAT GGACTGATTT TAATCCTTTG GGAGCACTAA GTATAGAGAT CCAAATGATG	960
TTGGATGACA ATTCGATAAA TACCGTGGGT GGAGAACGCT CCCATAACTT CCTGATCACT	1020
TACCCGGGCC ATTACGTATA TCCGAAGCAA TCTTTCAATT ATTCTCCCGG ACATACACCG	1080
ACAAAGAAAG ATCTGGTCTT TAAACACTGT ATAGGTATTC CGGCTTTGGC ATACGATAAG	1140

GAAGGCGATC	GTTATCTGAC	TACTTTTCAA	GATCACAATC	TAATGAGATA	CAGATGGATC	1200
AAATACGATG	ACATTAACTC	TTTTTATGGT	TGGAGTTGGC	CATATGTATA	TGCAAAAGAA	1260
GCTAAAGATA	AAAAGAGGCG	CCGTCCGCAA	GTAGCACTCA	ATCCTACCAA	TGGAAAGGCT	1320
TGTTGGGTAT	GGCATACTCG	CAAGAGCCCA	TATGATGAAA	CCAAACCACA	TCCTACTCCT	1380
GTAATTATTA	AACATTTTCT	ATGGTCCGAT	ACGGAGTGGG	TACATGCTCT	GGACGTGGGG	1440
GACGTATTGC	AGAAGGAGGG	TAGCATGAAG	CTCTACCCCA	ATCCTGCCAA	AGAATATGTT	1500
CTGATCAACC	TACCCAAAGA	AGGGGGGCAC	GAGGCAGTCG	TATACGACAT	GCAGGGCCGA	1560
ATCGTGGAGA	AAGTTTCATT	TTCAGGGAAA	GAATATAAGC	TGAATGTGCA	GTATCTGTCC	1620
AAAGGTACGT	ACATGCTGAA	AGTTGTAGCG	GATACGGAGT	ATTTCTGTGA	AAAAATCATT	1680
GTAGAG						1686

(2) INFORMATION FOR SEQ ID NO:6

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: UNKNOWN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

CAAATGAAAC	GATTACTCCC	CTTTCTCCTT	TTAGCAGGAC	TCGTAGCCGT	AGGAAACGTG	60
TCTGCTCAGT	CACCCCGAAT	CCCTCAAGTG	GATGTACACA	CTCGCATCGC	AAGAAATGCC	120
CGTTATCGAC	TGGACAAGAT	CAGTGTCCCG	GATTCTCGTC	AGATATTCEA	TTACTTCTAT	180
AAAGAAGAAA	CGATACCCAC	TAAAATACAA	ACGACCACAG	GAGGTGCAAT	TACAAGCATC	240
GATTTCGCTT	TCTATGAAGA	CGACAGGTTG	GTTCAGGTGC	GCTATTTTGA	CAATAACCTT	300
GAATTAAAC	AAGCGGAGAA	GTATGTATAC	GACGGTTCTA	AGCTGGTCCT	TCGAGAAATT	360
CGCAAGTCGC	CGACAGACGA	AACGCCAATA	AAGAAAGTTA	GCTATCACTA	TCTCTGTGGC	420
AGCGATATGC	CTTTTGAGAT	TACGACAGAG	ATGAGCGATG	GCTATTTTGA	AAGCCATACG	480
CTTAACATATC	TGAATGGAAA	GATTGCCCGA	ATAGATATCA	TGACTCAACA	GAACCCATCG	540
GCCGAATTGA	TCGAAACGGG	TAGAATGGTA	TATGAGTTTG	ATGCCAATAA	TGATGCTGTA	600
CTGCTTCGTG	ACAGTGTATT	TCTTCCTCTT	CAAAACAAGT	GGGTAGAAAT	GTTTACTCAC	660
CGTTATACAT	ACGACAATGA	GCATAATTGT	ATTCGTTGGG	AACAAGACGA	ATTCGGCACC	720
CTCACCCCTT	CCAACAACCT	CGAATACGAC	ACCACTATCC	CTCTGTCGTC	TGTATTGTTC	780
CCCACGCATG	AGGAGTTCTT	CCGTCCCTCT	CTCCCAATT	TTATGAAGCA	TATGCGTACG	840
AAGCAAACGT	ATTTCAATAA	CTCCGGAGAA	GGCTTGTCAG	AGGTATGCCA	TTACAACACT	900
TTCTATACCG	ATATGCAGGG	TAAATCACTG	ACCGATGTTG	CCGTGAACGA	ATCGATCAAG	960
ATTTATCTCT	GTCCTGCCAC	GGATTTTCTG	CGTATAGAAG	GTTCGCAACT	GCTTCGCCTT	1020
TCGCTATTCG	ACATGAACGG	GAACTCATC	AGAGCTACCG	AATTGACAGG	CGATTGGGCC	1080
ATTATCGGAG	TTGCATCTCT	TCCGAGAGGC	ACTTACATCG	CAGAAATAAC	TGCTGCAAAAC	1140
AGCAAAACCA	TACGTGCAAA	AGTATCGCTC	AGA			1173

(2) INFORMATION FOR SEQ ID NO:7

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

AAGAGGAATC	CCTTACCTTT	GACGGCATCA	AATCGAAAGA	TTTTTATAAA	AATGAGACAG	60
CATTTATCTC	TATTTCTTTT	TATCTTGTTT	CTGCTTCTTG	CCTTCTCTTA	TGTCGGTTGC	120
AGAACAGTCC	GACAAACACC	TAAGCAGTCG	GAACGGTACG	TCGTAGTCCT	GTCTTTGGAC	180
GGCTTCCGAC	CGGACTATAC	CGATCGGGCA	CGTACACCGG	CGTTGGATCG	GATGGCACAG	240
GAGGGATTGA	GCGGGTCGCT	CCAACCATGC	TTCCCCTCGC	TTACATTTC	CAATCATTAC	300
AGCATGGCTA	CGGGGCTTTA	CCCCGATCAT	CACGGTATCG	TAGCCAATGA	GTTTGTGGAT	360
TCGCTACTGG	GCATCTTTCG	TATATCCGAC	CGAAAAGCCG	TGGAGACCCC	CGGATTTTGG	420
GGCGGCGAGC	CGGTTTGGA	TACGGCCGCA	CGCCAAGGCA	TCCGTACCGG	TGTCTACTTT	480
TGGGTAGGAT	CCGAAACGGC	TGTGAACGGA	AATCGGCCGT	GGCGGTGGAA	AAAATTCTCC	540
TCCACCGTTC	CGTTTCGTGA	CCGTGCCGAC	TCCGTCATCG	CGTGGCTCGG	ACTGCCCAGAA	600
AAGGAGCGAC	CGCGCTTGCT	CATGTGGTAC	ATCGAGGAGC	CGGATATGAT	CGGACACAGC	660
CAAAAGCCCC	AAAGCCCCTG	GACACTGGCA	ATGGTAGAGC	GGTTGGACAG	TGTGGTCGGC	720
TATTTCCGCA	AGCGGTTGGA	CTCTCTGCC	ATAGCCGCAC	AGACCGACTT	CATCATAGTA	780
TCCGATCAGC	GTATGGCCAC	GTACGAAAAT	GAGAAATGTG	TCAATCTGTC	GCATTATCTG	840
CCTGCGGACA	GTTTCCTCTA	CATGGCCACC	GGGGCCTTCA	CCCACTTGTA	CCCGAAGCCC	900
TCCTATACCG	AGCGAGCCTA	TAGATCCTG	CGGGCCATTG	CACATATATC	GGTTTACCGC	960
AAGGGGGAGG	TGCCCAAGCG	TTTGCCTGT	GGCACCAATC	CTCGTTTGGG	CGAACTGGTC	1020
GTGATTCCGG	ACATAGGCTC	CACCGTCTTT	TTCGCAATAA	ATGAAGACGT	TCGTCCGGGA	1080
GCGGCACATG	GCTATGACAA	CCAAGCACCG	GAAATGCGGG	CTTTACTCCG	GGCTGTCCGA	1140
CCCGATTTC	GTCCGGGCGA	TAGGTGGAA	AACCTGCCGA	ATATCACCAT	CTATCCGCTC	1200
ATATGCAGGC	TGTTGGGTAT	AGAGCCTGCA	CCCAACGATG	CGGACGAAAC	GTTGCTGAAC	1260
GGCCTGATCC	GAGACAAACG	ACCA				1284

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

CTTCCCCGTG	GAGTTTTTCC	CCTGATGTAT	GGCCGAAGAG	GAAGCATTCG	TGCCTCTTCA	60
GGGCATAGGG	ACAAAATTTT	TAAGAATACA	ATTATCAGAT	TTATCACAAT	GAAAGTAGGT	120
TTGTTTCATCC	CCTGTTATGT	CAATGCAGTG	TATCCGGAAG	TGGGTATCGC	CACGTACAAA	180
CTGCTGAAGA	GTTTGGACAT	AGATGTCGAC	TACCCGATGG	ATCAGACATG	TTGCGGCCAG	240
CCTATGGCCA	ATGCCGGATT	CGAACAGAAA	GCTCAAAAGC	TGGCTTTGCG	ATTGGAAGAG	300
CTGTTTCGAGT	CGTATGATGT	AGTCGTAGGG	CCATCGGCCA	GTGCGTTGTC	TTTCGTGAAA	360
GAAGAACTATG	ATCATATCCT	CAGACCGACA	GGACATGTCT	GCAAGTCGGC	AGCCAAGGTT	420
CGGGATATAT	GCGAGTTCTT	GCACGATGAC	CTGAAGATCA	CCAGCCTCCC	CTCCCGATTC	480
GCCCATAGAG	TGAGCCTGCA	CAACAGTTGC	CACGGTGTGC	GCGAAGTCA	TCTGTCCACC	540
CCCAGTGAAG	TGCACCGACC	GTACCACAAC	AAGGTGCGCC	GGCTATTGGA	GATGGTGCAG	600
GGCATAGAGG	TATTCGAGCC	GAAGCGAATA	GACGAATGCT	GCGGTTTCGG	CGGTATGTAC	660
TCGGTGGAGG	AGCCGGAGGT	ATCCACCTGT	ATGGGGCATG	ACAAGGTGCT	GGATCACATA	720
TCCACAGGTG	CGGAGTACAT	CACAGGGCCG	GACAGCTCGT	GCCTCATGCA	TATGCAGGGA	780
GTGATAGACA	GAGAGAAATT	GCCGATCAAG	ACAATTCATG	CAGTAGAAAT	TTTAGCAGCA	840
AACTTA						846

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

CCTCTGAAAA	AACGAATGGA	TATTGTAAGT	ATGGCCGATA	AAGCTCTTGT	AGTGGAGATG	60
AGAGATGTGA	CGCTCTGTCA	GGAGGAAAAAC	GTCATTTTTC	AAAATTGAA	TCTGACCCTT	120
TCCGCCGGAG	ACTTCGTCTA	TCTGATAGGC	TCAGTGGGAT	CGGGGAAGAG	CACTTTGCTG	180
AAGGCTTTGT	ATGCTGAGGT	GCCTATCTCT	GCCGTTATG	CCCGCGTGAT	AGATTATGAT	240
CTGGCAAAGT	TGAAACGGAA	GCAGTTGCC	TATCTGCGCA	GGAATTTGGG	CATTGTGTTT	300
CAGGATTTCC	AGTTGCTGAA	CGGACGTACT	GTTGCGGAGA	ATTTGGATTT	CGTTTTCGA	360
GCTACGGACT	GGAAAAACCG	AGCCGATCGC	GAGCAGCGTA	TCGAGGAGGT	TTTGACCCGT	420
GTGGGAATGT	CTCGGAAGGC	TTATAAGAGA	CCGCACGAAC	TGTCGGGAGG	GGAGCAACAA	480
CGTGTGGGTA	TAGCCAGAGC	TTTGCTGGCG	AAGCCTGCGT	TGATCCTGGC	CGACGAACCC	540
ACAGGCAACC	TCGATTTCGT	GACCGGATTG	CAGATCGCTT	CTCTGCTCTA	CGAAATCAGT	600
AAGCAGGGCA	CTGCAGTACT	TATGAGCAGC	CACAACAGCA	GCCTGCTGTC	GCATCTGCCG	660
GCACGGACAT	TGGCCGTTCG	TAAGAATGGC	GATGCCTCCT	CTTTGGTCGA	GCTGAGTGCA	720
GATGCTGTTT	CAAGAAAAAA	TACGGAAATA	GAT			753

(2) INFORMATION FOR SEQ ID NO:10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...714
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

ACCAGGCATT	GTCCGGCTTG	TCGCTCTTCC	TTTCACCTCA	TAAAAACAAG	TAAAACAATG	60
ATTGAAATCA	GCAACCTCAC	CAAGGTTTTC	AGAACAGAAG	AAATAGAGAC	GGTAGCCCTC	120
GATGGCGTAT	CGCTCAAAGT	GGACAAAGGC	GAATTTATCG	CCATAATGGG	GCCTTCGGGA	180
TGCGGTAAGT	CACTCTGCT	CAATATCCTC	GGCCTTCTCG	ACAATCCAC	TTCCGGTATC	240
TACAAGCTCG	ATGGGGCAGA	AGTGGGCAAC	CTCCGGGAAA	AAGACAGGAC	TGCCGTCCGT	300
AAGGGCAATA	TCGGCTTCGT	ATTCCAGAGC	TTCAACCTCA	TCGAAGAGAT	GACGGTAAGC	360
GAGAACGTGG	AGTTGCCGCT	CGTCTATCTG	GGTGTGAAGG	CCTCCGAGCG	GAAAGAGCGA	420
GTGGAGGAGG	CACTGCGCAA	GATGAGCATC	AGCCACCGGG	CCGGCCACTT	CCCCAATCAG	480
CTCTCCGAG	GACAACAGCA	GCGCGTGGCT	ATCGCCCGTG	CCGTGGTGGC	CAATCCGAAG	540
CTCATCCTCG	CCGATGAACC	CACGGGTAAC	CTCGACTCCA	AAAACGGAGC	CGATGTCATG	600
GAACTGCTCA	GAGGTCTCAA	TCGCGAAGGT	GCAACCATCG	TCATGGTGAC	GCACTCCGAG	660
CACGATGCAC	GTAGTGCCGG	CCGATCATC	AATCTGTTCG	ACGGTAAGAT	TCGC	714

(2) INFORMATION FOR SEQ ID NO:11

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1812 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

```
AGCACAGAAA CAAATAGCAA ATCTGAAATG AAAGAATTTT TCAAAATGTT TTTCGCCTCG      60
ATCCTCGGGG TTATAACGGC AGGAATCATC TGTTCTGTGA TCTTTCTATT TATCTTTTTC      120
GGCATCGTAG CCGGTATTGC CTCCAAGGCA ACGGGAGGAA CCATTCCGAA GATCGAAGCA      180
AACTCCATCC TACATATANA CAATTCTTCT TTCCCTGAGA TCGTATCGGC CAATCCCTGG      240
AGCATGCTCA CAGGCAAAGA CGAGTCCGTA TCGCTCTCAC AGGCAGTCGA AGCCATCGGC      300
CAAGCCAAAA ATAATCCCAA CATAACCGGT ATCTTCTCTG ATCTGGACAA CCTTTCCGTC      360
GGTATGGCAT CGGCAGAGGA ATTGCGTCGC GCGTTGCAGG ATTTCAAGAT GTCGGGCAAG      420
TTCGTCTGAT CCTATGCCGA CAGATACACC CAAAAGGGTT ACTACCTCTC CAGTATTGCA      480
GACAACTCTT ACCTCAATCC GAAAGGAATG TTGGGGCTTA TCGGGATTGC GACCCAAACA      540
ATGTTCTACA AAGATGCCCT CGACAAATTC GGCGTGAAGA TGGAGATCTT CAAGGTAGGC      600
ACCTACAAGG CAGCCGTAGA GCCATTCTAT CTCAACAGGA TGAGCGATGC CAATCGCGAA      660
CAAATCACCA CATACATAAA CGGGCTTTGG GACAAGATCA CATCCGATAT TGCAGAGTCG      720
CGCAAGACGG CAATGGATTG CGTGAATGTT TTTGCCGACA AAGGCGAAAT GTTCGGTCTT      780
GCCGAGAAAG CCGTGGAGAT GAAGCTCGTG GATGAGCTGG CTTACCGTAC CGATGTGGAG      840
AAAGAACTCA AAAAGATGTC CCAACGCGGA GAGAAAGATG AACTTCGGTT CGTATCGCTT      900
TCTCAGGTTT TGGCCAATGG CCGCATGAAC AAAACGAAAG GCAGTCGGAT CGCCGTTCTC      960
TTTGCCGAAG GTGAAATAAC GGAAGAAATA ATAAAGAAGC CGTTCGACAC TGACGGTAGC     1020
TCCATCACAC AAGAACTCGC CAAAGAAATC AAGGCAGCAG CCGATGACGA TGATATCAAA     1080
GCCGTAGTAC TTCGTGTCAA TTCTCCGGGA GGTAGTGCTT TCACTTCCGA ACAGATATGG     1140
AAGCAGGTAG CCGATCTCAA GGCCAAAAAG CCTATCGTGG TCTCCATGGG CGACGTAGCA     1200
GCCTCGGGCG GATACTACAT AGCCTGCGCA GCCAACAGTA TCGTGGCAGA GCATACGACT     1260
CTGACCGGCT CCATCGGCAT ATTCGGCATG TTCCCGAACT TCGCGGGCGT AGCCAAGAAG     1320
ATAGGAGTGA ATATGGACGT CGTACAGACA TCCAAGTATG CAGACTTGGG CAACACCTTC     1380
GCTCCGATGA CGGTCAAGA TCGTGCCCTC ATCCAACGCT ACATAGAGCA GGGCTACGAC     1440
CTCTCTCTCA CTCGCGTATC GGAAGGCCGC AACCGCACCA AGGCACAGAT CGACAGCATC     1500
GCTCAAGGCC GTGTATGGCT CGGCGACAAA GCTCTTGAC TCGGTTTGGT GGATGAGCTT     1560
GGAGGTTTGG ACACAGCTAT CAAACGGGCC GCGAAGCTGG CTCAGCTCGG TGGCAACTAC     1620
AGCATAGAGT ATGGCAAGAC CAAGCGCAAC TTCTTCGAAG AGTTGCTCTC CTCATCAGCA     1680
GCGGATATGA AGTCTGCCAT CCTGAGTACC ATTCTCTCCG ATCCGGAAAT AGAAGTTCTG     1740
CGCGAACTCC GCTCCATGCC GCCCGTCTCT TCGGCATAC AGGCACGTCT CCCCTATTAC     1800
TTCATGCCGT AC                                     1812
```

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

```
CTAACGTTGT TTTGTTGCAA CTATTTCAAA CAGATGAGAG CAAACATTTG GCAGATACTT      60
TCCGTTTCGG TTCTCTTTT CTTCGGGACA GCGATCGGAC AGGCTCAGAG TCGAAACCGT      120
ACATACGAGG CTTATGTGAA ACAGTACGCC GACGAAGCTA TCCGACAGAT GAGCCGCTAC      180
AATATACCGG CAAGCATCAC CATAGCACAG GCTTTGGTGG AGACAGGAGC CGGAGCCAGT      240
ACACTGGCCA GCGTACACAA CAATCACTTC GGGATCAAAT GCCACAAATC GTGGACGGGC      300
AAGCGCACCT ATCGTACCGA CGATGCGCGG AACGAATGCT TCCGCAGCTA TTCGGCCGCT      360
CGCGAATCGT ATGAAGATCA TTCCCGATTT CTGCTCCAAC CACGTATATG TCCCTGTGTC      420
AAACTCGACA GAGAAGACTA TCGGGGCTGG GCTACGGGGT TGCAACGCTG TGGCTATGCC      480
ACCAATCGGG GCTATGCCAA TCTGCTGATC AAGATGGTGG AGCTGTATGA GCTATATGCT      540
TTGGATCGCG AGAAGTACCC CTCATGGTTC CACAAGTCTT ACCCCGGGTC CAACAAAAAA      600
```

TCCCATCAAA	CGACCAAGCA	GAAGCAGAGC	GGACTCAAGC	ACGAAGCTTA	CTTCAGCTAC	660
GGACTGCTCT	ACATCATAGC	CAAGCAAGGC	GATACCTTCG	ATTCTTTGGC	CGAAGAGTTC	720
GACATGAGAG	CCTCCAAACT	GGCCAAATAC	AACGATGCTC	CCGTGGATT	CCCGATCGAA	780
AAGGGCGATG	TGATCTATCT	GGAGAAAAAG	CACGCATGCT	CCATCTCCAA	ACACACACAG	840
CACGTAGTGC	GTGTGGGCGA	TTCGATGCAC	AGTATCTCCC	AACGCTATGG	CATCCGGATG	900
AAGAACCTCT	ACAAGCTCAA	CGACAAGGAT	GGCGAATATA	TACCCCAAGA	GGGCGATATA	960
CTGCGCTTGC	GC					972

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

AGGATCCCCG	ACGAGCAGAC	CGGACGTATC	ATGGACGGAC	GTGATATTC	GGATGGCCTC	60
CATCAGGCTA	TGCAAGCCAA	AGAGCATGTG	AAAGTAGAGG	CTGCGACACA	GACATTTGCA	120
ACTATCACTT	TGCAGAACTA	TTTCCGCATG	TATCATAAGC	TGGCAGGGAT	GACCGGTACT	180
GCTGAAACTG	AAGCGGGAGA	GCTTTGGGAC	ATCTACAAAC	TGGACGTTGT	AGTTATTCCG	240
ACAAACAAGC	CTATCGCCCG	TAAGGATATG	AATGATCGTA	TCTATAAGAC	GGCACGTGAA	300
AAATATGCAG	CAGTTATCGA	AGAGATTGTA	CGTCTTGTCG	AAGAGGGCAG	ACCTGTACTT	360
GTCCGTACTA	CTTCGGTGGA	AATATCCGAA	TTGTTGAGCC	GTATGTTACG	CTTGCGTGCG	420
ATCCAACACA	ATGTACTCAA	TGCCAAATTG	CATCAGAAGG	AGGCCGAGAT	TGTAGCTCAG	480
GCCGGTCAGA	AAGGAACTGT	TACCATCGCA	ACGAACATGG	CCGGTCGTGG	TACCGACATC	540
AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	GGTTTGCTA	TCATTGGTAC	GGAAAGGCAC	600
GAATCCAGAG	GAGTGGACGA	ACAGCTTCGT	GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	660
TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	CATCTGATGC	GCCTCTTTGC	CACAGAAAAG	720
ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	780
CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	AAGGTGGAAG	AGAACAACCT	CGGTATCCGT	840
AAACATCTGC	TTGAGTACGA	TGATGTAATG	AATTCGCAGC	GTGAAGTCAT	TTATACCCGT	900
CGCCGTCATG	CTTTGATGGG	AGAGCGTATC	GGTATGGATG	TACTCAATAC	CATATACGAC	960
GTATGTAAGG	CTCTGATTGA	CAATTATGCA	GAAGCCAATG	ATTTCGAAGG	CTTCAAGGAA	1020
GATCTGATGC	GTGCACTCGC	GATAGAATCT	CCTATCACGC	AAGAAATATT	CAGAGGTAAG	1080
AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	1140
ATGGATCTGA	TGCGAGAAGT	GGCCCACCCT	GTGGTTCATC	AGGTATTCTGA	GACCCAAAGCC	1200
GCCGTGTACG	AGCGCATTCT	AATCCCCATT	ACGGATGGTA	AACGTGTCTA	TAACATAGGA	1260
TGCAATTTGC	GTGAAGCGGA	TGAAACTCAA	GGGAAAAGCA	TCATCAAAGA	ATTTGAGAAA	1320
GCTATCGTAC	TGCATACTAT	CGATGAGTCT	TGGAAAGAAC	ATCTGCGTGA	GATGGACGAG	1380
CTTCGTAATT	CCGTTTCAGAA	TGCCAGCTAC	GAAAACAAAG	ATCCACTACT	TATCTATAAA	1440
CTCGAATCTT	ACGAACGTGT	CCGCAAGATG	GTAGAAGCCA	TGAACCGTAA	GACCGTAGCG	1500
ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	GAGGCTCCTT	CCCAAGAAGA	GCTGGAACAC	1560
AGGCGGCAAA	TAGAAATCCG	ACATGCAACC	CAACAACGT			1599

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

```
AAATCTTGCC GTGTTATTGG CCAGACGAGG CGATACGGAT GCTGCCCTGT CGGACTACGA      60
CCGTGCCATC AAAGCCTATC CGGAGTTTGC CGATGCCTAT TTCAATCGCG GCCTGCTGTT      120
GCTTTCGCGC GGAAGGCCA AAGAAGGCAT CGCCGATCTG AGTCGGGCAG GCGAATACGG      180
GCTCTACAAG GCGTACAACA TCATCAAACG AATGAGCACG AAGTCATGAT CTCCGTCAAT      240
AACCTGACTG TCGATTTTCG CACCCGTCTG CTCTTCGATC AGGTATCATT CGTCATCAAC      300
AGGCGCGACC GTATCGCTCT TGTAGGGAAG AACGGTGCCG GCAAGAGTAC GCTGCTCAAG      360
CTGATTGCCG GCATGGAAGA ACCGACATCC GGACACATAG CACGCCCCAA GGGGATCCGC      420
ATAGGCTATC TGCCGCAGGT GATGCGTTTG CAGGACGGAC ACACGGTTTA CGAAGAGGTG      480
GAGCAGGCTT TCAACGATAT TCGCCAAATA GAGGAAGAGA TACGGCGTCT GTCCGATGAA      540
ATGCCCGGAC GTACGGACTA CGAATCGGAT GACTATATCC GACTGATAGA GCATTATACG      600
AATATGAGCG AGACCCTCTC TCTCATGCAG CAGGGCAACT ATCATGCTGC GATCGAACAG      660
ACATTGATCG TCGTGCGGTT CGGCCGAGAG GACTTCCACC GCCCACAGC CGATTTCAGC      720
GGAGGATGGC GTATGCGGAT AGAGCTGGCC AAACCTTCTGC TCCAACGCCC CGAAGTTTTG      780
CTGCTCGACG AGCCGACCAA TCACCTCGAC ATCGAATCCA TCGGCTGGCT GGAGCAGTTC      840
ATCGCCACCA ATGCAGGAGC CGTTATCCTG GTGTCGCACG ACAGGGCATT CATCGACAAT      900
ACCAGCACAC ACGTGCATCG AATAGAAGT GGACATATAT ACGACTACAA GACCAAGTAC      960
AGCCACTATG TGGAGCTGCG CGAAGAGCGG CTGCGACAGC AGATGCGTGC CTACGAGAAT     1020
CAGCAGAAAG TGATCCGCGA TACGGAGGAC TTCATCGAAC GATTCAGATA CAAGGCCACG     1080
AAGTCCGTAG AGGTACAGAG CCGGATCAAA CAGTTGGAGA AAGTAGAGCG CGTGGAGATA     1140
CTGGGGCACA ATCGTTTCGG ATTTCACTTC CGCTTTATCC CGGCACAGCC TTCCGGCAGT     1200
TATCCGCTAA TAGTGGATGA TTTGGCCAAG GCTTATGGCG ATCACCAGGT GTTTTCCGGA     1260
GCTACATACA CCATCGAAAG AGGCGAAAAG GTGGCTTTTC TAGGCAAAAA CGGTGCCGGC     1320
AAAAGTACCA TGGTCAAGTG TATCATGGGA GAGCTGACAG ACTACACCGG CAAGCTCGAA     1380
CTGGGGCACA ACGTGCATCG GGGCTACTTT GCCCAAAACG AAGCCCAAGA GCTAAGAGGG     1440
GATCTCACGG TATTCGACAC GATAGACCGT GAGGCCGTGG GCGACATCCG TCTGCGCCTG     1500
AACGATTTGC TCGGGGCTTT TCTCTTCGGG GGCGAAGCAT CGGAAAAGAA AGTAAGTGTC     1560
CTGAGTGGAG GAGAACGAGC ACGATTGGCT ATTATCAGGC TTTTGCTACA GCCGGCTAAC     1620
TTCCTTATTC TCATGAGACC GACCAATCAC CTCGATATGC GCTCGAAGGA TGTAAGTAAA     1680
GAGGCGATCA AGAAGCTTCA TGGGACTGTC ATCGTAGTAT CTCACGACCG TGAGTTCCTC     1740
GATGGGCTTG TCAGCAAGGT GTATGAATTT GCAGATGGAC AGGTGAACGA ACACCTCGGA     1800
GGTATATACG ACTATCTCCG GACCCGCCGT ATGCAGACGC TGACAGAGCT GGAGCGAACC     1860
ACTACGATCG AAACAAAAAC CACACGGGAG GCTATACCTG AAACGGAAGC CAAAGCGGAC     1920
TACCGTCGGC AAAAGGAGGT AGCCAAACAG CTGCGCACGT TGGAGCGAAC CGTAGCAACC     1980
TGCGAGGAGC GGATCGGAAA ATTGGAGTCG GAATTACAGG CAATAGAGAT GCTACTGCAA     2040
GATCCGAAAC ATGCGACTGA CGCGAATCTG TTCGAGCGAT ACGCCGGCAT GAAACAAGAA     2100
CTCGAAAAGG CCATGGAGGA CTGGGAACAG GCTTCCGAAG CTTTATCCGA AGCCCAAGGA     2160
```

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```
TATTTGAAGC TATTAATACT ACAAATAGCC TTGATGAATT TCTTAAAAA AGAACCGTTT      60
AAAATATTCT CTATGATTTA TCTGCTGTTA GATACAATAA CAAACCGTGC CGGTACAGAA      120
CGCGCCGTGA TCAACTTGGC TAACAACCTG CATGCCAATG GTCATCGCGT ATCATTAGTC      180
AGCGTTTGTA CAAAAGAAGG AGAGCCTTCC TTCCAAGTAG AAAAAGGAAT AGAAGTACAC      240
CATCTCGGAA TTAGGCTTTA TGGCAATGCA TTAGCCCGCA AAACAGTATA TTTCAAGGCT      300
TATCGAAGGA TAAAAGCCCT ATACAAGAAG CGTGAACCGG TTTTATTGAT AGGGACTAAT      360
ATTTTATCA ATACAATTTT GTCTCAGATC AGTAACAGAG GCAGAATATT TACGATCGGA      420
TGCGAACATA TCTCTTATGA TATTGCCCGC CCTATTACAA AACGCATAAG GGGGTTTCTG      480
TATTCAGGGC TTGATGCCGT TGTAGCACTG ACAAAAAGAG ATCAGCAATC GTTCGAGGCA      540
```

ATCTTACGTG	GACGCTCTAA	AGCATATGTC	ATACCCAATC	AAGTTTCATT	TACTACAGTC	600
CAAAGAGATG	CTACTACTCA	CAAACAAATG	TTGGCGATTG	GCAGGCTTAC	CTACCAGAAG	660
GGTTTTGAAT	TCATGATAGA	AGATGCATCA	CGAGTGCTGC	GAGAAAGGCC	TGATTGGAAG	720
CTTATCATAG	TCGGAGATGG	CGAAAATGAA	TCGATGCTAC	GTAAAGAAAT	TGCATCTCGC	780
AATATGGAGT	CGCAAATAGA	AATACATCCA	TCTACACCGG	AAATTCGCAA	ATACTACGAA	840
TCATCTGCTA	TTTATCTAAT	GACGTCCCGT	TTCGAAGGAC	TACCAATGGT	ACTTCTCGAA	900
GCAGAAGCAT	ATGCACCTAC	TATAATCTCA	TACGATTGTC	CGACCGGCCC	GAGGGAAGTG	960
ATCGAAAACG	GTCGCAATGG	TTTCCTTGTG	CCAATGGAAG	CACATGAAGA	CTTCGCGGAT	1020
AAGTTACGCT	TATTGATGGA	TGATGAAACT	CTTCGTAAGA	AAATGGGACA	AGAATCAGAG	1080
TTGATGGTCA	AATCCTACTC	TCCGGCAAAT	ATCTATGAAT	GTGGAAGAA	ACTATTTCGT	1140
GAAATCGGCT	ACATGAAT					1158

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1965 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ACAACGAAAG	AAAACGAGAC	AACAACAAAA	AACGAATATA	GAATTATGGG	AAAAATCATT	60
GGAATTGACT	TAGGCACAAC	GAACTCTTGT	GTCTCTGTAT	TGGAAGGTAA	CGAACCTATC	120
GTTATTACAA	ACAGTGAGGG	CAAGCGCACA	ACGCCCTCGG	TAGTGGCTTT	TGTGGATGGT	180
GGCGAGCGTA	AGGTGGGCGA	TCCGGCCAAG	CGTCAGGCCA	TCACCAATCC	GACCAAGACG	240
ATATACTCTA	TCAAACGCTT	CATGGGCGAA	ACTTACGATC	AGGTTTCCAG	AGAAGTGGAG	300
AGAGTGCCAT	TCAAGGTAGT	ACGTGGGGAC	AATAATACTC	CGCGCGTAGA	TATAGACGGT	360
CGTCTCTATA	CGCCGCAGGA	AATTTCGGCC	ATGATCCTTC	AGAAGATGAA	GAAGACGGCC	420
GAAGACTACC	TCGGTCAGGA	AGTAACGGAG	GCCGTGATCA	CTGTGCCCCG	ATACTTCAAC	480
GACGCTCAAC	GTCAGGCAAC	GAAAGAAGCA	GGAGAGATCG	CCGGCCTGAA	AGTTCGCCGT	540
ATTGTGAACG	AGCCTACGGC	AGCTTCTCTG	GCCTACGGTC	TGGACAAGTC	CAATAAGGAT	600
ATGAAGATCG	CTGTCTTCGA	CTTGGGTGGC	GGTACCTTCG	ATATCTCTAT	CTTGGAATTG	660
GGCGACGGCG	TTTTCGAAGT	GAAATCGACC	AACGGTGATA	CGCACCTCGG	AGGAGACGAC	720
TTCGACCACG	TGATCATTGA	CTGGCTGGCA	GAAGAGTTCA	AGTCTCAGGA	AGGTGTGGAT	780
CTTCGCCACG	ATCCTATGGC	TATGCAGCGT	CTGAAAGAAG	CTGCCGAAAA	AGCCAAGATA	840
GAGCTCTCCA	GCACTTATC	TACGGAGATC	AACCTCCCCT	ATATCATGCC	GGTGAACGGC	900
ATCCCCAAGC	ACTTGGTGAT	GACGCTTACA	AGGGCTAAGT	TCGAGCAGTT	GGCCGATCGT	960
CTGATTGAGG	CATGTGTGGC	ACCCTGCGAA	ACGGCCTTGA	AAGATGCCGG	TATGTCACGT	1020
GGCGATATCG	ATGAAGTGAT	TCTCGTAGGT	GGTTCACAC	GTATTCTCTG	TATTCAGGAG	1080
ATTGTGGAGA	AGATCTTCGG	TAAGGCTCCG	TCCAAGGGTG	TGAATCCCGA	CGAAGTGGTA	1140
GCTGTGGGTG	CCGCTATTCA	AGGCGGTGTT	CTGACCGGTG	AGGTAAAGGA	TGTCTTGCTG	1200
TTGGACGTTA	CCCCCTTGTC	GTCGGTATC	GAGACTATGG	GAGGCGTGAT	GACTCGCTTG	1260
ATCGATGCCA	ATACCACTAT	CCCAGCAAG	AAGAGCGAAA	TCTTTACCAC	AGCAGTGGAC	1320
AATCAACCTT	CGGTAGAGAT	TCATGTACTT	CAGGGTGAGC	GTCTTTTGGC	TAAGGACAAT	1380
AAGAGCATCG	GCCGTTTCAA	CTTGGACGGT	ATTGCTCCGG	CGCCCCGTCA	GACACCGCAG	1440
ATCGAAGTAA	CGTTTGACAT	CGATGCCAAC	GGTATCCTGA	ATGTAACGGC	TCATGACAAA	1500
GCTACCGGCA	AGAAGCAGAA	TATCCGCATC	GAAGCCTCCA	GCGGTTTGTC	CGATGATGAG	1560
ATCAAGCGCA	TGAAGGAAGA	GGCGCAGGCC	AATGCCGAAG	CAGATAAGAA	AGAGAAAAGAA	1620
CGTATCGACA	AGATCAATCA	GGCCGACAGC	ATGATCTTCC	AGACGGAAAA	GCAGTTGAAG	1680
GAGTTGGGAG	ACAAATTCCC	GGCCGACAAG	AAGGCTCCGA	TCGATACCGC	TCTCGACAAA	1740
CTGAAAGAAG	CACACAAAGC	ACAGGATGTA	GCTGCTATCG	ATACAGCCAT	GGCCGAAGTG	1800
CAAACCGCTC	TTTCCGAGC	GGGCGAAGAG	CTTTACAAGA	ATGCCGGAGC	AGCCCAAGGT	1860
GGCGCACAAAC	CCGGTCCGGA	CTTCGGCGGT	GCTCAAGGTC	CCTCTGCCGG	TGATCAGCCC	1920
TCTGACGACA	AGAACGTCAC	AGACGTAGAC	TTGAGGAAG	TGAAG		1965

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

AAGTGGGCAC	GTACAACTAC	TTTAAGGATA	TCGAACGCAA	CAATCTATAA	AACTATGCGC	60
TACGACTTAG	CTATCATCGG	TGGAGGGCCG	GCCGTTTATA	CGGCTGCCGA	ACGTGCTGCC	120
AAAGGTGGCC	TGAAAACCTT	CCTAATTGAG	AAGAATGCTC	TCGGTGGTGT	ATGCCTCAAC	180
GAAGGATGTA	TACCGACCAA	GACGCTACTC	TACTCGGCCA	AAGTGCTACA	TCAAATTGCT	240
ACGGCATCTA	AATATGCAGT	AAGTGGAACG	GCCGATGGAC	TTGACCTCGG	CAAGGTGATT	300
GCCAGAAAAG	GTAAAATCAT	TCCCAAGCTG	ACTGCAGGCA	TCCGTTTACG	CCTGACAGAG	360
GCCGGAGTAG	AGATGGTGAC	GGCAGAAGCT	ACCGTAACGG	GATGCGATGC	AGACGGCATC	420
ATCGGCATTA	CTGCGGGCGA	AGCACAGTAC	AAAGCTGCCA	ACCTGCTACT	ATGTACCGGT	480
TCGGAGACGT	TTATTCCACC	CATCCCCGGA	GTGGAGCAGA	CAGAGTATTG	GACAAACCGT	540
GAAGCTCTAC	AGAAACAAAG	GATTCCGACC	TCTCTCGTCA	TCATCGGTGG	TGGAGTGATC	600
GGAATGGAGT	TCGCTTCTTT	CTTCAACGGT	ATCGGTACGC	AAGTGCACGT	GGTGGAGATG	660
CTGCCGGAAA	TACTCAACGG	TATCGATCCC	GAACATGCAG	CTATGCTACG	CGCTCACTAT	720
GAAAAAGAAG	GAATCAAATT	CTACCTCGGG	CACAAAGTAA	CATCGGTTTC	CAACGGAGCT	780
GTACCGTAG	AATACGAAGG	AGAAAGCAAA	GAGATCGAAG	GAGAACGTAT	CCTGATGAGT	840
GTGGGACGTC	GCCCCGTGCT	GCAAGGATTC	GAGTCGCTCG	GATTGGTGCT	TGCCGGCAAA	900
GGTGTAAGA	CTAATGAGAG	GATGCAAACT	TCCCTGCCCA	ATGTCTATGC	TGCAGGTGAT	960
ATTACAGGCT	TCTCGCTTTT	GGCACATACG	GCTGTACGGG	AAGCAGAGGT	AGCAGTAGAT	1020
CAGATTTTGG	GCAAAACAGA	CGAAACGATG	AGCTACCGTG	CCGTACCAGG	TGTGGTGATC	1080
ACCAATCCCG	AGGTCGCCCG	TGTGGGAGAG	ACGGAAGAAT	CGCTTCGCAA	AGCAGGACGT	1140
GCCTACACTG	TTCGTCGCCT	TCCTATGGCC	TTCTCCGGTC	GATTGTAGC	AGAAAACGAA	1200
CAAGGCAATG	GAGAGTGCAA	ACTACTACTT	GATGAAGAGA	ACCGCTTGAT	CGGAGCACAC	1260
CTCATTGGCA	ATCCGGCCGG	CGAACTCATC	GTAACCGCTG	CCATGGCCAT	CGAGACCGGC	1320
ATGACGGATC	GACAAATCGA	ACGAATCATA	TTCCCTCATC	CGACTGTAGG	CGAAATCCTA	1380
AAAGAAATCT	TCGCCGGAGG	T				1401

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2835 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

CCTAAGATAC	TTATGGAATT	GAAAAGATTT	TTATCACTTG	GTCTTCTGCT	TGTGGGATTC	60
ATTCCGATGA	AGCTTTTCTGC	CCAACAGGCT	CAGCCACTCC	CTACAGATCC	GGCTGTTTCGT	120
GTCGGTAAGT	TGACAAACGG	ATTGACTTAT	TTATCCGTC	ACAACGAGAA	CCCGAAAGAT	180
CGTGCGGATT	TCTTTATCGC	ACAAAAGGTA	GGTCTATTTC	TTGAAGAAGA	TAGCCAGTCC	240
GGTTTGCTC	ACTTCTTGGA	ACACATGGCT	TTCAACGGTA	CGAAGAACTT	CCCGGTAAG	300
AACTTGATCA	ACTATCTCGA	AACGATCGGT	GTACGTTTCG	GTCAGAACCT	GAACGCTTCT	360
ACCGGATTTC	ACAAGACGGA	ATATACGATA	ATGGATGTGC	CGACTACACG	TCAGGGAATC	420
ATCGACTCCT	GCTTGCTTAT	CCTGCATGAT	TGGAGTAACA	ATATTACCCT	CGACGGGCAT	480
GAGATCGACG	AGGAGCGCGG	TGTGATCCAG	GAAGAGTGGC	GTGCTCGTCG	CGATGCCAAC	540
CTTCGTATGT	TCGAGGCTAT	ACTTGCCAAG	GCTATGCCGG	GTAATAAATA	TGCAGAACGC	600
ATGCCCATCG	GTCTGATGGA	CGTCGTGCTC	AACCTCAAGC	ATGATGAGCT	GCGCAACTAT	660

TATAAGAAAT	GGTATCGTCC	CGACCTGCAA	GGTCTGGTGA	TCGTGGGAGA	TATCGATGTG	720
GACTATGTGG	AGAACAAGAT	CAAAGAACTC	TTCAAGGACG	TTCTGTCTCC	CGTGAATCCA	780
GCAGAGCGTA	TCTATACGCC	GGTAGAGGAC	AACGATGAGC	CTATCGTAGC	CATTGCTACC	840
GATGCTGAGG	CTACTACCAC	GCAGCTCTCC	ATCAGCTTCA	AGAGCGACCC	CACTCCTCAA	900
GAAAGTGCGAG	GATCGATATT	CGGACTTGTG	GAAGACTATA	TGAAACAGGT	GATCACTACA	960
GCCGTGAATG	AGCGTCTGTC	CGAGATTACT	CACAAGCCTA	ACGCTCCTTT	CCTCAGTGCA	1020
GGAGCTTTCT	TCTCTAACTT	CATGTACATC	ACCCAGACTA	AGGACGCATT	CAATTTTGTT	1080
GCCACGGTTC	GTGAGGGTGA	AGCGGAGAAA	GCGATGAACG	CATTGGTGGC	AGAGATAGAA	1140
AGCCTCCGTC	AGTTCGGTAT	CACCAAAGGC	GAATACGATC	GTGCACGCAC	GAATGTGCTC	1200
AAGCGATACG	AGAATCAATA	CAACGAAAGA	GACAAGCGTA	AGAACAATGC	TTATGCCAAT	1260
GAATACTCCA	CCTACTTCAC	CGATGGCGGC	TATATCCCGG	GTATTGAGGT	GGAATATCAG	1320
ACGGTGAATG	CTTTTGCTCC	TCAGGTTCCT	CTGGAAGCAT	TCAATCAGGC	TATTGCCCAA	1380
ATGATCGATC	CGGTGAAGAA	TGCTGTCTGT	ACCTCACCAG	GTCTTCAAA	GGCTGAAGCC	1440
AAGATTCCGA	GCGAAGCAGA	CTTCCTCGCT	GCTTTCAAAG	CTGCTCGTCA	GCAGAAAGTA	1500
GAAGCCAAGA	AAGACGAAGT	CTTCGACCAA	AAATTGATGG	AGAAAGCTCC	TAAGGCCGGA	1560
AAGATCGTTT	CCGAGAAGAA	AGATCAGAAG	TTCCGTACCA	CGGAACCTAC	CCTTAGCAAT	1620
GGCATCAAAG	TATACCTCAA	GAAGACCGAT	TTCAAATCAA	ACGAAATCCT	GATGAGTGCT	1680
CTCAGCCCGG	GTGGTATCCT	CTCCGGAAAG	CATGCTCCCA	ACCAATCTGT	GATGAATTCG	1740
TTCATGAACG	ACCGGTGGCT	TGCGTGGTGC	GATGCTATCC	AGCTGGATAA	GGTGCTGACA	1800
GGTCGCTCTG	CTTCCGTATC	TCCTCTTTTG	TCTCTGCTCA	GTGAAGGTCT	TTCGGGCAAA	1860
ACGACTGTAG	AAGATATGGA	AACTTTCTTC	CAGTTGATCT	ATCTCCAAAT	GACTGCTAAC	1920
CGCAAGGATC	CCGAAGCGTT	CAAGGCCACA	CAGGAAAAGT	TGTACAATAA	CTTGAAAAAT	1980
CAGGAAGCCA	ACCCGATGGC	TGCGCTTAGT	GACTCTATCC	GTACATACCA	GTACGGCGAT	2040
AATCCGATGA	TGAAACCCAT	GAAAGCTGCT	GACGTGGAGA	AAGTAAATTA	CGATCAGGTA	2100
ATGGCTTTCT	ACAATGAGCG	ATTGCTGAT	GCCGGCGACT	TTATGTTCTT	CTTTATCGGT	2160
AATCTGGATG	AAGCCAAGAT	GAAGCCATTG	ATCGAACTT	ATCTTGCTTC	ATTGCCCAAC	2220
CTCAAGCGTG	CGGATAAGAT	GAATAAGGCT	CAGGTACCGG	CTGCCCGTTC	GGGAAAGATC	2280
GATTGCAAGT	TCGAGAAGGA	AATGGATACT	CCTTCGACTA	CTATATTCTG	TGTCGTGTCC	2340
GGAAATGTGG	AATATACGCT	CAAGAACAGT	CTCCTGCTGG	AAGTCTTCTC	AGCCGTAATG	2400
GATCAGGTGT	ACACGGCTAC	CGTTCGCGAG	AAGGAAGGCG	GTGCATACAG	TGTGGCTGCA	2460
TTCGGCGGTC	TCGAGCAATA	TCCTCAGCCC	AAGGCTCTGA	TGCAGATCTA	TTTCCCACG	2520
GATCCTGCTC	GTGCCGAGGA	AATGAATGCT	ATCGTTTTTG	CTGAGTTGGA	GAAGCTTGCC	2580
AAGGAGGGCC	CCAATGTGGA	ATACTTTAAG	AAGACTATCG	AAAACCTGAA	TAAGCAGCAC	2640
AAAGAAAGTC	TGCGTGAGAA	TCGTTTCTGG	CTCGAAGCCA	TGAAGGCGTC	TTCTTCGAA	2700
GGAAATGACT	TCATCACAGA	CTACGAATCC	GTACTGAACG	GTCTTACTCC	TGCTGAATTG	2760
CAAAAGTTTG	CGGCAGACCT	CTTGAAGCAG	CAGAATCGGG	TTGTTGTCAT	GATGGCTCCT	2820
GTTGCAAAGG	CTCAA					2835

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

TACACTATGA	GTAAGAAAGG	AACAATCGGG	GTAACGAGCG	ACAATATATT	CCCCGTCATC	60
AAAAAATTCC	TGTACAGCGA	CCATGAGATA	TTCTGCGTGG	AGATCGTCTC	CAATGCCGTG	120
GATGCTACGC	AGAAGCTGAA	AACGCTTACA	TCCGTGCGCG	AATTCAAAGG	CGAGACGGGT	180
GACCTCCGCG	TAACGGTCAG	CGTGGATGAA	GTGGCAGCGA	CGATCACGGT	CAGCGACCGC	240
GGCGTAGGGA	TGACCGAAGA	GGAGGTGGAG	AAGTACATCA	ATCAGATTGC	TTTCTCCAGT	300
GCGGAAGAGT	TTCTTGAAAA	GTACAAAGAC	GACAAGGCCG	CCATTATCGG	CCACTTCGGA	360
CTCGGATTTT	ACTCGGCTTT	CATGGTGCTC	GAGCGAGTGG	ACGTGATCAC	GCGCTCTTTC	420
CGAGAAGATG	CTACGGCGGT	GAAATGGAGC	TGCGACGGAT	CGCCCCAATA	CACGCTCGAA	480
CCTGCGGACA	AGGCTGACCG	TGGCACCGAC	ATCGTGATGC	ACATCGATGA	GGAGAATAGC	540
GAGTTCCTCA	AAAAAGAAAA	GATAGAGGGG	CTCCTCGGCA	AATACTGTAA	GTTCTTACC	600
GTGCCGATCA	TTTTCGGCAA	GAAGCAGGAA	TGGAAAGACG	GCAAGATGCA	AGATACGGAC	660
GAGGACAATC	AGATCAACGA	CACACATCCT	GCCTGGACCA	AAAAGCCTGC	CGACCTCAAG	720
GACGAAGACT	ATAAGGAATT	TTACCGTTTC	CTCTATCCCA	TGTCCGAAGA	GCCTCTCTTC	780
TGGATCCACC	TCAATGTGGA	CTATCGTTTC	AATCTGACAG	GTATCTCTTA	TTTCCCGAAG	840
ATCAAAAACA	ACTTGGATCT	GCAGCGCAAC	AAGATTGAGC	TCTACTGCAA	TCAGGTTTAC	900

GTCACCGATG	AAGTACAGGG	TATCGTGCCG	GA	CTTCCTCA	CCCTCCTGCA	CGGGGTCATC	960
GATTCCGCCG	ATATTCCCCT	CAACGTATCG	CG	CTCCTATC	TGCAGAGCGA	TGCCAATGTG	1020
AAGAAGATCT	CGTCTCATAT	CACCAAGAAG	GT	GGCAGACC	GTCTGGAAGA	AATTTTCAAA	1080
AACGACCGCC	CCACATTTCGA	GGAGAAATGG	GAT	AGTCTCTGA	AGCTCTTCGT	CGAATACGGT	1140
ATGCTGACGG	ATGAGAAGTT	CTATGAGCGT	GC	AGCCAAAT	TCTTCCTTTT	CACCGATATG	1200
GACGGACACA	AGTACACGTT	CGACGAATAC	CG	AACGCTCG	TCGAAGGTGT	ACAGACGGAT	1260
AAGGACGGAC	AGGTAGTGTA	TCTCTATGCT	AC	GGACAAGC	ATGGACAGTA	CAGCCACGTG	1320
AAACGTGCAT	CCGACAAAGG	CTACACGCTG	AT	GTGTTGG	ATGGTCAGTT	GGATCCGCAT	1380
ATCGTGAGCC	TGCTGGAGCA	AAAGTTGGAG	AAG	ACACACT	TTGTCCGTGT	CGATAGCGAT	1440
ACGATCAACA	ATCTGATCCG	CAAGGAGGAA	AG	AGCCGAAG	TGAAACTGTC	CGATACGGAG	1500
CGCGCCACTC	TCGTGAAGCT	GTTTGAAGCA	CG	CTGCCAC	GGGACGAGAA	GAAGCACTTC	1560
AATGTAGCTT	TCGAATCGCT	CGGAGCCGAA	GG	TGAAGCCA	TCCTTATCAC	ACAAGCCGAA	1620
TTCATGCGCC	GTATGCGCGA	TATGGCACAG	CT	GCAGCCGG	GAATGAGCTT	CTACGGCGAA	1680
TTCCCCGATT	CGTACAACT	GGTACTTAAT	AC	CGATCATC	CGCTCATCGA	CAGGGTACTC	1740
CTCGGTGAGA	AAGAATCGGT	AGAGCTTCG	CT	CACAGAGC	TTAGAGCGAA	AATCGCCGAG	1800
CTGAAAGCGG	AAGAGGCCAA	GCTGCTCGAT	GAG	GAAGAAAC	GGAGGAAATC		1860
CCTGTTGCCA	CGAAGGAAGC	CAAGGAGAAC	AAC	CGCCGTCG	AACAGGCCAA	AACCGAAGGC	1920
AGTATCAACG	ATCAACTGAC	CAAATATGCT	CAG	GACAACG	AGCTGATAGG	TCAGCTCATC	1980
GA	CTTGGCTC	TGCTCGGAAG	CG	GATTGCTG	ACGGGAGAGG	CTTTGGCCGA	2040
CGCAGCCAGC	GTCTTCTC					ATTCAATTCG	2058

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

GACATTTCGAC	AGAAAAGACC	GTGCTTCAAC	GCCAATTGT	ACTTTTACCG	TGCAATGGAA	60
AAACTGATCG	ATATTTTGGT	CGTAGACGAT	GATGTGGCAG	TCTGTGCCGC	ACTGCGTCTG	120
GTGCTCAAGC	GAGCGGGCTA	TAATCCCGTT	ATAGCCAACA	GTCCCGACGA	AGCTTTGTCC	180
ATAATGCGGA	ATCCTGATGG	CGGCTGTAAG	CCGGCTGTGA	TTCTGATGGA	TATGAATTTC	240
TCCCTTTTCGA	CCTCCGGCAG	GGAAGGATTG	GA	ACTACTGG	AGAAGATGCA	300
TCCTGCCCTG	TCATACTGAT	GACGGCTTGG	GCTTCGATTC	CACTGGCAGT	GGAGGGAATG	360
AGGCTTGGAG	CTTTCGACTT	CATAGGCAAG	CCATGGGACA	ACGATCGGCT	CCTTCGTACC	420
ATAGATACGG	CCTTGCACT	GGCTGCTCCC	TCAGCTGTGG	CGAATCCATC	GGAACAGTCT	480
GACAGAGATA	CAGCCCGTCA	GCCGAAAGCT	ACAGTCCAAG	AGAATGACCC	CTGTGCCCAT	540
ATCATAGGCC	GGAGCGATGC	CATCTGTAAG	ATCAAGGAAC	GGATACGCCG	CATAGCTCCC	600
ACCCATGCCT	CTGTGTCTGAT	CACGGGCGAG	AGCGGTACGG	GCAAAGAGTT	GATAGCCGAA	660
GCTCTGCACC	GTGGGAGCAA	ACGAGCCTCA	GCCCCATTCT	TCAAGGTCAA	TTTGGGTGGG	720
ATTCCCGAAA	GTTTGTTCGA	AAGTGAGCTG	TTCGGACATA	AGAAAGGAGC	TTTTACCAAT	780
GCTTTTTC	ACAGGAAAGG	ACGGTTCGAG	CTGGCTGATG	GCGGCACGAT	CTTCTGGAC	840
GAAATAGGCG	AACTACCGGT	CGGAACCAA	GTAAAACTGC	TGCGAGTGCT	ACAGGAACAG	900
ACATTTCGAGC	CGTTGGGCGA	GAGCGTCTCC	CACCGAGTGG	ACATCCGTGT	GGTATCGGCT	960
ACGAATGCTT	CCTTGGAGCG	AATGGTAGCC	GAAGGACGTT	TCAGAGAGGA	CCTCTACTAT	1020
CGAATCAACC	TGATACATCT	GCATCTGCCT	CCGCTGCGTG	AGCGTCAGGA	GGATATACAG	1080
CTGCTGGTGG	AAGCCTTCAG	TGAAGCCTTT	GCCCAATCGA	ACGGATTGCC	CCATGCCGTT	1140
TGGAGTGCGG	AAGCTATGCG	ACGTATCTGT	GCCATGCCCC	TACCGGGCAA	TGTACGCGAA	1200
CTGAAAACG	TAGTGGAGCG	TACGCTATTG	CTCTCGGGAT	CGAGAGAAAT	CAGTGCCCGG	1260
GATGTGGCTG	ACTTCGGTTC	GCAGGTGACG	GCAGCAGACC	ACTCCGACGA	ACGGGCTTTG	1320
ACCGACATGG	AGGAAGCTGT	TATCCGAGAG	ACGCTGACTA	AATACAACGG	CAACGTTAGT	1380
CGTGCTGCAC	GAGCCTTGGG	ATTGAGCCGG	GCAGCTCTTT	ACCGGCGAAT	GGAGAAATAC	1440
GGACTG						1446

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

AGATCTCTGC	AATCATTTC	AAATAAAAA	CACTCAAGTA	TGCTTAAGAT	AAAGAACCTC	60
CACGCCACAG	TACAGGGCAA	AGAGATATTG	AAAGGAATCA	ATCTGGAGAT	CAATGCCGGA	120
GAGATTTCATG	CTATCATGGG	GCCGAACGGA	TCGGGGAAAA	GTACGCTCTC	TTCCGTTTTG	180
GTGGGACATC	CCTCCTTTGA	AGTCACGGAA	GGAGAGGTGA	CATTCAATGG	AATCGACCTG	240
CTCGAACTCG	AACCGGAAGA	ACGTGCACAC	CTCGGACTCT	TTCTCAGTTT	CCAATATCCG	300
GTGAGATCC	CGGGCGTCAG	CATGGTGAAT	TTCATGAGGG	CAGCTGTCAA	TGAACATAGG	360
AAAGCGATCG	GAGCAGAACC	CGTATCGGCA	AGCGACTTCC	TCAAGATGAT	GCGAGAGAAG	420
CGTGCCATTG	TGGAGCTGGA	CAACAAATTG	GCCAGCCGTT	CTGTGAACGA	AGGCTTCTCC	480
GGTGGAGAAA	AAAAGAGAAA	CGAAATCTTC	CAAATGGCTA	TGCTCGAACC	CAAGCTGGCT	540
ATTTTGGACG	AAACCGATAG	CGGGCTCGAT	ATCGACGCTC	TCCGCATCGT	AGCAGGCGGG	600
GTAAACCGAC	TCCGCTCTCC	GGAGAATGCT	GCTATTGTGA	TCACACACTA	TCAGCGTTTG	660
CTCGAGTACA	TCAAGCCGGA	CTTCGTACAC	GTCCTTTACA	AGGGGCGCAT	CGTCAAGTCG	720
GGAGGAGCCG	AGCTGGCTCT	CACGCTCGAA	GAAAAAGGCT	ACGACTGGAT	CAAGGAAGAG	780
ATAGGAGAA						789

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1386 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

AGCATGGCTA	AGGAGAAAAC	GATCTACGTC	TGCCGTTGCT	GCGGAACCAA	ATACGCCAAA	60
TGGCAAGGCA	ACTGCAATGC	CTGTGGAGAG	TGGAAGTGA	TTGATGAGGA	GAAGGTGCCG	120
GCACCGGCAT	CGGGCAAGCA	TGCAGCCAAG	AGTTTTATGC	CTCGGGAGCA	GGACAACCGG	180
CCAAGACTCT	TACAGGATGT	GGAGTCCGGC	GATGAAGAGC	GTATTGCGCT	CGCGGATGAA	240
GAGTTCGACC	GCGTACTGGG	TGGAGGAATT	GTCAAAGGAG	CATTTGTCTC	GCTTGGCGGC	300
GAGCCGGGAA	TCCGTAAGTC	CACGCTTATC	CTCCAGACGG	TGCTGCGTCT	GCCGCAGTTG	360
CGCACGCTCT	ATGTGTCCGG	CGAAGAAAGT	GCCCCACAAC	TGAAGATGCG	CGCCGAACGA	420
CTGGGGCAAG	CCATGAATGG	GTGCTACGTA	TACTGCGAAA	CGAATATAGA	GAGGATACTC	480
TCCCGTGCG	AAGAACTCAC	ACCCGATCTC	CTCGTGATAG	ACTCTATACA	GACGGTCTAT	540
ACCGAGGAAA	TGGAAAGCTC	GGCCGGCAGC	GTGGGGCAGA	TCCGCGAATG	TGCCGCCTTA	600
CTGCTCAAAT	ACTGCAAGAC	TACGGGTATC	CCCGTCATCG	TCATCGGACA	CATCACCAAA	660
GAAGGTAGCA	TAGCCGACCG	GAAGGTGCTG	GAGCATATAG	TGGATACGGT	GCTTCTCTTC	720
GACGGGGATA	AGCATCATCT	CTACCGGATA	CTCCGAGGAC	AGAAGAACCG	CTATGGCAGT	780
ACTTCCGAGC	TGGGGATATA	CGAGATGCGG	CAGGACGGTC	TGCGTGCGCT	GGAGAATCCG	840
AGCGAACATC	TCATCACACG	CAATAGGGAA	GACCTCAGTG	GCATAGCCAT	AGCCGTAGCG	900
ATGGAGGGCA	TTCGCCCGAT	ACTCATCGAA	GCGCAGGCTT	TGGTCAGCTC	GGCCATTAT	960
GCCAATCCGC	AGCGTTCGGC	CACGGGCTTC	GATATTCCGG	GGATGAACAT	GCTCTTAGCC	1020
GTAAGTGGGA	AACGTGCCGG	CTTCAAGCTC	ATACAGAAGG	ATGTGTTTCT	GAACATTGCC	1080
GGAGGTATCA	AAATAGCCGA	TCCGGCTACG	GATCTGGCCG	TTATCTCGGC	AGTGCTGGCG	1140
TCGAGTCTGG	ACATCGTTAT	CCCGCCGGCC	GTATGCATGA	CGGGCGAGGT	CGGACTCTCC	1200

GGAGAGATAC GTCCCGTGAG CCGCATCGAG CAGCGCATAA CGGAAGCGCG TCGCATAGGG	1260
TTCAAAGAGA TATTGGTACC GGCCGATAAT TTCCGGCAGG AGGATGCCGG CCGCTTCGGT	1320
ATTCCGGCTCG TGCCGGTCAG AAAGGTGGAG GAAGCCTTCC GCCATCTGTT CTCGAAAGGA	1380
AGAGAA	1386

(2) INFORMATION FOR SEQ ID NO:23

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

GGGTCTTGTG GAAGTAGCCC AGCAATTGGC CGATCAGGGT GTTCGCGTTG TGATCGCCGG	60
ATGGGACATG GACTTTTCGAC GTGACGCTTT CGGACCTATG CCGGGCTTGT GTGCCATAGC	120
CGACTCCGTG ACCAAAGTTC ATGCCGTGTG TGTGGAATGC GGCCGATTGG CCAGCTATTC	180
TTCCCGTCGT GTCCAAGGCG ATCAGCAAGT GATGCTGGGC GAACTGAACG AATACAGTCC	240
CCTCTGCAGA ACCTGCTACA GGAAATGCAG TTCTCCCCCA CAAACAGAAG AAATCCATTC	300
GACAATATGA ATAGCAGACA TCTGACAAAT ACAATCATTG CCGGCCTCTC CCTCTTTGTA	360
CTGACATTGG GCGGCTGCTC CGTAGCCCAA CAAGATACGC AGTGGACTCT CGGCGGAAAG	420
CTCTTTACTT CGGCGTGGAT ACAACGTTTC GCCGAATATC AAGCGCTTTC CATTCAGGCA	480
TACAACATCG CTACGGAAAG AGTGGAGCCT CTACCGGCAG AACGTAAACA AGGAGATAGG	540
CCTTATGCCA TCGTAACGGA CATAGACGAA ACCATTTTGG ACAATACGCC TAACTCCGTG	600
TATCAGGCTC TCAGGGGCAA GGATTATGAT GAAGAGACTT GGGGGAAATG GTGTGCACAG	660
GCCGATGCCG ACACACTGGC AGGAGCTTTG TCTTTCTTCC TCCATGCAGC GAACAAGGGG	720
ATCGAGGTCT TTTACGTCAC CAACCGCAGA GACAATCTGC GCGAAGCAAC TCTTCAGAAC	780
CTTCAGGTTT ACGGATTCCC CTTTGCCGAT GAAGAACATT TGCTTACGAC CCATGGGCCA	840
TCCGACAAAG AACCCCGTCG GCTCAAAATA CAAGAACAGT ATGAAATAGT ATTGCTCATA	900
GGAGACAACT TGGGCGACTT CCACCACTTC TTCAATACGA AAGAAGAGTC CGGACGCAA	960
CAGGCTCTGG GCCTGACAGC CGGGGAGTTT GGCCGGCACT TCATCATGCT GCCCAATCCC	1020
AACTACGGAT CTTGGGAACC GGCATGGTAC GGCGGGAAGT ATCCGCCACT GCCCGAAAGA	1080
GACAAAGCAC TTAAACAACT GCACTCACAG AACAGCAGA	1119

(2) INFORMATION FOR SEQ ID NO:24

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

CGTTGGGGTT TTTCTAATTT TGTGGCCATG AGCACCATA TAGATGTACA ACAGATCAAA	60
CAGCGTTTCG GCATCATCGG TAGCAGTCCG CTGATGGAAC ATGCCATACG AGTGGCAGCA	120
CAGGTGGCTC CTACCGACAT GTCCGTCTTC GTGACGGGGG AGAGCGGTTT GGGGAAAGAG	180
TTCTTCCAC AGATAATCCA CTACTACAGC GCCCGGAAAC ATCATAGCTA CATTGCAGTC	240

AATGCGGAG	CCATCCCCGA	AGGAACCATC	GATTCCGAGC	TGTTCCGACA	CCGCAAAGGT	300
TCCTTTACCG	GAGCCGTATC	GGATCGCAAG	GGGTACTTCG	AAGAAGCATC	CGGCGGCACG	360
ATCTTTCTCG	ACGAAGTGGG	CGAACTGCCT	TTGCCACGC	AGGCGAGGCT	GCTGAGGGTG	420
CTGGAGACGG	GCGAGTTCAT	CCCCGTAGGA	GCCAGCCAGT	CGCAGAAGAC	GGATGTCCGT	480
ATCGTAGCGG	CGACGAATGT	GAACCTCAAG	GAGGCGGTAG	CGAACGGGAA	GTTCCGGGAA	540
GACCTCTTCT	TCCGGCTCAA	TACGGTACCG	ATCGAGGTGC	CTGCGCTGCG	TATGCGACCG	600
GACGACGTGC	CCTTGCTTTT	TCGCCGATTG	GCCGCCGACA	GCGCCGAGAA	GTATCGGATG	660
CCTCCGCTGC	GCCTATCGGA	CGAAGCCCGT	ACCATATTAA	TGCGTTACCG	CTGGCCCGGC	720
AATGTGCGAG	AGTGCGCAG	TATAACCGAC	AGGCTGAGCA	TCCTGGAGGA	GGAGCGGACG	780
GTATCGGCAG	AGACCATCAC	TCGCTACCTG	GACGCTGAGG	GGATGCAAGA	CCTCCACCCC	840
GTCTGTATCC	GACGGAACGA	AACGACCGAA	GCGGACAAAC	AAATCCCCCA	TTACGAGCGC	900
GAAATCATCT	ACCAGGTGCT	ATACGATATG	AAGAAAGAGA	TAGCCGATTT	GAAGGGGATG	960
ATGAACCGCC	TGGCGCACCA	CGAACAGCCC	TCATGGCCTG	TAGGGTCGGA	CGTCTGGGGC	1020
AACGACGACA	AGCGCACCGC	AGATCCGAAG	TGGGGCGTCA	GCACGCACAA	GGCCCCCATC	1080
GCGAACGCGG	CAGAACCCGT	GGAGCCGATA	CAGGAAGCCA	GCGAATACAC	CGAGGATCCG	1140
GTTTCGCTGG	AGGAGGTAGA	GAAGAAAATG	ATTTCCCTTG	CATTGGAACG	CCACGGCGGA	1200
AGGCGCAAGC	AGACAGCCGA	GGAAGTGAAG	ATTTCCGAGC	GGACACTATA	CCGTAAAATC	1260
AAGGAGTATG	GACTGGAA					1278

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

AAAAATCTTC	CGAGGTACGC	TCCGGCATTT	GCGAGAAATC	GTAAAAGGGA	ACAACCTGAC	60
CCTGACAAAC	ATGATAGTCG	TGGGAGAAGC	CATAGACAAT	CGGGAAGGGC	TGTCACGGTT	120
GTATGCCGAC	GAAATCAAAC	ACCTCTTCCG	CACATGATCC	TACTCTTCGG	CGGTACTACG	180
GAAGGCCGTG	CGCAGTTCG	CTGCTGGAT	GAAGCGGGAA	GTCCGTTTTT	CTACTCCACC	240
AAAGGCAATC	TGCAAGAGAT	CCAGAGTAGC	CACGGCCATC	GTCTGACAGG	AGCCATGACG	300
GTTGCCGACA	TGGTTTCGTT	TTGTCGGAAA	GAAGAGATCC	GAATGATCGT	GGACGCCGCT	360
CATCCTTTTC	CGGAAGAATT	GCACGCTTCA	GTGGCAGAAG	CCTCTGAACA	AACAGGTATC	420
CCCGTAGTAA	GATACGAGAG	ACAATACCCT	CCACGCGAAG	AAGGTATCGT	CTGGTGTGCA	480
AACACGATA	CGGCTGCCGA	GCGGATGCTT	GGCGATGGCG	TGCAGCGCTT	GCTGATGCTC	540
ACAGGAGTGA	ATACGATCCC	CAAGCTGGCT	GCTTTCTGGA	AAGAGCGCAC	CACCTTTTGC	600
CGCATATTGA	AGCGAGACGA	ATCGGTTGCT	TTGGCAGAGA	AGAACGGGCT	TCCTGCGGAG	660
CGCATCGTTT	CTTTCGAACC	CGATGCGGAC	GAGGAGCTGA	TGCAAGCCGT	TCGCCCCGAT	720
GCCATTATCA	CAAAAGAAAG	CGGAGAGAGC	GGTTACTTCC	GAGAAAAGAT	AGAAGCTGCC	780
CGACGGATGG	GCATCCGTAT	ATATGCCGTC	GTACGTCCCC	CTTGCCTCC	TTCATTCAAT	840
CCCGTAGGCG	GGCCTGTCCG	TTTGAGACGG	GCGGTAGAAC	GCCTCGTGCC	GGGATTCTTT	900
TCACTCCGAA	GCGGATTAC	TACCGGCACC	ACAGCTACCG	CTGCAGTAGT	AGCAGCCATG	960
TACCGATTGA	TGGGGCTTGG	CTCTCTCGCC	GAAGCTCCCG	TAGAATTGCC	TTCGGGCGAA	1020
ATAGTCAGTC	TGCCCATAGC	GGAAATTCGA	GAGGAAGAAG	ATGCTGTCTG	ATCCGAGTC	1080
CTGAAAGATG	CAGGTGATGA	TCCGGATGTG	ACCAATGGCA	TGGCGGTATG	CGTACGATC	1140
AGGCTCAATC	CGGAACATGA	GGAAGTCCGC	TTCTGTCAGG	GTGAAGGGGT	GGGGGTAGTG	1200
ACGCTCCCCG	GCCTCGGTCT	GAGGTCGGA	GGTCCGGCTA	TCAACCTCGT	ACCTCGACGA	1260
ATGATGACAG	CAGAGGTACG	CCGACTCTAT	GCGCAGGGAG	GTGTGGATAT	TACGATTAGC	1320
GTACCCGAAG	GCCGAGAGGC	TGCTACCCAG	ACATTCAATC	CCCGACTCGG	CATACGGGAC	1380
GGCATCTCTA	TTATCGGAAC	ATGCGGATGC	GTGAAACCTT	TTTCGGCCGA	AGCGTTCGTT	1440
GGTGCCATCC	GTAAGCAAAG	GGGTATTGCC	ACCGCCTTGG	GAGCCAATCA	TATCGTCTCT	1500
AATTCCGGAG	CCAAGAGTGA	GCGTTATGTA	AAAGGAGCCT	ATCCGGCACT	CATTCCACAG	1560
GCCTTTGTGC	AGTATGGCAA	TTTCGTGCGC	GAATCACTCA	GTGTGTGATG	TTCTTCCCTT	1620
TCTGTCCGTT	CGGTAACGGT	AGGAATCATG	CTCGGCAAG	CAGTGAAACT	CGCCGAAGGC	1680
TATCTGGATA	CGCACAGTAA	AAAGGTAGTG	ATGAATCGGG	ATTTCTTGCA	CGAACTGGCT	1740
CGTCAGGCAG	GTTGTTCCGA	AGACATCCAT	GCCATAATAG	ACAGCCTGAA	TTTGGCTCGT	1800
GAGCTATGGA	CTATGCCGAG	TGCGGAGGAC	AGCGATCGAC	TGCTACGAAA	GATTGCCGAA	1860
CGATCTTGGG	AAACTTGCCG	CCATCGGTA	CCATCGGCGG	AATTAGAACT	CCTGCTGATC	1920
GATGAGTCCG	GAGCGATTCC	TTTTCGTATC	GGTGAGAGAA			1959

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

```
CAACAAAGAC CACATAGAAT TATTATGTTG AGGACTTTCC GAATCGGTGG TATTCACCCC      60
CCCGAAAACA AGTTGTCGGC AGGCAAGCCC GTAGAGGTGT TGCCTATCCC CTCACAGGTA      120
GTCATCCCTC TTGGTCAGCA CATCGGTGCA CCGGCAACTG CCACGGTCAA GAAAGGGGAT      180
GAAGTTAAGG TCGGGACTAT CATTGCTCAG GCCGGAGGAT TCGTATCAGC TAATATCCAC      240
TCATCTGTGT CGGGTAAGGT GCTGAAGATC GATAACGTAT ACGACTCAAG CGGCTATCCC      300
AAGCCCGCAG TCTTCATTAG CGTAGAAGGT GACGAATGGG AAGAGGGCAT CGATCGCTCA      360
CCAGCCATCG TCAAAGAATG CAATCTGGAT GCAAAAGAAA TCGTAGCCAA AATTCTGCA      420
GCCGGTATTG TGGGTCTTGG CGGTGCTACC TTCCTTACCC ATGTGAAGCT GTCCCTCCT      480
CCGGGCAACA AAGCTGAGAT CCTGATCATC AACGCCGTAG AGTGCGAGCC TTATCTGACG      540
AGCGACCATG TCCTTATGCT GGAGCACGGC GAAGAGATCA TGATCGGCGT GAGTATCCTG      600
ATGAAAGCCA TTCAGTAAA CAAGGCCGTC ATCGGAGTTG AGAATAATAA GAAAGATGCT      660
ATTGCTCACC TCACAAACT GGCCACTGCA TATCCGGGCA TAGAGGTAAT GCCGTGTAAG      720
GTGCAATATC CTCAAGGCGG TGAGAAGCAG CTGATCGATG CAGTGATCCG CAAGCAGGTA      780
AAAAGCGGTG CCTTGCCTAT CAGCACAGGT GCCGTAGTAC AAAACGTGGG TACGGTATTC      840
GCCGTGTACG AAGCAGTACA GAAGAACAAG CCTCTGGTCG AGCGCATCGT GACGGTTACA      900
GGAAAAAAAC TGTCTCGTCC GTCTAACCTC CTCGTTGCGT TAGGTAATCC TATTGCGGCT      960
TTGATCGAAG CAGCAGGTGG CTTGCCGGAG AATACGGGCA AGATCATCGG CGGAGGTCCG     1020
ATGATGGGAC GCCTCTGCT GTCAACCGAT GTGCTGTGA CCAAAGGCAG CTCGGAGTA     1080
TTGATTCTCG ATAGAGAAGA GGCAGTTCGC AAGCCTATGC GCGACTGTAT CCGATGCGCC     1140
AAGTGCGTCG GAGTGTGTCC GATGGGACTC AATCCGGCTT TCCTTATGCG CGACACCTTA     1200
TATAAGAGCT GGGAAACAGC GGAAAAAGGC AACGTGGTTG ACTGTATCGA ATGCGGTTCTG     1260
TGAGCTTCA CCTGTCCGGC CAACCGTCCT CTGCTGGATT ATATCCGCCA AGCCAAGAAG     1320
ACTGTGATGG GTATCCAAAG AGCACGTAAG CAA                                     1353
```

(2) INFORMATION FOR SEQ ID NO:27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

```
ATGAACTCTC AAAAGAAAGA GGCTTTTAAT ATGAAAAGAA TACAACTAAC TCTTATCGCT      60
CTCTTCGCCG CTGTTGCCGG TTTGGTCGCT CAAAATGCTT ACGAGGGAGT AATTTTCATAT      120
AAAATTTTGT TGGACAAAAC CGGAAACAAG GTTGTAAGTA ATGGTGCGGC AGATATGAGT      180
AATTTAAAGC TCAAGAGCAC TCAGATGATC ATTGTTACGC CTATTCTTCG TTCAGAAGAT      240
GGTACCAGCC GGGTGAATT TCCTTCGGTA GTCATTACAG GCCGCAATAG AACAAAAGCT      300
```

CTCAAGCGTG	AAATCGCATT	TAGTTCGGCT	TTGCCCAAG	CAAAACATGC	AGCTCAATAC	360
ATTCGCCGTC	ATAATGGGAA	GAGCGAGCAG	TTTGCTTTTA	CAGGAGAACA	TGCTTATGCA	420
TCATGGATGA	TGGATGCCAA	GTTTGTGGTT	CGTGAGGAGG	TACGAGGTTG	TGCTAAATGC	480
CCTGTAGGTC	TCTCGAGTAA	TATTGTTCCT	TTTGATCCAC	TCTTCAATCC	GGCAGAGGCT	540
CCTTATTTGT	TGGCACACAT	TACTCCGGCA	GAAGAAGTGG	AAAAACAGCG	AGAGTCCAGC	600
TTTCGATGCTT	ATATCAACTT	CAAAGTCAAT	AAGGCAGATG	TCCTTCCTGA	GTATCGCAAC	660
AATAAGGCGG	AGTTAGAGAA	AATCAAAGAA	TTTGTAAGCA	CCGTAAAGGC	TAATCCAAAC	720
TATTCGGTCA	ATAAAATGAT	CATCGAAGGG	TTTGCTTCTC	CCGAGGCTTC	AATAGCCAC	780
AATAAGGCTT	TGTCGGAGCG	CCGTGCTAAA	AGACTCGCGG	AAGAATTGGT	GCGTAAGTAT	840
GGCAAAACAT	TGCCGAATAT	AACCACTGAA	TTCCGGCGTG	AAGATTGGAA	GGGGCTGAAA	900
CTGGCTATCG	AAAAGAGTGA	TATAGCCGAT	CGTGACCGCG	TATTGGAGAT	AATCAACTCC	960
GATAAATATG	CCGATGATGA	TGCACGTGAA	CAGGCTCTGA	AGCAACTTTC	GTCTTATCGT	1020
TATATCTTGG	ATCAGATCTA	TCCGAATTGG	CGTCGCAATA	CGATAACCAT	GGGGTATATC	1080
GTTTCGTGATT	ATACCCTCGA	AGAAGCTCGT	GAAATCATTA	AGACTGCTCC	GAAAGAACTT	1140
AGTGAGGCGG	AAATGTACCG	TGTGGCAATG	TCTTATCCTG	AGGGGCACCA	AGAGCGTTTG	1200
TTTGCTCTGA	ATACGACCTT	TAAGTATTTT	CCTGAAAGTG	TAACGGGCGG	AATCAATTTG	1260
GCTGTAGCCG	CTTTTAATGG	TGGAGACGTT	CAACAGGCAA	TTGCTCTGTT	GAGTCCGATT	1320
CAGACAGAAA	AGGGTGTAA	CAATATCCTT	GGAGCTGCTT	ATGCTCGTAC	GGGAGATTTT	1380
GCTCGTGCCG	AAACCTTCTT	CCGTAAGGCC	GTTGCAGAA	GAGATGCAAA	TGCGCAGCGC	1440
AACCTCGATA	TGCTGCTTGG	CAAAAAG				1467

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

GACATGGCAG	AAAAAAGAGA	CTATTACGAA	GTCTCGGTG	TATCGAAGAA	TGCCACCGAC	60
GATGAAGTGA	AAAAAGCATA	TGCAAGAAG	GCTATCCAAT	ACCATCCTGA	TAAGAACCCC	120
GGTGACAAGG	AGGCCGAAGA	GCACTTCAAA	GAGGTAGCTG	AAGCCTACGA	CGTATTGAGC	180
GATCCGCAGA	AGCGCAGTCA	ATATGACCAG	TTCCGGCCATG	CCGGATTGGG	CGGAGCTGCC	240
GGTGGAGGTT	TCAGCGGAGG	CGGTATGTCC	ATGGAGGATA	TTTTCAGTCG	CTTCGGTGAT	300
CTATTTCGTT	GGTTCGGCGG	TTTCGGCGGA	TTCTCCGATA	TGGGCGGTGG	CAGTCGCAGA	360
CGTGTTTCGA	GAGGGTCTGT	GCTGCGAGTA	CGAGTGAAGC	TTTCTTTTGGC	CGATATAAGT	420
AAAGGTGTGG	AGAAGAAAGT	GAAGGTAAAA	AAGCAGGTAG	TGTGCAGCAA	ATGTCGTGGC	480
GATGGCACGG	AAGAAGCCAA	TGGCAAGACT	ACCTGCCAGA	CCTGCCATGG	AACCGGCGTG	540
GTTACACGTG	TGAGCAACAC	TTTCCTTGGG	GCCATGCAGA	CCCAGAGCAC	TTGTCCCACT	600
TGCCACGGAG	AGGGTGAGAT	CATCAGGAAG	CCATGCTCCA	AGTGTAAGGG	CGAAGGTGTG	660
GAGATCGGCG	AAGAGGTGAT	CTCATTTCCAC	ATCCCTGCCG	GTGTAGCCGA	AGGAATGCAA	720
ATGTCCGTGA	ACGGCAAGGG	AAATGCCCGG	CCCCGAGGAG	GCGTGAATGG	CGACTTGATA	780
GTCTGTATCG	CCGAGGAACC	GGATCCGAAT	CTGATCCGCA	ATGGCAACGA	TCTGATATAC	840
AATCTGCTTA	TATCCGTTCC	GTTGGCTATA	AAAGGAGGTA	GTGTGGAAGT	GCCGACGATA	900
GACGGACGAG	CCAAGATCCG	CATCGAGGCG	GGGACACAAC	CCGGCAAGAT	GCTGCGTTTG	960
CGCAATAAGG	GGTTGCCCGG	CGTAAACGGC	TATGGCATGG	GAGACCAACT	GGTGAATGTC	1020
AATGTCTATA	TCCCGGAATC	GATCGATGCC	AAAGATGAGC	AGGCTATCGC	AGCGATGGAA	1080
AACTCGGACA	GCTTCAAACC	TACCGATGCT	GCTCGTAAGG	ATATAGACAA	GAAATACAGA	1140
GAGATGCTGG	AT					1152

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...927
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

CGATTCGATT	CAACAACATA	TGTCTCACAA	ATTAATTTAA	GAACAGAGAT	GAAAAAAGT	60
ATTTTAGCGA	CTTTGGGACT	TATGGCCATT	GCCATGCTCT	CATGTTCAAG	CAACAACAAG	120
GATTTGGAGA	ACAAAGGGGA	GGCTACTCTT	TTGGTAACGT	TTGGTAGCTC	CTATAAAGCT	180
CCACGCGAAA	CCTATGCGAA	GATTGAGAAG	ACTTTTGCCG	CAGCTTATCC	CGATCAAAGG	240
ATAAGCTGGA	CATACACGTC	TTCTATTATC	CGAAAGAAAC	TGGCTCAGCA	GGGTATTTAT	300
ATCGATGCTC	CGGATGAGGC	TTTGGAGAAA	TTGGCTCGTC	TGGGTATATA	GAAGATCAAT	360
GTACAGAGTC	TTTATGTGAT	TCCCGGCCGA	GAATATGATG	AGATGATCGA	CTTTGTCAAT	420
AAGTTTAAGG	CAGCACATAG	TGATATTACT	GTGAAGGTAG	GGGCTCCGCT	TTTCGATACC	480
GATGAAGATA	TGCGCGAGGT	GGCAGAGATC	TTGCACAAGC	GTTTTCAGCA	AACGATAGAG	540
AAAGGTGAAG	CTATTGTATT	CATGGGACAC	GGCACCAGAG	ATGCTGCCAA	TGACAGGTAT	600
GCCCGTATCA	ATAAGATCAT	GAAGAAGTAT	AGCAAGTTCA	TGATCGTCGG	AACCGTCGAG	660
TCCGATCCCT	CTATCAATGA	TGTATTGACC	GAAGTGAAG	AAACCGGTGC	CACGCCCGTA	720
ACAATGATGC	CGCTGATGAG	TGTGGCAGGC	GACCATGCTA	CGAATGATAT	GGCCGGAGAT	780
GAGGACGATA	GCTGGAAGAC	GTTGCTGACC	AATGCCGGCT	ACACAGTTTC	TATAGACAAG	840
CTGGACAATG	GCAATTTCTC	AGCTCTTGGA	GATATAGAAG	AGATCCGGAA	TATCTGGCTC	900
AAGCATATGA	AAGCCACCTC	TGTCGCGC				927

(2) INFORMATION FOR SEQ ID NO:30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1473
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

CGGAGAGATG	CGCGGAGGCA	ACTGGTACGC	CGTAGGAGGA	AAGAGCTATC	TGGCACAGCA	60
AATACGCGAT	GCCGGAGGAG	AGTATTTCTT	GAAAGACGAT	CAGCGATCCG	GTGGTGTTC	120
CCTCGACTTC	GAGACGGTCT	ACAGCCGATC	CGATTCGGCT	CGCTACTGGC	GAATCCTCAA	180
CAGCTATCCC	GGGGAGTTTC	GTTACGAAGC	TTTGAAAGCC	GAAGACAGCC	GATATGCCGA	240
TTTCAGGGCA	TTCAAGGAAA	AAGGCGTGAT	ATACTGCAAC	CTGAGGGAAA	CAGCCTTCTA	300
CGAACTCATG	CCCATGCATC	CCGATTGGGT	GCTGGCCGAT	CTTATCGCTA	TCTTGCACCC	360
CGGACTACTT	CCCGACCACC	AACCGCATTT	CTATTATTTC	CTCCAATGAC	ATCCGTACGC	420
CACTTACGTA	CAATTTCTGT	CGCAGGTATC	CTGGCTGCGC	TGGGAGGGGC	TGTAATCATT	480
CTCTTCGGGG	TTAATCTCTT	CCTCGGCTCG	GTGGCTATTC	CGATGAGCGA	GATCTTCCGA	540
CATCTTTTTT	CAGATCGTCC	CGAAGGAGGA	GAAGCACTCG	TGCACTACAA	TATCCTATGG	600
AAATCCCGCC	TGCCCAGAGC	CCTCACGGCT	GCTTTTGCCG	GCGCAGGTTT	ATCCGTTAGT	660
GGCTTGACAG	TGCAGACCGT	CTTTTCGAAT	CCTTTGGCCG	GTCCGTCCGT	TCTCGGCATC	720
AGCTCCGGTG	CCGATTTTGG	TGTTGCTTTG	GTGCTTCTGC	TGAGCGGCTC	GCTGGGAGGA	780
GTGGCATTGA	GTAGCCTGGG	TTATATGGGC	GAGGTGGCCA	TGAATATAGC	CGCTGCCGTA	840
GGCTCGCTGG	CAGTAATGGG	GCTGATCGTT	TTGTTCAGCA	CCAAGGTGCG	CAGCCACGTT	900
ACGCTGCTCA	TTATCGGCGT	TATGATCGGA	TATGTAGCCA	CTGCCGTCAT	CGGGGTATTC	960
AAGTTTTTTT	GTATCGAAGA	AGATATTCCG	GCATACGTAA	TTTGGGGGTT	GGGACAGTTT	1020
TCCCGTGCCA	CGGATTCGCA	ACTGAGTTTC	TTTGCCATTC	TGATGTTGAT	CTTTATTCCG	1080
GCCGGTATGC	TCCTTGTCAA	GCAGTTGAAT	CTCTTATTGC	TGGGAGAAAG	CTACGCACGT	1140
AATCTGGGAC	TGAATACTCG	TGGGGCACGG	CTGCTCGTGA	TCTCTTCCGC	CGGTTTGCTC	1200
ATCGCTACCG	TCACGGCCTA	TGCGGTCC	ATCGGCTTTT	TGGGGATGGC	TGTGCCACAC	1260
TTGGCACGGG	TTATCTTTCA	CACATCGGAT	CATCGGATCC	TGATGCCTGC	TACCTGTTTG	1320
ATTGGAAGTG	CTCTGGCTCT	TTTCTGCAAT	ATCATTGCTC	GTATGCCGGG	GTTTGAGGGG	1380

GCTTTGCCCC TCAATTCCGT AACGGCTTTG GTGGGAGCAC CTATTATCGT CACCGTTTTG 1440
 TTCGGCGCA GACGCTTCAA GGAAGAAACC GAC 1473

(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

CATTTTTTAG	TAACGATTAT	GCGGACAAAA	ACTATCTTTT	TTGCGATTAT	CTCTTTTATT	60
GCCTCTATGT	CGTCTTCTCT	GTCCGGCTCAG	AGCAAAGCCG	TTTAAACCGG	TAGTGTGTCTG	120
GATGCCGAAA	CCGGAGAGCC	TCTTGCCGGT	GCTCGAATCG	AAGTCAAACA	CACCAACATA	180
GTAGCCGGTG	CCGATGCCGG	CGGACATTTC	GAGATCAAGA	ACCTGCCGGC	AGGGCAGCAT	240
ACTATTATAT	GTTCGTTGGG	GGGGTATGGA	CAGAAAGAGG	AGGTGGTTGC	CATCGAAGCC	300
GGACAGACCA	AAACGATCTC	TTTTGCATTG	CGACTGCGAA	CGAACAACCT	GGAGGAAGTC	360
GTGCTTACCG	GTACCGGTAC	ACGTTACCGC	TTGGTCGATG	CTCCTGTGGC	AACGGAAGTC	420
GTTGCCGCTA	AGGACATAGC	CTCTTTCTCG	GCTCCTACTT	CCGAGGCCCT	ATTGCAGGGG	480
CTGAGTCCGT	CTTTTGACTT	CGGCCCCAAT	CTGATGGGCT	CTTTCATGCA	GCTGAACGGC	540
CTTAGCAGTA	AGTATATCCT	CATCCTTATC	GATGGTAAGC	GTGTGTACGG	CGATGTAGGC	600
GGTCAGGCCG	ATTTGAGTCG	TATTTCTCCT	GATCAGATCG	AACGGATCGA	ACTGGTGAAA	660
GGTGCTTCGA	GTTTCGCTCTA	CGGATCCGAT	GCCATCGCCG	GGGTAATCAA	TGTGATCACA	720
AAAAAGAATA	CGAATCGACT	GAGTGCATAT	ACGTCACATC	GCATATCGAA	GTACAACGAT	780
CGGCAAAACA	ATACTTCGCT	CGATATAAAC	ATCGGTAAGT	TCAGTAGCAA	TACCAACTAT	840
TTCTTCTACC	ATACGGATGG	CTGGCAGAAT	AGTCCGTTCG	AAATAAAAAA	GAAAAAAGGA	900
TCCGGCGAAC	CGGTCTTTGGA	GGAAACGTAT	AAGAAAACCT	TTCTGTGCACA	GGAAAATCAG	960
GGTGTAAGCC	AATCGCTTTC	CTATTATGCA	ACTAACAATC	TTAGCTTCAG	CGGAAATGTG	1020
CAGTACAATA	AACGTCAGAT	CTTCACTCCG	ACTTTTTCCG	AAAAGAAGGC	CTATGACATG	1080
GATTATCGTG	CTTTGACGGC	TTCACTCGGT	ACGAACATATC	TTTTCCCCAA	TGGTCTGCAT	1140
ACGCTTTCTT	TCGATGCCGT	CTACGATCGC	TTCCGTTTCG	GATATTTGTA	TCATGACAAG	1200
GACAGCAGTG	AGAGCCTGAT	CAACAACCAA	GGTCAGACCG	AGCAACCCAC	ATTCTTTCCG	1260
GGTCAGCTAC	GCAATAAAAA	CGATCAGATC	CGATACACGG	CAGAGGCTCG	CGGTGTATTT	1320
ACACTGCCTT	ATGCGCAGAA	ACTGACCGGC	GGTTTGGAGT	ATTTCCGTGA	GGAATTGATC	1380
TCTCCCTATA	ATTTGATTAC	CGACAAGGCA	GATGCTTCCA	CGCTCTCTCG	TTATGTACAA	1440
GATGAATGGA	AACCGCTCGA	TTGGTTCAAT	ATGACAGCCG	GTTTCCGTCT	GGTACACCAT	1500
CAGGAGTTTC	GTACACGAAT	GACGCCAAG	GTATCCATAC	TCGCCAAGTA	TGGGCCGCTG	1560
AACTTCCGCG	CTACGTATGC	TAACGGCTAT	AAGACTCCCA	CGCTGAAAGA	GCTTTTTGCA	1620
CGGAACGAAC	TCACCACTAT	GGGTTCGCAC	AATCTCTATC	TCGGCAATGC	GGATCTTAAG	1680
CCACAGATGT	CGGATTATTA	TGCTTTGGGC	TTGGAGTACA	ATCAAGGCCC	TATCTCGTTC	1740
AGTGCAACGG	TTTATGACAA	TGAACCTCGC	AATCTGATCT	CCTTTATGGA	TATACCGACC	1800
TCACCCGAGC	ACGAAGCTCA	GGAATCAAG	AAAACCAAGC	AGTATGCCAA	CATAGGAAAA	1860
GCTCGCAGCC	GCGGCCCTGA	TGTCCTATGT	GATGCCTCTA	TCGGTTGGGG	TATCAAGTTA	1920
GGAGCCGGAT	ACAGCCTCGT	GGAAGCTAAG	AATCTCCAGA	CGGATGAGTG	GCTGGAAGGA	1980
GCTGCACGTC	ATCGTGCCAA	TGTGCACGCC	GATTGGGTTC	ACTACTGGGG	TCAGTATAGA	2040
CTTGGCGTGA	GCCTTTTCGG	CCGTATTTCAG	AGCGAGCGTT	ACTACAAAGA	CGGCAATGCT	2100
CCGGACTATA	CCTTGTGGCG	ACTCGCCACA	TCGCATCGTT	TCGCTCATTT	CCGCCACATC	2160
ATCCTGGATG	GAACGCTCGG	TATAGACAAC	CTGTTTGACT	ACGTGGATGA	TCGTCCTATG	2220
GGTGTCAATT	ATGCTACCGT	AACGCCGGGA	CGTACTTTCT	TTGCTCAAAT	AGCGATTCTGA	2280
TTCAACAAC						2289

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

TGCTGCGCAA	GGCTTCGGGA	CACCTCTCCC	CGGAAGAAGT	CGTTTCGGAA	TGATACCGTT	60
TTTCCTTATT	TCGTTATTCA	TCTGATCAAA	CATATTATCA	TTATGACGGA	CAACAAACAA	120
CGTAATATCG	TATTCCCGGC	GTTTCTCCTC	TTGCTGGGAG	TCATCGCAGT	GGTGACGATC	180
GTTGGTTTTT	TCATGCTCAG	ACCGGCCGAG	GAGATTATCC	AAGGACAGAT	AGAAGTGACC	240
GAATACCGAG	TGTCCAGCAA	AGTGCCCGGG	CGCATCAAGG	AACTTAGGGT	ATCCGAGGGA	300
CAGCAGGTGC	AGGCCGGCGA	TACCCTCGCT	GTCATCGAAG	CCCCGACGT	AGCGGCTAAG	360
ATGGAGCAGG	CAAAGGCTGC	CGAAGCAGCT	GCACAGGCTC	AGAACGCCAA	GGCTCTCAAA	420
GGAGCACGCA	GCGAACAGAT	ACAGGCAGCC	TATGAGATGT	GGCAGAAAGC	TCAGGCCGGC	480
GTAGCCATAG	CGACCAAGAC	ACACCGCGC	GTGCAGAACC	TCTATGACCA	GGGAGTG GTA	540
CCGGCTCAGA	AGTTGGACGA	AGCCACTGCC	CAGCGCGATG	CGGCCATCGC	TACGCAAAAA	600
GCGGCCGAAG	CCCAGTACAA	TATGGCTCGC	AACGGTGCCG	AACGCGAAGA	CAAGCTGGCA	660
GCTTCTGCCC	TCGTGATAG	AGCGAGAGGA	GCCGTCGCCG	AGGTGGAGTC	GTACATCAAC	720
GAAACCTACC	TCATCGCCCC	ACGGGCAGGC	GAAGTGTCGG	AGATATTCCC	CAAAGCCGGC	780
GAATCGTAG	GTACCGGCGC	ACCTATCATG	AATATCGCCG	AGATGGGCGA	TATGTGGGCC	840
AGCTTTGCCG	TTCGTGAGGA	TTTCCTCAGC	AGCATGACCA	TGGGAGCCGT	TCTGGAGACT	900
GTGGTGCCGG	CTCTGAATGA	AGAAAAAGTA	CGCTTCAAGA	TCACATTTCAT	CAAGAACATG	960
GGTACCTATG	CTGCCCTGGA	AGCGACCAAG	ACAACAGGGC	AGTACGACCT	GAAGACCTTC	1020
GAGGTAAAGG	CCACCCTTGC	GGATAAAGAC	AAGGCACAAA	AGCTACGCCC	GGGTATGTCC	1080
GTGATCATAC	GCAAG					1095

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 960 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

CCGCAATCCT	CTCCTGATCG	AAGAAGCTTC	CAAAACGTCA	TGAATAAATA	TCATTCTCAA	60
AGCGTTTTAG	AGGTCGGCAA	AATTGGGATT	GTGATTATCT	TTGCGCCCAT	AGTACGGAAT	120
GTACATCAAC	AACCCCTTTT	TTTAAGCCAT	AAATCAATTA	TGCGTATTGT	CAGTAATTTT	180
TTGTTTCGTCT	CTTTTTCGGT	TTTGCTTTTT	GCATCATGCC	GTTCCCAGCG	AGAAAAGGTC	240
GTTTACCTGC	AAGGATATCCA	AACTTTAAAT	CGGGAGATTA	TCGCTAAACC	ATATGACGTA	300
AAAATTGAGA	AGGACGATGT	GCTGAACATC	CTTGTCAGCA	GTAGAGACCC	GGAGCTTTCA	360
ACGCCCTACA	ACCAAGTGTT	GACCACTCGT	GCACTGGCCC	GCAACGGCTA	TGGAACGAAC	420
TCGAACGAAG	GCTTCCTGGT	CGATTGAAA	GGGTACATCA	ATTATCCTAT	TTTAGGCCAG	480
ATCTATGTAG	AAGGCCTTAC	TCGTACCGAA	CTGGAGAAGG	AGATACAGAA	GAGGATTATT	540
TCCAGTGGAT	TTATCAAGGA	TCCTACGGTA	ACGGTGCAGC	TTCAAAATTT	CAAGGTGTCTG	600
GTTTTGGGAG	AGGTGAATCA	TCCGGGTTCG	ATGTCGGTAA	AAGGAGAGCG	AATAACTCTT	660
TTGGAAGCGA	TCGGAATGGC	CGGAGACCTG	ACAATCTATG	GTCGCCGCGA	TCGGGTTTTT	720
GTGATTAGAG	AAACCGATGG	GCATCGCGAG	GTTTTCCAGA	CGGATCTCAG	AAAGGCCGAC	780
TTGCTCGCAA	GCCCCGTGTA	CTATCTGCAT	CAGAACGACG	TCATCTATGT	GGAGCCGAAC	840
GACAAGAAAA	CACAGATGAG	CGAGATCAAC	CAGAATAATA	ACGTAAACGT	ATGGCTGAGT	900
GTTACCTCCA	CTTTGGTATC	CATTTCCACG	CTGACGATTA	CGATAATAGA	TAAGACCAAA	960

(2) INFORMATION FOR SEQ ID NO:34

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

TCAAAAATAG	TACTACGAAA	GTTTTGTACC	TTAGCGCGCA	TGAAAAAGAC	CAATCTGTTT	60
TTATCTCTGC	TGGTGATCTT	TATCACCGGT	AGTTTTATGA	CTGCCTGTGC	ACAGAAGTCC	120
AAGACGAACA	AACTCACCGA	AGAAGATCGG	AGCCGCAATG	AGTATGTACA	GTCGATGGAT	180
GTGCTTAGCA	ATATTATCGG	TAACGTCAGG	CTGTATTTTCG	TCGATACCAT	AAGTATCAAA	240
CATATGACTC	GGCGTGGTAT	AGATGCGATG	TTGGGCGGGC	TTGACCCCTA	TACCGAATAC	300
ATTCTTTACG	AGGAAATGGA	TGAAGTAAA	TTGATGACTA	CGGGAGAGTA	TGCCGGAGTC	360
GGAGCTATCA	TATCGCAGCG	CCCGGATAGT	GCTGTGATTA	TCCAGAGACC	TATGGAAGGT	420
ATGCCCCGAG	ACGAAGCAGG	ATTGATAGCA	GGCGACCGCA	TCCTGACTAT	CGATGGGAAA	480
GACTTCCGCA	AATCCACCAC	ACCGAAAAGTA	AGCCAAGCAC	TGAAAGGGAT	AGCCGGTACT	540
GTTGCAAAGG	TGACAGTAAT	GCGCTATGGC	GAAACCAAAC	CTCGTACTTT	TTCCGTGAAA	600
CGTCAAAAAG	TGATTATGAA	TTCCGTCACT	TACAGCGGAA	TGCTCGATGG	CTCGATAGGA	660
TATATCCGCT	TGAACAACCT	TACGGACAAA	AGTGCAGAAG	AGGTGCGCAC	GGCCTTGTGT	720
GACTTTCGTG	ACAAACAAGG	AGCGAAAAGGT	CTCATTTTGG	ATTTAAGAGG	CAATGGTGGC	780
GGACTGATGC	AGGCTGCTAT	CGAGATAGTC	AATCTGTTCG	TCCCTAAGGG	CAAAGAGGTG	840
GTAACGACCA	AAGGTCGCAT	TGCAGAGTCG	GCGTCCGTAT	TTCGCACATT	GACTIONAACC	900
ATCGACACGA	AACTCCCGAT	AGTAGTCCTG	ATCGATGGAC	AATCGGCATC	TTCTCCGGAG	960
ATTGTAGCCG	GAGCATTGCA	GGATATGGAC	AGGGCTGTAC	TGATGGGACA	AAAGAGCTAT	1020
GGCAAAGGGC	TTGTACAAAC	GACTCGTCAG	CTACCATACA	ACGGCGTGAT	CAAATTGACT	1080
ACGGCCCAAGT	ACTACATCCC	AAGCGGACGT	TGTATTACAG	GTTTGGACTA	CAGCCGCACC	1140
AATCGGACAG	GTATGGCAAC	GGCCATTCCCT	GACAGTCTGC	ACAAAATCTT	TTACTACTGCT	1200
GCCGGAAGAC	GTGTAGAAGA	TGCAGGAGGA	ATCCTGCCTG	ACATCGAGGT	CAAACAAGAT	1260
ACAGCTGCGA	CATTACTTTA	TTATATGGCC	ATCAATAATG	ACGTTTTTCGA	TTTCGTCACA	1320
GGTTATGTGC	TCAAGCATAA	AACGATTGCC	AAGCCGGAGG	ATTTTTCAT	AACGAACGAG	1380
GACTATGCAG	CTTCTGCA	GATGATGGAA	GAAAAGAAAT	TTGACTATGA	TCGCCAGAGT	1440
GGCAAGATGC	TTGACAAACT	TGAGGAACCTG	GCTAAGATAG	AAGGCTACCT	GCCGGAAGCC	1500
AACTCGGAGC	TTAAAGCACT	ACGCGAAAAG	CTAAAACCCA	ACCTGTGCGG	TGATCTGCTA	1560
CGATTCAAAA	AGGAGATAAC	AACTATCTC	AACAATGAGA	TTGTCACTCG	CTATTATTAT	1620
GAGCGAGGCA	GTATCCGCCA	GAGTTTGCCG	GAAGATAAGG	TAGTCAAAGA	AGCTATTAAAG	1680
CTGCTGAAGG	ACCATCCGGA	ACAAATTGCA	CAGATCCTTG	CAGCTCCGAA	AGCAGAGAAT	1740
AAAGGG						1746

(2) INFORMATION FOR SEQ ID NO:35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2955 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2955
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

GTAACAGACA	AAATGCAAAA	CAAAGGATTT	GTGATTGTTA	TCACATCGGC	TCTGGCCATC	60
ATCTGTGCGT	TTTACCTGTC	ATTCTCTTTC	GTTACGAACC	GTTACGAAAA	GAAGGCTAAG	120
GCGATGGGCG	ATGTTGCCGG	AATGGCCTAT	CTTGATTCCA	TGTCGAATGA	GAAGGTCTGG	180
TTCGGCTACA	CGCTGAAAGA	AGCTCAAGCC	CAGCAAATTG	GTCTTGGCCT	TGACTTAAAG	240
GGGGGTATGA	ACGTTATCTT	GAAACTTAAC	GCAAGCGATC	TGCTTCGTAA	CCTCTCTAAC	300
AAAAGTTTGG	ATCCCAACTT	CAACAAAGCT	CTGGAGAATG	CTGCCAAGAG	CACGGAGCAA	360
TCCGACTTCA	TCGATTATTT	CGTGAAGGAA	TATCGCAAGC	TCGATCCCAA	CGGTCGCTTG	420
GCCGTTATCT	TCGGTTCGGG	TGACCTTCGC	GACCAGATTA	CCGCAAAGTC	TACGGATGCA	480
GACGTAGTGC	GTCTGCTCAA	AGAAAAATAT	AATAGTGCTG	TAGAAGCTTC	GTTCAATGTG	540
CTCCGTGCTC	GTATCGATGC	TTTCGGTGTG	GTTGCACCTA	ATTTGCAGCG	ATTGGAAGGG	600
CAAGGGCGTA	TCCTTGTGCA	ACTCCCCGGA	GTGAAAGACC	CTGAGCGTGT	TCGTACCCTT	660
TTGCAACGCA	GTGCCAACCT	ACAGTTCTGG	CGTACATACA	AATTGCAAGA	GGTCAGCGGA	720
GACTTGATCG	CTGCCAATGA	TCGTCTGAGC	GAATTGGCTA	TGAACAACAC	GGATGCTACC	780
CCGGAAACAG	AGCCTGCAAC	TACTGACTCT	GTAGCTGCAA	CAGCCGATTG	TGCTGCTGTA	840
CAAGTGTGTA	TCGATTATTC	CGTGTAGCA	CAAAAAGAGG	CCAAGGATGC	TACTCGTAAA	900
GACGCACTCT	TCTCTCTGCT	TACTCCCGTG	AATCGTGGCG	GTGCAGTAGT	GGGTGTGGCT	960
CGTCGTGCTA	ATATGGCTCA	GATATCTGAA	ATGCTCCAGC	AAGCTCACGA	TCTGAAGGTT	1020
ACACGTGAAG	ATGTGCTTTT	CCTCTGGGGT	GCTAAAGCAA	TCGAAGACCC	CGAAACCAA	1080
AAGGAGACCG	ATGCTGATGC	ATTCGTACCA	ATCGTACGGG	AGATCCTGAT		1140
TTGGGAGGTG	ATGTAGTGAC	TTCCGCCAAG	AGTGATATCC	AAAATGACTT	CGGTCGTTCC	1200
GAACCGATCG	TTTCGATGAC	GATGAATGAA	GAAGGTGCTC	GTAATGGGC	GCGTATCACA	1260
AAGGATAACG	TGGGACGGGC	AATCGCTATC	GTTTTGGATG	GTGTGGTTTA	TTCTGCTCCG	1320
TCGAGTGAATG	ATCGAAACAC	CGGCGTGC	TCTCAGATCT	CCGGGCACTT	CACCGTGGAG	1380
GAGGCCGGTG	ACCTTGCCAA	CGTACTCAAC	TCCGGTAAAA	TGGATGCTAC	GGTAAGCATC	1440
GAACAGGAAA	ACGTGATTGG	TCCTACGCTG	GGTGCCGAGT	CCATTAAAGC	CGGATTCTTG	1500
TCGTTCTCTG	TCGCTTTGGT	TATCCTGATG	TGTTACATGT	GTCTGGCTTA	CGGTTTCTTG	1560
CCGGGTCTTA	TCGCAAAACG	CGGATTGATT	GTAACACAGT	TCTTCACATT	GGGCGTATTG	1620
GCTTCTTTCC	ATGCCGTGCT	GACCCCTCTG	GGTATCGCAG	GTTTGGTGCT	GACGCTGGGT	1680
ATGGCTGTGG	ATGCCAACGT	ACTTATCTTC	GAGCGTATCA	AAGAAGAGCT	TCGTGCCGGT	1740
AAGACTCCGA	TTCGTGCCGT	TACGGATGGT	TATGGCAACG	CTTCTCTGCT	CATCTTCGAC	1800
TCGAACGTTA	CGACTATTAT	TACCGGTATC	ATCCTATTCC	TCTACGGGAC	GGGCCCATTG	1860
CGCGGTTTTG	CCACTACGTT	GATTATCGGT	CTTATCGCTT	CTTTCATTAC	GGCTGTCTTC	1920
TTGACTCGTA	TCGTCTTCGA	GAAACTGGCG	AAAAAAGGTC	GTTTGATAAA	GATTACATTC	1980
ACTACGAGCA	TTACTCGCAA	TCTCCTTGTC	AATCCCTCAT	ACAACATCTT	GGGTAAGCGC	2040
AAGACC GGCT	TTATCATTTT	GGTGATTATC	ATCGTTTTGG	GACTTATAGC	TTTCAATTTA	2100
ATCGGTCTCA	ATAGGGGTAT	TGAATTCTCC	GGAGGACGTA	ACTACGTAGT	TAAATTCGAC	2160
CAGCCTGTAT	CTTCCGAAGC	CGTTCGTTTG	GCCTTGCTTT	CTCCCTGCA	GGAAAAGGTA	2220
TTGGTTACCT	CCATCGGTAC	TGAAGGGACA	GAGGTGCGTA	TATCTACGAA	CTATAAGATC	2280
CAGGAGGAAA	TCGAGAGAAA	TGAAGCAGAG	ATTACTGACA	AATTGTATCA	GAGCCTGAAA	2340
GGTTTCTACA	CCCAGCAGCC	TACTGCTGAT	CAGTTCTTGG	ACAATATCAT	TAGCTCTCAG	2400
AAAGTAAGTC	CCAGTATGTC	GAGTGACATC	ACGAGAGGTG	CTATTGGGCG	TGTGCTGTTA	2460
TCGATGATCT	TCATGGCCAT	TTATATTCTG	ATTCGCTTCC	GTGACATTTC	TTTCTCTGCC	2520
GGGGTATTCT	TATCTGTGGC	CGTACTACA	TTCTGCATTA	TTGCTCTGTA	TGCGTTGCTG	2580
TGGAAGATTTC	TGCCCTTCAC	CATGGAGATC	GATCAGAACT	TCATCGCTGC	TATTCTGGCT	2640
ATCATCGGTT	ACTCGCTCAA	TGACACCGTG	GTTGTATTTG	ACCGTATCCG	AGAGACGATG	2700
AAATTGTACC	CCAACAGAGA	TCGCTATCAG	GTGATCAACG	ATGCCCTTAA	TTCAACATTG	2760
GGTCGAACAT	TAAATACGTC	TTTGACTACG	TTTATCGTTA	TGTTGGTAAT	CTTCATCTTT	2820
GGAGGTGCTA	CGATGCGTAG	TTTCACGTTT	TCGATCCTGC	TCGGTATCGT	TATCGGTACA	2880
TACTCTACGC	TCTTTGTTGC	TACACCCCTT	GCCTACGAGA	TCCAAAAGCG	CAAGCTCAAC	2940
AAAGCAGCTA	AGAAA					2955

(2) INFORMATION FOR SEQ ID NO:36

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GACTTCCCTT	GGGTTAGGGT	AAAACCGGAG	AAGAAAAGAA	AACAACATAA	CAGTAATAAT	60
TTTAAGTTTA	ACGCAAAAGA	AAAGTCTATG	AAAAGAATGA	CGCTATTCTT	CCTTTGCTTG	120

CTGACGAGCA	TTGGGTGGGC	TATGGCCCAG	AATAGAACCG	TGAAGGGTAC	AGTTATCTCC	180
TCCGAGGATA	ATGAGCCCTT	GATCGGCGCG	AATGTCGTGG	TTGTCGGAAA	CACCACTATC	240
GGTGCTGCAA	CCGACTTGGG	TGGCAACTTC	ACGCTTAGCG	TGCCTGCCAA	TGCCAAAATG	300
TTGAGAGTGT	CCTATTCCGG	TATGACTACC	AAAGAGGTCG	CCATCGCTAA	TGTGATGAAG	360
ATCGTACTGG	ATCCGGACTC	TAAGGTTCTG	GAGCAGGTAG	TTGTATTGGG	TTACGGGTACG	420
GGACAGAAAC	TCAGCACTGT	TTCGGTTCTT	GTGGCCAAAG	TGTCCAGCGA	AAAGCTCGCG	480
GAAGAGCCCG	TTGCCAATAT	CATGGATGCC	CTCCAAGGTC	AGGTAGCCGG	TATGCAGGTT	540
ATGACTACAT	CCGGTGACCC	TACTGCCGTC	GCTTCTGTGG	AGATCCATGG	TACAGGGTCG	600
TTGGGGGCAA	GCTCTGCACC	ATTGTATATC	GTGGATGGTA	TGCAAACTTC	TTTGGATGTT	660
GTGGCTACGA	TGAATCCGAA	TGATTTTGAA	TCTATGTCCG	TTTTGAAAGA	TGCTTCTGCA	720
ACATCTATTT	ATGGAGCTCG	TGCTGCAAAC	GGAGTCGTTT	TCATTCAAAC	GAAGAAAGGT	780
AAAATGAGCG	AGAGAGGTCG	TATTACCTTT	AATGCCAGTT	ACGGGATTTC	TCAAATCCTG	840
AAATACTAAGC	CCCTTGATAA	TATGATGACT	GGAGATGAAT	TGCTGGATT	TCAGGTGAAG	900
GCAGGTTTTT	GGGGGAACAA	TCAAACCGTT	CAGAAGGTTA	AAGATATGAT	CCTTGCCGGA	960
GCTGAAGATT	TTGATGGCAA	ATCATATTCT	TTGAAAGATG	AGTATGGTAA	GACATTGTTC	1020
CCAGTGGATT	TTAATCATGA	TGCAGACTGG	CTCAAGGCTT	TGTTTAAAC	AGCACCCACC	1080
AGTCAAGGTG	ATATTTCTTT	CTCCGAGGGG	TCTCAGGGAA	CTTCATATTA	TGCTCTATA	1140
GGCTACTTCG	ATCAGGAAGG	TATGGCTCGT	GAACCGGCAA	ATTTTAAGCG	CTATAGTGGC	1200
CGCTCAACT	TCGTAAGTAA	TGGCTGAAAG	TTGGTGCAA	TTTGTCTGGT		1260
GCGATAGCGA	ATAGACGATC	TGCCGACTAT	TTTGGAAAGT	ATTATATGGG	GTCAGGTACT	1320
TTCGGTGTGT	TAACGATGCC	TCGTTATTAT	AACCTTTTGG	ATGTGAATGG	GGATTTAGCA	1380
GATGTCTATT	ACATGTATGG	AGCTACCAGA	CCTTCTATGA	CAGAACCCTA	CTTCGCAAAA	1440
GATGACCGT	TCAGTTCGGA	ATCACATCAG	GCCAATGTAA	ATGGTTTCGC	CCAGATTACT	1500
CCGATCAAAG	GCCTTACTTT	AAAGGCACAG	GCTGGTGTGG	ATATTACTAA	TACTCGCACT	1560
TCTTCTAAGA	GAATGCCCAA	TAATCCGTAT	GATTCCTACTC	CTCTTGGGGA	AAGAAGAGAA	1620
AGAGCTTATC	GAGATGTTAG	CAAGTCTTTT	ACAAATACGG	CTGAATATAA	GTTTTCAATT	1680
TATGAAAAAC	CTAGTCTTAC	AGCATTTGATG	GGGCATGAAT	ATATTGAATA	TGAAGGGGAT	1740
GTTATTGGGG	CATCTTCTAA	AGGATTTGAA	AGTGATAAGT	TGATGTTACT	GAGCCAGGGA	1800
AAAACCGGAA	ATAGTTTGTC	TTTGCCTGAA	CACAGAGTCG	CTGAATATGC	CTATTTGTCT	1860
TTCTTTAGTC	GTTTTAATTA	CGGTTTTGAC	AAATGGATGT	ATATAGATTT	CTCTGTTCTG	1920
AATGACCAAT	CTCTCGATT	CGGATCCAAT	AATAGAAGCG	CGTGGTTCTA	TTCTGTCTGGT	1980
GGAATGTTTG	ACATATATAA	TAAATTCAAT	CAAGAAAGTA	ATTGGCTCAG	TGATCTTCGA	2040
CTGAAAAATGA	GTTATGGTAC	AACGGGTAAC	TCGGAGATTG	GTAATTACAA	CCACCAAGCA	2100
CTCGTTACTG	TGAACAATTA	TACTGAAGAT	GCTATGGGGC	TTAGCATTTT	TACAGCAGGC	2160
AATCCCGACC	TCTCGTGGGA	AAAGCAGTCT	CAGTTCAACT	TCGGTTTGGC	TGCAGGGGCT	2220
TTCAATAATC	GCTTATCTGC	AGAGGTAGAT	TTCTATGTCC	GCACTACGAA	TGATATGTTG	2280
ATTGATGTCC	CGATGCCTTA	TATCAGTGGT	TTCTTCTCAC	AGTATCAGAA	TGTAGGCTCT	2340
ATGAAAAATA	CGGGTGTAGA	CCTTTCTCTT	AAGGGGACGA	TCTACCAAAA	TAAGGACTGG	2400
AATGTATATG	CTTCTGCGAA	TTTCAACTAC	AATAGACAGG	AAATAACAAA	GCTTTTCTTC	2460
GGTCTCAATA	AGTACATGTT	GCCTAATACC	GGTACTATAT	GGGAAATTGG	GTACCCCAAT	2520
TCGTTCTATA	TGGCTGAATA	TGCTGGAATC	GACAAAAAAA	CCGGTAAGCA	GTGTGGGTAT	2580
GTTCTTGGTG	AAGTCGATGC	GGATGGTAAT	AAAGTTACAA	CAAGCCAGTA	CTCAGCTGAC	2640
TTGGAGACAC	GAATTGATAA	GCTCTTACT	CCTCCTATTA	CAGGTGGTTT	CTCCTTAGGT	2700
GCTTCTTGGA	AAGGACTTTC	TTTAGATGCT	GATTTTGCCT	ACATCGTTGG	TAAATGGATG	2760
ATCAATAATG	ACCGTTACTT	TACAGAGAAT	GCAGGTGGAT	TGATGCAATT	AAATAAAGAT	2820
AAAATGCTAT	TGAATGCCTG	GACAGAGGAT	AATAAAGAAA	CAGATGTTCC	AAAATTGGGA	2880
CAGTCTCCTC	AGTTTGATAC	GCATTTGTTG	GAGAATGCTT	CTTCTCTGCG	TTTGAAGAAT	2940
CTCAAACTCA	CCTATGTACT	CCCCAATAGT	CTTTTGTCTG	GGCAGAATGT	GATTGGTGGA	3000
GCTCGTGTCT	ATTTGATGGC	GCGCAATCTG	TTAACTGTTA	CGAAGTATAA	AGGCTTTGAC	3060
CCTGAAGCAG	GGGGGAATGT	GGGAAAAAAT	CAATATCCTA	ATTCTAAGCA	GTACGTTGCG	3120
GGTATTCAGT	TGTCTTTT					3138

(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

TGGCATAGGA ATATTTTAT CTTTGGCAGT ACATTAGACC CGAAAAATAT GCTCCCACTG

CCATACCGTT	ATGCAAAAAC	CGAGCACCTT	TTTCTCGCAA	AAGGATACTG	CAAGAATCCA	120
ATAACAAACA	TAATTATCCT	ATTTATGAAG	AAAAAGAATT	TTTTGCTTCT	TGGCATT TTC	180
GTTGCTTTGC	TGACTTTTCAT	CGGCAGCATG	CAGGCACAAC	AGGCCAAAGA	TTATTTCAAC	240
TTTGACGAAC	GGGGCGAGGC	CTACTTCTCA	TTCAAAGTGC	CTGATAGGGC	CGTTCTACAA	300
GAGCTGGCTC	TGATCATGTC	CATCGACGAG	TTTGACCCCG	TAACCAATGA	AGCCATTGCC	360
TATGCCAGCG	AAGAGGAGTT	CGAGGCATTG	CTGCGCTATG	GGCTCAAGCC	TACATTCTTG	420
ACTCCTCCAT	CCATGCAGCG	CGCTGTCGAG	ATGTTGCTGAG	ACCGCTCAGG	AGAAAAATAC	480
GAATGGAATG	CTTACCCAC	CTATGAAGCC	TATATCAGCA	TGATGGAAGA	GTTCCAAACA	540
AAGTATCCAT	CACTTTGTAC	TACTTCCGTC	ATTGGCAAAT	CCGTAAAGGA	TCGTAAACTG	600
ATGATTTGCA	AGCTGACGTC	CTCTGCCAAT	ACAGGGAAAA	AGCCTCGCGT	GCTCTATACT	660
TCTACGATGC	ACGGAGACGA	AACGACCGGA	TATGTGGTAC	TGCTCCGACT	CATAGACCAT	720
CTGCTGTGCA	ACTACGAATC	CGATCCGAGG	ATTAAGAACAA	TTCTGGATAA	AACGGAAGTA	780
TGGATCTGCC	CTTTGACCAA	TCCGGACGGA	GCATACAGAG	CCGGAACCA	CACCGTACAA	840
GGAGCTACTC	GCTACAATGC	AAACAATGTC	GATTTTGAACC	GTAACCTCAA	GGATGATGTA	900
GCCGGTGATC	CCCCGAGTGC	AAACCTTGG	CAGCCGGAGG	CAACTGCATT	CATGGATT TG	960
GAAGGAAACA	CCTCTTTCGT	GCTCGGTGCC	AATATACATG	GAGGAACAGA	GGTGGTGAAC	1020
TATCCATGGG	ATAATAAAAA	AGAAAGACAT	GCAGACGATG	AGTGTACAA	ACTGATCAGT	1080
CGCAACTACG	CAGCCGCTTG	TCAGAGTATT	TCCGCCAGCT	ACATGACCTC	CGAAACCAAT	1140
TCCGGAATCA	TCAAGAGTTC	AACATGCTAT	GTAATTCGCG	GAAGTCGTCA	GGACAATGCA	1200
AATTATTTCC	ATCGTCTGCG	AGAAATTACC	CTTGAAATCA	GCAACACGAA	GTTGGTGCCG	1260
GCCTCTCAAC	TTCCAAAGTA	TTGGAATCTG	AACAAAGAAT	CTCTGCTTGC	TCTGATCGAA	1320
GAATCCTTAT	ACGGCATCCA	TGGTACAGTG	ACTTCCGCTG	CGAACGGACA	GCCTCTCAAA	1380
TGCCAGATCT	TGATAGAAAA	CCATGACAAG	CGCAACTCCG	ATGTTTACTC	CGATGCTACC	1440
ACAGGCTACT	ACGTACGTCC	TATCAAAGCC	GGCACTTATA	CGGTGAAATA	CAAAGCCGAG	1500
GGTTATCCTG	AGGCAACTCG	TACCATTACG	ATCAAGGACA	AAGAAACCGT	CATCATGGAC	1560
ATTGCATTGG	GCAACTCGGT	TCCTCTGCCT	GTACCCGATT	TCACAGCTTC	TCCTATGACC	1620
ATCTCAGTAG	GCGAAAGCGT	CCAATTCCAA	GATCAAAACGA	CAAATAACCC	CACGAATTGG	1680
GAGTGGACGT	TCGAAGGCGG	ACAGCCTGCC	ATGAGTACAG	AGCAGAATCC	GCTCGTATCC	1740
TATAGTCATC	CCGGTCAGTA	CGACGTTACG	CTCAAAGTGT	GGAATGCAAG	TGGTTCCAAC	1800
ACGATTACGA	AAGAAAAATT	CATCACTGTC	AATGCCGTTA	TGCCTGTAGC	TGAATTCGTC	1860
GGTACCCCGA	CGGAAATAGA	AGAGGGCCAG	ACGGTATCTT	TCCAAAACCA	ATCCACCAAT	1920
GCCACCAACT	ACGTATGGAT	ATTCGATGGC	GGCACTCCCG	CTACCACTGA	AGACGAAAAC	1980
CCGACTGTGC	TTTACAGCAA	AGCCGGCCAA	TACGATGTCA	CGCTCAAGGC	GATCAGTGCT	2040
TCCGGTGAAA	CGGTGAAGAC	GAAAGAAAAA	TACATCACTG	TCAAGAAAGC	TCCGGTCCCT	2100
GCTCCGGTAG	CCGACTTCGA	AGGAACACCT	CGAAAAGTAA	AGAAAGGCGA	GACAGTTACT	2160
TTCAAAGACT	TGCTACGAA	CAATCCGACT	TCATGGCTTT	GGGTGTTCTGA	AGGCGGCTCT	2220
CCTGCCACCA	GCACGGAGCA	AAACCCGGTG	GTCACTTACA	ATGAAACAGG	CAAGTACGAT	2280
GTCCAGCTGA	CTGCCACCAA	CGAGGGCCGA	AGCAATGTGA	AGAAAGCAGA	AGACTACATT	2340
GAGGTTATCC	TCGATGACAG	TGTCGAGGAC	ATAGTGGCAC	AGACGGGTAT	CGTCATTCTG	2400
CCGCAAAACG	GAACGAAGCA	GATCTCATA	GAAGCCAACG	CTGCTATCAA	AGCGATCGTT	2460
CTCTATGACA	TCAATGGACG	GGTCGTACTC	AAAATACTC	CGAATCAGCT	CCGCTCGACC	2520
GTAGATCTTT	CCATCCTGCC	CGAAGGAATC	TACACCATCA	ATATCAAAAC	GGAAAAATCC	2580
GCTCGCACGG	AAAAGATCCA	TATCGGG				2607

(2) INFORMATION FOR SEQ ID NO:38

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...318
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CTTTCGTACA	GTGGAGAGAG	CGATGCAAAA	GAGTCTGATC	AGAATTGCCG	GAAATGTACC	60
TTCATCGGCT	TTGAAAACG	AGTAAATACG	ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	120
CTCTTACTGC	TCCCCATTTT	CTTCTACAAG	CGGTTTATAT	CGCCGCTTAC	ACCGCCTTCA	180
TGCCGGTTTA	CCCCCTCATG	TTCGTCTTAT	GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	240
GGCAAAAGGAC	TATTGCTGAG	CATCAAGCGT	ATTCTCCGCT	GTCACCCGTG	GGGTGGAAGT	300
GGCTATGACC	CCGTTCCG					318

(2) INFORMATION FOR SEQ ID NO:39

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2583
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

```

TTAGAGATGG CATACGACTT TACACAAACA TTCCGCAACA GCCTGGAGTA CAGCTATCAG      60
GAAGCAACCC GTCTCGGCGT CGTAGCCGTG ACGCAAGATA TGCTCGTACT CGGTATCATT      120
CGCGACGAGG ACAATGGCGC GATCGACATC ATGCGGCACT ATGGGATCAA CTTGTACGAA      180
CTCAAACGGT TGATCGAGTT GGAAGCCATC GCCGAGAGTT TGCCTGCTTC GCCTGAGGGA      240
TCGCCCCATCT TCACCCCTTC GGCTCGGGAG GCTATCGATG ATGCCACAGA CATCTGTGCC      300
GACATGGAGG ACGAGGCCGT CAGCCCGGTC CATCTGTTGC TGAGTATCCT CAACTCGACA      360
CAGGAGAGCT TAGTACAAAA GATATTTATG AAACAAGGTA TAAAATACGA CACCATCCTG      420
TCGGATTACT TCGGACAGCG CAACCCCTCC GAAGGGAAGT CTCCCTCCGA AATGGAGATC      480
CTCGACGGGT ACCAAGACAA CGACTTCGAC GACGAAGAGG ACGAATCCTC TCCGCCTTCC      540
GGGAATAGCG GGACAGGCGG AGGCTCCGGC GACGCCCCCG AACAGAATAC CGGCGGAGGC      600
GATACTACCA CCACGACACG GAGTGGAGGC GACACGCGTG CACTGGACAC CTTCGGCACC      660
GACATCACTG CCATGGCGCG AGCAGGCAAG CTCGACCCGG TAGTGGGTCG GGAGCAGGAG      720
ATCGAAAGGG TGAACATCAG ACTCAGCCGG CGCAAAAAGA ACAATCCGGT GCTCATCGGC      780
GAACCCGGTG TAGGCAAGAG TGCCATCGTG GAAGGACTGG CCGAACGCAT CGTGAACAGG      840
AAGGTGAGCC GTATTCTTTT CGACAAGCGG ATCATCAGCC TCGATTTGGC TCAGATGGTA      900
GCCGGCACCA AATATCGCGG ACAGTTCGAA GAGCGGTTGA AAGCCGTGCT CGATGAGCTG      960
AAGAAGAATC CGCAGATCAT CTTCTTCATC GACGAGATAC ATACCATCGT GGGAGCAGGC     1020
TCTGCAGCCG GATCGATGGA TACGGCCAAT ATGCTCAAAC CCGCTCTTGC CCGTGGACAG     1080
GTACAGTGCA TCGGAGCCAC TACGCTGGAT GAGTATCGTA AGAACATAGA AAAGGACGGA     1140
GCACCTCGAA GCCGCTTCCA GAAGGTGCCG ATAGCCCCCT CGACTGCAGA AGAAACGCTG     1200
ACCATCCTGC AAAACATCAA AGAGAAATAC GAGGACTATC ACGGTGTACG CTATACGGAC     1260
GAAGCGATCA AAGCGGCAGT GGAAGTACC GATCGCTATG TATCCGATCG TTTCTTCCCA     1320
GATAAGGCGA TAGATGCCAT GGACGAGGCC GGCGCGAGCG TCCATATCAC CAATGTGGTG     1380
GCTCCGAAAG AAATCGAGAT ACTGGAGGCC GAATTGGCAT CGGTGCGAGA GAACAAGCTC     1440
TCGGCCGTAA AGGCTCAGAA CTACGAACTG GCTGCCTCCT TCCGCGATCA GGAGCGGCGC     1500
ACTCAGCAGC AGATAGCGGA AGAGAAGAAA AAATGGGAAG AGCAGATGTC CAAGCACCGC     1560
GAGACGCTGG ACGAGAATGT AGTGGCGCAT GTAGTGGCGT TGATGACAGG CGTTCGGCT     1620
GAGCGGCTGA GCACGGGCGA AGGCGAACGT CTGCGCACGA TGGCAGATGA TCTCAAGACC     1680
AAAGTAGTAG GTCAGGACAC AGCATCGAA AAGATGGTGC ATGCCATCCA GCGCAATCGT     1740
CTGGGACTTC GCAATGAAAA GAAACCGATC GGTTCCTTCC TTTTCTCGG CCCCACGGGG     1800
GTAGGCAAGA CCTATTGGG CAAGAAGCTC GCCGAATACC GTTTCGAGGA TGAGAATGCC     1860
ATGATCAGGG TGGATATGAG CGAGTATATG GAGAAGTTCT CCGTTTCGCG TCTCGTGGG     1920
GCCCCCTCGG GATATGTGGG TATGAAAGAA GGCGGCCAAC TGACGGAGCG CGTAAGACGC     1980
AAACCCTATT CCGTGGTTCT CTTGGATGAG ATCGAAAAGG CGCATGCCGA TGTCTTCAAT     2040
CTGCTCTTAC AGGTGATGGA CGAAGGTCAG CTGACCGACA GTCTGGGACG GCGCGTGAAT     2100
TTCAAGAAAC CCGTGATCAT CATCACCTCC AACGTGGGTA CACGCCAGCT CAAAGACTTC     2160
GGGCAGGGTA TCGGGTTCCG TTCGGAAAAA GACGAGGAAG CGAACAAGGA GCATAGCCGT     2220
TCCGTGATCC AAAAAGCTCT GAACAAGACG TTCAGCCCCG AATTTCTCAA CCGTTTGGAC     2280
GATATCATCC TCTTCGACCA ACTGGGCAAG ACGGAGATTC GCCGGATGGT GGACATAGAG     2340
CTTAAAGCCG TCTTGGCGCG CATCCATCGT GCCGGATACG ACCTCGTCCT TACCGATGAA     2400
GCCAAGGATG GATAGCGAC GAAGGATAC GACCTCCAAT ACGGAGCACG ACCGCTCAAG     2460
CGCACACTCC AGAACGAAGT GGAGGATCGC CTCACGGATC TTATCCTCTC CGGACAGATC     2520
GAGAAAGGGC AGACGCTTAC GCTCTCTGCT CGCGATGGCG AGATCATCGT ACAAGAACAA     2580
GCA                                         2583

```

(2) INFORMATION FOR SEQ ID NO:40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

AGAGGAGGAC	AAATCCGCGG	ACACCATACC	GATTCGTCAA	GGGGATCGGA	CAGCAAAGCC	60
TGCCGCTTCT	CCTTTCATGC	CGAGACCATC	GGTTTCTCCA	ACCACCAAAG	AGCAAAAATG	120
AATTACCTGT	ACATACTGAT	TACACTTTTA	CTCTCCGGCT	TTTTTTCCGG	TGCTGAGATT	180
GCTTTCCTTT	CTTCGGACAA	ACTGCGTCTT	GAGTTGGACA	GGAATAGAGG	CGATCTCACA	240
GGCAGAGCGT	TAAACTTGCT	GTATCGACAT	CCGGACCAAC	TGGTGACTAC	TCTCCTTGTT	300
GGTAATAATA	TCGTTTTGGT	AGTCTATGGT	CTGCTGATGG	CGGGATTGCT	GGCCGCACCT	360
TTGGCGCAAT	GGATTGATAA	CGATGCTATG	ATCGTCGTTC	TCCAATCTGT	CTTATCCACT	420
ATCATCATAC	TGTTTACCGG	GGAATTTCTA	CCCAAAGCCA	TTTTCAAGAC	CAATGCCAAT	480
ATGATGATGA	GGGTATTGCG	CTCCCTATC	GTAGCGATCT	ATTATCTGCT	TTATCCTCTG	540
TCTAAACTCT	TCACCGGTTT	ATCTCGCTCT	TTTATTCGTC	TGGTGGACAA	GAATTATGTG	600
CCTACAACAG	TAGGGTTGGG	GCGCGTAGAT	CTCGATCATT	ATTTGGCAGA	AAATATGTCC	660
GGAGAAAACG	AACAGAACGA	CTTGACTACC	GAAGTGAAAA	TCATCCAGAA	TGCGCTGGAT	720
TTTTCCGGTA	TTCAGGTGCG	AGATCGCATG	ATCCCACGCA	ATGAGATGAT	AGCATGTGAG	780
TTGCAAAACG	ATATTGAAGT	ACTCAAAACG	ACTTTTATCG	ATACCGGTTT	GTCCAAGATC	840
ATTATCTACA	GACAGAACAT	AGATGACGTA	GTAGGATATA	TCCATTTCGAG	CGAAATGTTT	900
CGTGGGCAAG	ACTGGCAAAA	ACGTATCAAT	ACTACTGTAT	TCGTACCCGA	AAGCATGTAT	960
GCCAATAAAC	TGATGCGACT	ACTCATGCAG	CGCAAGAAAA	GCATTGCGAT	CGTCATCGAT	1020
GAACTTGAG	GTACGGCCGG	AATGGTCACA	TTAGAGGATT	TGGTAGAAGA	GATTTTCGGT	1080
GACATTGAGG	ACGAACACGA	CACTCGCAAG	ATCATAGCCA	AACAGCTCGG	CCCTCATACC	1140
TATCTGGTCA	GTGGTCGTAT	GGAATAGAT	GATGTGAACG	AACGTTTTGG	GTTGTCCTTG	1200
CCTGAGTCTG	ACGACTACCT	TACCGTGGCC	GGATTTATCC	TGAATAGCCA	TCAAAATATC	1260
CCACAGGCCA	ATGAGGTCGT	GGAGATTGCT	CCTTATACTT	TTACCATTCT	CAGATCTTCT	1320
TCCACCAAGA	TCGAAGTGGT	GAAATGTCC	ATCGACGACC	AATCGAAC		1368

(2) INFORMATION FOR SEQ ID NO:41

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 897 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

TTAAAAAAGG	AGATAACTAT	GAAACAGAAC	TACTTCAAAA	GAGTCTGCTC	ACTGCTTTGG	60
CTGGTTTTAC	CCATGCTTAT	TATGCCATTG	GAAGTAGCAG	CTCAAGAGAT	TATTCCGAAC	120
GAAGAGGTGT	TGAATCATT	GACTTTCGTT	GCACCGGTG	AGGAGACAGA	CGCAATAGAG	180
GCAGAGGTAG	AAGCTCTGCA	GGAGATAGTC	GCTACTGAGG	AGATTGCGGA	GCAGGCTGTT	240
CGTTCTTATA	CCTACACGGT	CTATCGTGAT	GGCGTGAAGA	TTGCTTCAGG	ATTGACTGAG	300
CCCCTTTTC	TCGATGAAGA	TGTTCTTGCC	GGCGAACATA	CCTACTGCGT	AGAAGTACAG	360
TATCAGGGAG	GCGTATCCGA	CAAAGTATGC	GTGGACGTAG	AGGTGAAGGA	CTTCAAACCG	420
GTTACCAATC	TCACCGGAAC	TGCTTCCAAT	GACGAAGTTT	CTTTGGACTG	GGACGGTGTG	480
GAAGAGAAAG	CTGAAGAGCC	GGCAAGTGAT	AAAGCAGTCA	GCTACAACGT	CTACAAGAAAT	540
GGAACCTTGA	TCGGTAATAC	AGCTGAAACT	CATTATGTGG	AGACCGGTGT	AGCCAATGGT	600
ACATACATCT	ACGAAGTGGA	AGTAAAGTAT	CCTGACGGTG	TATCTCCGAA	GGTGGCTGTA	660
ACCGTGACCG	TGACCAACAG	CTCATTGAGC	AATGTAGATG	GACAGGCTCC	TTACACATTG	720
CGAGTAGAAG	GCAAGAAGAT	TATTGCGGAA	GCCCATGGTA	TGATCACGCT	CTACGACATC	780
AACGGACGTA	CCGTGGCCGT	AGCCCCGAAT	CGATTGGAAT	ACATGGCGCA	AACCGGTTTC	840
TATGCAGTGC	GCTTCGATGT	GGGGAATAAA	CACCATGTAT	CGAAAATACA	AGTAAGA	897

(2) INFORMATION FOR SEQ ID NO:42

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1131
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```
TTGTTTAAATC ATAAAAAATC ATGGTATGAA ACATTTCAAT TTTATCTCGT TGTTTTCCGC      60
TCTGGCTTTA TTCTTTTGTG TGAAAAATACC CTGACACAAC AAAAAACAGA GGAGTTTGCA      120
CCTGTGTCCG ATTTACGTGC AGAAGCGTAC GGCTCTACCG TTTTCCTCCA CTGGACTCCG      180
CCGTATGACA ATCCGATGAT TCTCTAAGC GAGAGTTTGT AATCAGGTAT TCCAGCTATA      240
TGGAAGACCA TTGACGCAGA TGGCGATGGC TATAATTGGA TGCATTTGAC CAATTTACG      300
GGACAGAGTG GTCTCTGTGT CTCTTCGGCT TCATACATAG GCGGCGTCGG AGCTTTGACT      360
CCGACAAATT ATCTGATAAC ACCCGAATTA AAACACCCA CAGACGCGTT GGTGGAAATA      420
ATCTATTGGG TATGTACTCA AGATCTCACT GCTCCATCGG AGCACTATGC CGTTTATTCC      480
TCTTCTACAG GCAATAATGC TGCTGACTTT GTTAATCTCT TATATGAAGA GACTTTGACT      540
GCCAAACGGA TACAATCCCC CGAGTTGATC CGCGGAAATC GGACACAAGG TGTTTGGTAT      600
CAAAGAAAGG TGGTACTCCC TAACGATACT AAATATGTTG CTTTCCGCCA TTTTAATTCC      660
ACGGATAATT TCTGGCTCAA TTGGATGAA GTATCTATCC TGTATACCCC TCTCCCCGGA      720
AGAGCTCCGT GTCCGCATCC GGGTGGTTAC ACTTATTCTG TATTCCGTGA TGGACAAAAG      780
ATAGCGAGTG GATTGTGGC ATTGGCATAT ATCGATACGG ATGTACCGTA TGGGACTCAA      840
GACTATTGTG TCCAAGTCAA TTATCTGCAA GGAGACTCGT ATAAAGTCTG CAAAAATATA      900
GTGGTGGCAA ATTCTGCAA CATCTATGGG GCGGATAAGC CTTTGTGCGT GACCGTGGTT      960
GGCAAGACCA TTGTAGCGAG TGCTTTTCAA GGAGAGATCA CTCTTTATGA CATTCGTGGC     1020
CGGCTGATAG CTTCCGCTG CGATACGCTT AGGTACAAAG CGGAAAATGG TTTTACCTC     1080
ATTAAATAC AGGTAAACGG AACTGTCTAT ACTGAGAAAA TCCAAATCCA A             1131
```

(2) INFORMATION FOR SEQ ID NO:43

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2547
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

```
TTCGGAATAT CACCTTCAAT GAAAAAAGT TTTCTTTTAG CCATAGTAAT GCTCTTTGGC      60
ATTGCCATGC AGGGACATTC TGCTCCGTT ACGAAAGAGC GAGCTTTGAG TCTGGCTCGG      120
CTGGCTTTGC GACAGGTATC CTTGCGAATG GGACAAACAG CAGTATCTGA CAAGATTTC      180
ATCGATTACG TTTATCGGCA AGGAGATGCT GAGAGGGGTA TCACATCACA AGAGGAAGGC      240
TCTCCTGCAT ATTTTATATG AGCTAATCGT GGAAATAATG AGGGCTATGC TCTTGTAGCA      300
GCAGATGACA GAATACCGAC AATTTTAGCC TATTCACCCA TTGGCCGTTT CGACATGGAC      360
AGTATGCCCG ACAATCTTCG CATGTGGCTA CAAATTTACG ATCAGGAAAT AGGCCTGATA      420
CTTTCCGGAA AAGCTCAGCT CAATGAAGAG ATATTACGTA CCGAGGGCGT ACCGGCTGAA      480
```


GTACATGCTC	TGATGGATAA	CGGTCATTTT	GCCAACGATC	CCATGCGATG	GAATCAAGGT	540
TACCCATGGA	ACAATAAGGA	ACCACTGCTT	CCTAATGGCA	ATCATGCCTA	TACCGGCTGT	600
GTTGCTACTG	CTGCAGCACA	ACCATGCGC	TACCATAGCT	GGCCGCTTCA	AGGTGAAGGC	660
TCTTTTCGATT	ATCATGCAGG	TTCATTAGTT	GGCAACTGGT	CCGGCACATT	TGGTGAAATG	720
TACGACTGGA	TCAATATGCC	CGGAAATCCC	GACCTTGATA	ATCTGACTCA	ATCTCAAGTG	780
GATGCCTACG	CCCACTGAT	GCGTGTATGT	AGTGCATCTG	TTTCGATGAG	TTTTTATGAA	840
AATGGGAAGTG	GTACGTACAG	CGTTTATGTA	GTAGGAGCCT	TGCGAAACAA	CTTTCGCTAC	900
AAGCGTTCAC	TGCAGCTACA	TGTACGCGCC	TTATATACCT	CACAGGAGTG	GCACGATATG	960
ATCCGCGGGG	AACTTGCCCTC	CGGAAGGCCG	GTCTATTATG	CAGGGAATAA	CCAGAGCATA	1020
GGACATGCTT	TCGTTTGCGA	TGGTTATGCT	TCGGATGGTA	CTTTCATTAT	CAACTGGGGT	1080
TGGGGAGGTG	TTTCCAACGG	CTTCTACAAA	CTAACACTCC	TCTCGCCGAC	TTCGTTGGGT	1140
ATCGGAGGTG	AGGGAATAGG	TTTTACCATT	TATCAAGAGA	TCATCACCGG	TATCGAACC	1200
GCTAAGACTC	CCGCTGAAGC	CGGTACAGAT	GCCTTGCCGA	TCTTGGCACT	GAAAGACATA	1260
GAAGCCGAGT	ATAAAAGTGA	ATCCGGATTG	AACGTAGGGT	ATTCGATATA	TAATACAGGT	1320
GAAGAGCAAT	CAAATCTTGA	CCTCGGATAC	AGATTGAACA	AGGCTGACGG	AGAAGTCATA	1380
GAGGTGAAAA	CTTCATCTAT	CAATATCTCT	TGGTACGGAT	ACGGAGAGCA	TCCCGAGAGT	1440
TTCTCATTGG	CACCTAATCA	GTTGTACAAA	GGAATCAACA	CCATCACCTT	ACTTTATCGT	1500
CGCACAGGCA	CCGAACAGTG	GGAGCCGGTA	CGGCATGCAC	AGGGAGGATA	TGTCAATAGC	1560
ATTAAGATAA	ATACGCAACT	CCCGAACAA	GTCTAGTACA	CGGTAGATAA	TACGAAGGC	1620
AAGCTCAGTA	TCGTCCCAAA	CAGCTTTGTC	GCAGATCTGA	ATTCTTATGA	ACATAGTACG	1680
ATTACAGTAC	AGTTCAATAG	CGACAGCCCT	GATGAGATCC	GTACACCCGT	AGCCTTTGCT	1740
CTATCTACAG	GAGTACTGCT	GGACGATGTA	ATATCTTTGG	GCTGGGTAAT	GGCTGAAGTT	1800
CCGGGCGGTA	GCAGCAACTA	TCCGGTGGTT	TGGTCTAAAG	ACGTTCTCAC	TCTCTCGGAA	1860
GGCGACTATA	CATTGTGGTA	TAGATTTTCC	ATCAACAACC	AAAAGGATGA	ATGGAAAAAG	1920
ATCGGAAGCG	TGTCAGTAAA	AACACCGACA	GAGTATACGC	ACCCCTTATT	CGAAGTGGGC	1980
CATAATCAAA	CTTCTACCTA	TACGCTGGAT	ATGGCACACA	ACAGAGTATT	GCCCGACTTT	2040
ACACTCAAAA	ATCTCGGATT	GCTTTTCAAT	GGTGAGTTGG	TTGTGTGTTT	CCGCCAAACA	2100
CAATCCTCAT	CGGGGTCTTT	ATGGGCAGCT	CAAGAAACAG	TACATATCAA	GCAAGGAGAA	2160
ACTTTCGTAT	ATAAACCTGT	TGTCGAAGGC	CCTATACCTG	ATGGATCCTA	TCGTGCGACC	2220
CTCCATGCAT	TCGTAAACGG	ACAACAACAG	TTGTACCTCA	AGGGGAAAAG	GAATACACG	2280
GTGAAGATCG	TCAATGGTAC	AGCGGTAGAA	GCAATAGAAT	CGTCAGAAGA	GATCAGAGTA	2340
TTCCCTAATC	CGGCACGCGA	TTATGTGGAA	ATATCGGCAC	CTTGCAATTCC	CCAAGAAACA	2400
TCTATCATTC	TTTTCGATCT	GTCAAGGCAAG	ATTGTCATGA	AGAATAGTTT	ATCAGCGGGG	2460
CATGGCAGAA	TGGATGTCAG	CCGACTTCCT	AATGGGGCCT	ACATCCTTAA	GGTGGATGGA	2520
TATACGACGA	AAATAAATAT	AGTGCAC				2547

(2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

ACGAAGAAAA	CACTGATGAA	AAAGCTATTT	CTCTCGCTCA	CGAGTCTTGT	AATGGTCTTC	60
GCTGTTGCAA	GTTGCGATAT	AATCGACAAG	GATCAAAACC	TCTTGCCGGC	TCCGACCAAT	120
GTGACACCCG	ATAATCCGGA	TGACAATCCT	TCGGAGATCG	ACATTACGCA	GACGCACACA	180
GAAAAATATG	TTTTGGCTGA	AGAATTACC	GGCCAAAAAT	GTCTCAACTG	TCCGAAAGGT	240
CATCGCAAA	TGGCGGCTCT	CAAGGAGCAA	TACGGTAAGA	GATTGACTGT	TGTCGGTATA	300
CATGCCGGCC	CTGGATCTCT	CGTGCCACCT	CTTTCCGTA	CAGAAGCCGG	AGACGCATAT	360
TATAGCAAGT	TCGCCAATAA	TACCCCTCTC	CCTGCGCTGA	TGGTTTCGCG	CAAAAAGTTC	420
GGCTCTTCCT	ACGTTTATGA	TAAGAGCTAC	AAAACGTGGG	ACGTGCCTAT	TGCCGAGCAG	480
ATGGAGCAAA	AGGCGAAGAT	CAATATCTTT	GCCGTGGCCG	AATACACCGA	TACCCAAAAG	540
ATCAAGGTGA	CTGTAAAGGG	TAAATACTG	GAGGGGAATA	CACTCCCGAA	GTCCATGGTT	600
CAGGTGTATC	TGTTGGAGGA	TAAGCTGATC	GCTCCGCAGG	TGGATGGCAA	TACGACAGTC	660
GAGAATTACG	AGCACAAATCA	CGTGTGCGT	GGAGCCGTTA	ATGGTATTTG	GGGCGAAGAA	720
TTTGTGAATC	TCAAAGATTA	TTTGTATACT	TACGCCGTTG	AACCGCTCTC	GGGTATGTCC	780
TTCTAGCCG	AGAATTATTC	GATTGTGGCT	TTTGTATACG	ATGTGCAGAC	GTTCGAAGTG	840
TATGACGTTG	TGCATGTAAA	GATCAATCCG	CAATCCGATG	GCAAA		885

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

ACGAATAAAA	AAGAAGAGAC	AATGAAGAAA	TCAAGTGTAG	TAGCCTCAGT	TTTGGCCGTG	60
GCTCTCGTGT	TCGCCGGTTG	CGGACTGAAC	AATATGGCAA	AAGGCGGCCT	TATCGGCGCC	120
GGAGTAGGAG	GTGCCATTGG	TGCCGGAGTA	GGTAACGTAG	CCGGAAATAC	GGCTGTCCGT	180
GCCATCGTCG	GTACTGCAGT	CGGTGGAGCA	GCCGGTGCTC	TCATCGGAAA	GAAGATGGAC	240
AAGCAGAAAA	AAGAACTGGA	GGCCGCAGTA	CCCGATGCTA	CGATTGAGAC	AGTAAATGAC	300
GGAGAGGCTA	TTCTGGTTAC	TTTCGATAGC	GGTATCCTCT	TTGCGACGAA	CTCCAGCACT	360
CTGAGTCCCA	ACTCACGCAC	TGCGCTGACG	AAGTTTGCTG	CAAACATGAA	CAAAAACCCC	420
GACACGGATA	TTCTATCTGT	AGGCCATACG	GACAATAACG	GCTCCGACAA	GATCAACGAT	480
CCTCTGTCTG	AGAGACGTGC	AGCCAGCGTA	TATTCCTTCC	TGAATTCTCA	GGGTGTGAGT	540
ATGTCGCGCA	TGGCAGCCGA	AGGGCGTGGG	AGCCATGAAC	CGGTGTCAGA	CAATAGCACA	600
GTTGCCGGAC	GTTCCGGCAA	CCGCCGTGTG	GAGGTTTATA	TCTTGCCGAA	TGCCAAGATG	660
ATCGAACAAG	CACAGCAAGG	TACGCTGAAG				690

(2) INFORMATION FOR SEQ ID NO:46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

AACAGGAACA	GAAATATGTC	GAAAAAATCG	ATCCTTCTGC	TTTGCTGTTC	GCTGTGCTTC	60
ATTCTGCTA	CGAAGGCTGT	GACCCCGGTC	AGAAATGTGC	GCAATAGCCA	AGTGAACAGC	120
AAAGCAAAGA	CCGAACGTAC	AAAGCCCTCG	GACTCTGTAC	GGTACATTAG	CAACATGATT	180
GCAGATCGGC	TGGAGTTCCG	CAACAAGATT	TCTTCCGAAA	AAGAGGTAAG	AAAAGCCGAA	240
TATGAAAATC	GGCTGGCGAT	GGAAGCACTC	AATTACCCTG	CCATAGATTT	ATATGGTGAA	300
GATTCTTGGA	GCGAGTATGT	AAACCCCTTC	GTGGGTGCAG	GAACCGATGT	CGAAATTCG	360
AACTCCTATG	ACATTGATTG	CTCTTCGTTC	GTGATGCCCC	TCGAAGATAA	GCAGGTCACC	420
TCTCAATTTG	GCTACCGTCG	GCGTTTCGGA	CGGATGCACT	ATGGTATTGA	TCTTTCAGTG	480
AATCGTGGCG	ATACGATACG	AGCAGCCTTT	GACGGGAAAG	TTCTGTACG	CAGCTATGAA	540
GCGCGTGGCT	ATGGCTACTA	CATAGTCTTG	CGCCATCCGA	ACGGACTGGA	GAAGGCTTTC	600
GGACACATGA	GTCGCCAATT	GGTAGACGAG	AATCAGATCG	TTGAGCAGG	ACAACCGATC	660
GGATTAGGAG	GCAGCACGGG	TCGAAGCACC	GGTCTTCATC	TTCATTTCGA	GACCCGCTTC	720
ATGGGTATTG	CCATCAATCC	GAGTACCATT	ATAGACTTCG	ATAACGGAGT	GCCGCTCCGA	780
GACATTTACA	CATTCAAACG	AGGGAGCAAT	TCTCGCTATG	CAAAAGCCTC	TAAGACTTCT	840
TCTCGCTATG	CAAAAAAAGG	GAAGAAAGGC	AGACAAGCTT	CTTCTCCTAT	GACCTATAGA	900
ATCAAAAAAG	GCGATACTTT	GGAAACAATA	GCCAAAAGGC	ACGGCACTTC	TGTTCAGAAA	960
CTCTGTGCTA	CCAATGGCAT	TGGCAAGAGT	AAAATTTTGA	CTCCGGGCAA	AGCCTTGAGG	1020

(2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

CCGAGCAAAA	CGATAATTAA	GACAAATGGCA	AAAATCAATT	TCTATGCTGA	AGGCGTCAGC	60
CTTCCTCGGA	TCAGAAGACG	GATCGTCGGT	AAGTGGATAG	CCGAAGTATG	CAGCCGATAT	120
GGGAAAGCGG	TGGGAGAAAT	CTCCTATCTT	TTCTGTGATG	ACGAATATAT	CCTGAAAGCC	180
AATCAGGAAT	TTCTCGATCA	TGACTACTAC	ACCGACATCA	TCACCTTCGA	TTCTGCGGAA	240
GCGGATACGG	TGAATGGCGA	CCTGCTTATC	AGTCTCGATA	CCGTACGCTC	GAATGCCCGT	300
GCTCTTGATC	TTGATACGCA	AGACGAACTG	CATCGTGTCA	TTATCCACGG	CATACTGCAT	360
CTTTGCGGAT	TGAAAGACAA	GAGCAAAAAG	GATGAAGCCC	AAATGCGTGC	AGCCGAAGAG	420
AAAGCCCTTG	TCATGCTGCG	AGAAACCATC	GGATCGGAGC	TTTCCCTATT	GCATACA	477

(2) INFORMATION FOR SEQ ID NO:48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

AAAAGTAAAA	CTATGAAGGT	AAAGTACTTA	ATGCTCACAT	TGGTTGGAGC	AATTGCACTG	60
AACGCAAGTG	CACAGGAGAA	TACTGTACCG	GCAACGGGTC	AGTTACCCGC	TAAGAATGTT	120
GCTTTTGCTC	GCAATAAAGC	AGGCAGCAAT	TGGTTTGTA	CACTGCAAGG	CGGTGTTGCA	180
GCGCAGTTCC	TCAATGACAA	CAACAACAAA	GACCTCATGG	ACCGCTTAGG	AGCCATAGGT	240
TCTCTTTCTG	TCGGAAAGTA	TCACAGCCCT	TTCTTTGCAA	CTCGTTTGCA	AATTAACGGA	300
GGTCAAGCCC	ACACTTTCCT	CGGAAAAAAT	GGCGAACAA	AAATCAACAC	CAATTTTGGT	360
GCAGCTCACT	TCGACTTTAT	GTTTGATGTG	GTAACTACT	TTGCACCATA	TCGCGAAAAA	420
CGTTTCTTCC	ATTTAATTCC	ATGGGTAGGT	GTTGGCTACC	AACACAAATT	CATCGGTAGC	480
GAATGGAGCA	AAGACAATGT	GGAATCACTG	ACGGCGAATG	TAGGAGTTAT	GATGGCTTTC	540
AGATTAGGAA	AGCGAGTAGA	CTTTGTGATC	GAAGCACAAG	CAGCTCACTC	CAATCTCAAT	600
CTAAGTCGCG	CATACAATGC	CAAGAAAACT	CCCGTATTTC	AAGATCCCGC	AGGACGTTAT	660
TACAATGGAT	TCCAGGGGAT	GGCTACAGCA	GGTCTTAATT	TCCGCCTGGG	AGCCGTAGGC	720
TTCAATGCCA	TTGANCCAAT	GGACTACGCA	CTTATCAATG	ATCTGAATGG	TCAGATTAAC	780
CGTTTTCGCG	GCGAGGTCGA	AGAAGTCTCA	AAACGTCCTG	TATCATGCCC	CGAATGTCCT	840
GAAGTAACTC	CTGTTACTAA	GACAGAAAAA	ATACTGACGG	AAAAAGCTGT	ACTGTTCCGT	900
TTGACAGGCC	ACGTTGTGGA	CAAAGATCAA	TTGATCAACC	TGTATGACGT	AGCTCAGTTT	960
GTAAGAGAAA	CTAACGAGCC	GATTACCGTT	GTTGGTTATG	CTGATCCTAC	GGGTAATACT	1020
CAATACAACG	AGAAATTGTC	TGAGCGTCGG	GCTAAAGCCG	TTGTTGATGT	TCTGACAGGT	1080

AAATATGGTG TGCCTTCCGA ATTAATCTCT GTAGAATGGA AGGGCGACTC TACGCAACCG 1140
 TTCAGCAAGA AAGCTTGGA TCGTGTGTA ATCGTTCGCT CCAAG 1185

(2) INFORMATION FOR SEQ ID NO:49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

TATAAAATGA	CATACAGAAT	TATGAAAGCT	AAATCTTTAT	TATTAGCACT	TGCGGGTCTC	60
GCATGCACAT	TCAGTGCAAC	AGCCCAAGAA	GCTACTACAC	AGAACAAAGC	AGGGATGCAC	120
ACCGCATTCC	AACGTGATAA	GGCCTCCGAT	CATTGGTTCA	TTGACATTGC	AGGTGGAGCA	180
GGTATGGCTC	TCTCGGGATG	GAATAATGAT	GTAGACTTTG	TAGATCGTCT	AAGTATCGTT	240
CCTACTTTTCG	GTATCGGTAA	ATGGCATGAG	CCTTATTTTCG	GTAATTCGCT	CCAATTCACA	300
GGATTCGACA	TCTATGGATT	CCGCAAGGG	AGCAAGGAGC	GTAACCACAA	TTACTTTTGA	360
AACGCCCCAC	TTGACTTTCAT	GTTCGATCTG	ACGAACTATT	TCGGTGTATA	CCGTCCCAAT	420
CGTGTCTTCC	ATATCATCCC	ATGGGCAGGT	ATAGGATTG	GTTATAAAT	CCATAGCGAA	480
AACGCCAATG	GTGAAAAGT	AGGAAGTAAA	GATGATATGA	CCGGAACAGT	TAATGTCGGT	540
TTGATGCTGA	AATTCGCTC	ATCAAGAGTC	GTAGACTTCA	ATATTGAAG	ACAAGCTTTT	600
GCCGGAAGA	TGAACCTTAT	CGGGACAAAG	AGAGGAAAAG	CAGACTTCCC	TGTAATGGCT	660
ACAGCAGGTC	TAACGTTCAA	CCTTGGCAAG	ACAGAGTGGA	CAGAAATTGT	TCCTATGGAC	720
TATGCTTTGG	TCAATGACCT	GAACAACCAA	ATCAACTCAC	TTGCGGTC	AGTGAAGAG	780
TTGAGCCGTC	GTCTGTTC	ATGCCCTGAA	TGCCCTGAGC	CTACACAGCC	TACAGTTACT	840
CGTGTAGTCG	TTGACAATGT	GGTTTACTTC	CGTATCAATA	GTGCAAAGAT	TGATCGTAAT	900
CAAGAAATCA	ATGTTTACAA	TACAGCTGAA	TATGCGAAGA	CCAACAACGC	ACCGATCAAG	960
GTAAGTAGGT	ACGCTGACGA	AAAAACCGGT	ACTGCGGCCT	ATAACATGAA	GCTTTCAGAG	1020
CGTCGTGCAA	AAGCGGTAGC	CAAGATGCTT	GAAAAGTATG	GTGTTTCTGC	GGATCGCATT	1080
ACAATTGAAT	GGAAGGGCTC	ATCAGAGCAA	ATCTATGAAG	AGAACGCTTG	GAATCGTATT	1140
GTAAGTAATGA	CTGCAGCGGA	A				1161

(2) INFORMATION FOR SEQ ID NO:50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

GTAATTGGCA	TCATTATGGA	ATTTTTCATG	TTATTCATAG	CGGCGGTTTT	CGTTAATAAC	60
GTGCTGCTGT	CGCAGTTCTT	CGGTATATGC	CCATTCTTAG	GCGTATCGAA	GAAGGTAGAC	120
ACCTCAATCG	GTATGGGTGC	AGCCGTGACA	TTGCTATTGG	CCTGGCTAC	CTTGGTTACC	180
TTCTGATTC	AGAAGTTCGT	TTGGATCGT	TTGCTATTGG	GCTTTATGCA	GACCATTGCA	240
TTTATTTTGG	TCATTGCCGC	CTTGGTGAG	ATGGTGGAGA	TCATACTCAA	GAAAGTATCT	300

CCTCCCCTCT	ATCAGGCACT	GGGTGTATTC	TTGCCCTTGA	TTACGACGAA	CTGCTGTGTG	360
CTCGGTGTGG	CTATTTTGGT	TATCCAGAAG	GATTATACCC	TGCTCCAGAG	CTTCGTCTAT	420
GCAATATCCA	CGGCTATCGG	TTTCACCTTG	GCAATGGTTA	CTTTCGCAGG	TATTCGAGAG	480
CAACTCGATA	TGACCAATCT	CCCCAAAGCT	ATGAAGGGAA	TACCTTCGGC	ACTCTTGGCT	540
GCCGGTATAT	TGGCTATGGC	TTTCATGGGC	TTCAGCGGTA	TCGCC		585

(2) INFORMATION FOR SEQ ID NO:51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

TACCGATCTT	ATCGTGGGAT	AGGGAGTGGG	ACACACTCTC	CTAACCTCAA	AAACCGACTA	60
AAAAGGATCG	GAATAAGGAT	ACCGAACAGA	CACTATATCC	ATATCAAGCC	AATCAAACCA	120
AAAAATAAAA	TGAAACAACT	AAACATTATC	AGCTTCATCA	TTGCTTTCCT	ATTCTTAGGA	180
ACGAGCGCAT	CGGCTCAGCA	ATCGGGCGGA	TCCGTTACAG	GTACCGTAGT	GGACAAAAGC	240
TCAAAAGAAC	CTATCGCAT	CGTACAAGTA	TTCGTCAAAG	GAACCACTCT	CGGAACCTCC	300
ACGGATGCAA	ACGGAAACTA	CTCGATCAAG	GGAATCCCTT	CGGGTAATCA	AACTATCGTA	360
GCCCGACTCA	TGGGTACTCT	CACTTGCGAA	GAAAAAGTAC	ATATAGAAAA	GGGTGGTTCC	420
CGCCACGTAG	ACCTCTATCT	GACCGAAGAG	ATTCTCTCTC	TCGATGGGGT	AGTGGTATCT	480
GCCAATAGAA	ACGAGACTTT	CGGCCGTCAA	GCACCCTCGT	TGGTAACGGT	ACTGTCGCCG	540
GAACTTTTCC	TCAAAACCAA	CTCTACCAAC	CTGAGTCAGG	GACTTAAGTT	CCAGCCCGGT	600
CTGCGCGTGG	AGGACAACCTG	TCAGAACTGC	GGTTTCAACC	AAGTTCGTAT	CAATGGACTC	660
GAAGGAGCCT	ATTCGCAAA	TCTTATCGAC	AGCCATCCCA	TCTTCAGTTC	GCTTGCCGGT	720
GTCTATGGCT	TGGAGCAGAT	CCCTGCCAAT	ATGATCGAAC	GTGTAGAAGT	AATTCGCGGT	780
GGAGGTTTCG	CTCTGTTTCG	CTCTAATGCT	GTGGGAGGCG	TTATCAACGT	AATTACGAAA	840
GAACCGCTTC	GCAATTCGGC	CGAGATCAGC	CATTCTACGA	TGACCTTCGA	CCACGCGAAA	900
GGGTGGGGGA	GCTTCCAAA	TACGACCCAG	TTCAACGGTT	CTATGCTGAC	GGAAGACCCG	960
AAAGCCGGTG	TATGGTATT	AACTACCGTC	CCGGACAGGA	TATAGACGGC		1020
GACAACTTTA	CCGAACCTAC	CAATCTGCGC	AACCGCTCGC	TCGGTTTCCG	CTCATACTAT	1080
AAGACCGGTC	TCTACAGCAA	AGCAACCTCT	GAATATCACA	GCATGCAGGA	GTACCGTCGT	1140
GGTGGCGACA	GACTGGACAA	TCTCTCTTTC	GAAGCCCAGA	TAGCGGAATA	TCTCCAGCAC	1200
TATATCAATG	GCGGAAGTTT	CAAAATTCGAT	CAGGGCTTCA	CGGTGGCAA	GGATTTCTTC	1260
AGTCTGTATG	CTTCAGCACA	AGACGTTTCT	CGTCGTAGCT	ACTACGGGGG	TGGCGACTAT	1320
ACCGAAAATC	TGCTGAACGG	AGCAGTTTCT	AGTGGAAGCA	CCGAATCGGA	CGAATACAA	1380
GATGCTTTCA	CGGCTCTTAC	TTCTTACGGG	ACTACCAAGG	GATTTCGATT	GCAAGGAGGA	1440
GGTATGTACC	GTACATACCT	CGGAGAAAAC	TGGGACTTTA	CCGGCGGACT	CGAATATATC	1500
TACGGCCAAC	TCGATGACAG	AAGCGGTAC	AGACCGAGCA	AAATAGATCA	GAATACCTCT	1560
ACTTTTAGTC	AGTACGACCA	GCTCGAATAT	AAGACGGAGA	AGTTAAGTGC	CCTTATCGGA	1620
GCACGTATCG	ACTATGTTCT	CCTCAATCAG	GATGGCAAAC	GCTATATCGA	TCCGCTCTTC	1680
ATTTTCAGTC	CTAGAGCCAA	CGTACGATAC	AATCCCAATA	AGAATCTCAG	CTTCCGACTC	1740
TCATACAGCG	AAGGATTCCG	CGCTCCTCAG	TATTTTCGAT	AAGATCTGCA	CGTAGAGTTG	1800
GCCGGTGGTA	CTCCTATCAG	CCGTGTCCTT	TCCCCCAATC	TGAAAGAAGA	ACGTTACAG	1860
AGCATCAGTG	CTTCTTTTCA	TTATTACCAC	AGAGCCGACG	AATGGCAATT	CAATATCATG	1920
GGAGAAGCCT	TCTCCACCTT	TATCAGCAAT	CAGTTCAAAC	CATCCGATAA	GGTCGAAACC	1980
ACGAGCGATG	GCAAAGAATG	GATCATTCGT	ACCATCTACA	ACGACAAGGA	TGGAGTATCG	2040
AAGGTATATG	GTGTGAATCT	GGAGGGAAGA	ATCGCCTACA	ACAAATCGTT	CGACCTCCAG	2100
CTCGGCGGTA	CATGGCAGAG	AAGCCGCTAC	GGAAGCATCT	ATACCGCTGT	GGAAGCGGAC	2160
AAAACAACGG	GACAAGCGGA	GATCTCTGTG	AAAGACTATG	TACGCACTCC	GAATCTGTAC	2220
GGCTATTTTC	TTGCTACGGT	AGCTCCTACC	GAGCACTTCG	CCATCAATCT	CTCCGGTACA	2280
TTCACGGGCA	AAATGGATGT	AGTACACGAA	GCCTATGAAG	GCGATATTCC	CGCAGAACAC	2340
ATAGCTCCGG	ACGGATCGTT	CGACTTTGAA	ATGAATGGTC	AGCAATTCAA	AGGTTTGGCC	2400
GAAGGTCATG	CCAAGCTCGT	CAAGACTCCG	GCCTTCGCGG	ATATAGACCT	CAAGCTGAGC	2460
CACGACTTCC	ACCTTGCTTC	CACATGACCC	TTGGAATTGA	ATGCCGGAAT	ACAGAACATA	2520
TTCAACAGCT	ATCAGAAAAG	CACGGACAAG	GGACCGGGTA	GAGCTTCTAC	TTACGTATAC	2580
GGTCCTATGC	AGCCAGAAAG	GATTTTCGTC	GGTACAAAGA	TCAATTTT		2628

(2) INFORMATION FOR SEQ ID NO:52

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2697
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ATATTGAATC	ATTTGAGAAA	GACTATGTAC	AAAAAGATTA	TTGCCGTAGC	AGCTCTCTTC	60
TGCGCCAGCA	TAGGGATCCT	GAAAGGACAG	TCCTCGGATC	TGACCCCTCA	GGATACTATA	120
TATAGCCCTG	AAATATCCTA	TGCCAAGCCT	ATTCATAAGA	CCATAGCATC	TATTGAGATC	180
GAGGGAATGA	GGTCTTTTGA	TGACTTTTGT	TTGCGCAATC	TTTCAGGCTT	GGCTGTAGGT	240
GATGAAGTCA	TGATTCCTGG	AGATGCCATG	TCTGCTGCCG	TGAATAGAAT	TATGCGTCAG	300
GGCTACTTCT	CAAAATGTGG	AATCATCGCG	GATAAATATG	TCGGCAATAA	AGTCTATCTG	360
AAAATCATTG	TCACTGAACG	TCCTCGCATC	AGTAAGGTTA	CTTTTAGCGG	GGTAAAGAAG	420
TCTGAGAGAG	AAGATCTTGA	AATGAAAATC	GGTCTTCGCG	AGGGGATTCA	GATGACCAGA	480
AATAATGAAG	ACAAGGTCAG	GCAAATCGTA	CAGAAGTATT	TTAGTGAGAA	AGGTTATCGC	540
GATGCCAGCA	TACGGATAAC	GCAGGAACCG	GATCTTTCCA	AAGATGGCTT	TGTCAATGTG	600
CTTATCTCGA	TTGAGAAGAA	AAGCAAAACC	AAGGTGAATG	AAATTTATTT	TTCCGGCAAC	660
AAGGCCCTTA	GCAATCATAA	GCTAAGAATG	GCGATGAAGA	ACACCAATGC	CAAATTCAGT	720
CTTAGAAAAG	ATATTGCTTC	ATCTTTCTTG	AAACTTTTTA	GTACTCATAA	GTTTGTGGAA	780
GAGAGCTACC	GTGAAGATTG	GGTCCGATTG	ATAGAGAAGT	ATCAGGAATA	TGGATATCGT	840
GATGCTGAAA	TACTGACCGA	CAGTGTCTGT	AAGGCTCCTG	ACGGCAAAAG	AGTGGAATAT	900
TATCTCAACA	TGCAAGAGGG	GCAGAAGTAT	TATATTAAGG	ATGTCAACTT	TGTGGGCAAT	960
TCACAATATC	CATCGGAGTA	TTTGGAACGA	GTGCTCGGAA	TAAAATCCGG	AGATGTGTAC	1020
AATCAGAGAC	GATTGGCTAA	GCGTCTCAAT	GAAGATGAAG	ATGCTGTGGG	GAACCTGTAC	1080
TATAACAATG	GCTATATTTT	TGCGTGGGTC	GATCCCCTGG	AAACAAATGT	AGTGGGGGAT	1140
TCTGTTTCGC	TTGATATTCT	TATAGCGGAG	GGGAAGCAGG	CCAATATCAA	TAAGGTGATC	1200
ATCAAAGGAA	ATACTGTCTG	GTACGAAGAC	GTAGTACGCC	GAGAGCTTTA	CACAAAGCCC	1260
GGCCAGCTCT	TTAGTCGCGA	GGATATCATT	AACTCTATTG	GTCTCATCAA	TCAGCTTGGG	1320
CATTTTCGATG	CCGAAAAATC	TATTCCCCGT	CCGATTCCCA	ATCCCCGAAAC	AGGAACAGTG	1380
GATATAGAGT	ATGATTTGGT	GCCGCGTAGC	AGTGACCAAT	TGGAGCTTTC	TGTCGGTTGG	1440
AGTCAGTCCG	GACTTCTGTT	CCGAGGAGCC	ATTAAGTTCA	CGAAGTTCTC	TGTCGGCAAC	1500
TTGCTCCATC	CCTCGATGTA	TAAGAAAGGG	ATCATTCCGC	AAGGGGATGG	GCAAAACTA	1560
TCACTGAGTG	CTCAGACCAA	TGGAAAGTAC	TATCAGCAGT	ATAGTGTAC	ATTATGGAT	1620
CCATGGTTTG	GGGGCAAGCG	GCCGGATATG	TTCAGCTTCA	GTGCATTCTA	TTCCAAGACT	1680
ACGGCGATTG	ACTCCAAGTT	CTACAATAGC	AATGCCGGCA	ACTACTATAA	TGCCTACTAT	1740
AATAGCTACT	ACAACAATA	TAATAGTTAT	TACAACGGTA	TGTCGAACTA	TACCGGCGAC	1800
CTCTATACTC	AGGCCAGCGA	TCCGGATCGT	TCGCTTCAGA	TGTTAGGTAC	TTCGATCGGT	1860
TACGGTAAGC	GTTTGACTTG	GCCGGACAAT	TGTTCCAGA	TTTATACTTC	TCTGAACACT	1920
ACCTACTATA	GACTGCGAAA	TTGGAGCTAC	AATACCTTCC	AAAATTTCCA	TCATGGCTCG	1980
GCTAATGATC	TCAACTTGA	GCTGCGTCTC	TCTCGTACTT	CCATCGATAA	TCCTATTTAT	2040
ACCAGAAGCG	GATCGGATTT	CATGGTTTCT	GTGCTGCTA	CTCTTCCTTA	TTCTTTGTGG	2100
GACAATCATG	ACTATGCCAG	CCAGAACCCT	AGCGTAAGCG	ATCGTTACAG	ATTTATCGAG	2160
TATCACAAAGT	GGAAGTTTAG	AGGACGAGTT	TTTACTCCAT	TGCTCAATCC	TGCTACGCAT	2220
AAATATACAC	CGGTGCTCAT	GAGTCGAGTG	GAAGGAGCAG	TTCTTGTTTC	GTATAATTCC	2280
AATAAGAAAT	CTCCTTTTCG	TACTTTCTAT	ATGGGAGGTG	ATGGTATGTC	CAGCTATTAT	2340
GGTGGCTACA	TGAATGAGAC	TATAGGTTTG	CGTGGTTATA	AGAACGGATC	TATTGCCGGT	2400
AATAACTACG	ACTATGCATA	TGCTTATATG	CGGCTTACGA	TGGAAGTACG	TTTCCCGATT	2460
CTGTTTGAAA	ACTCATTCAA	TGCGTGGCTC	TTAGCTTTTG	CCGAAGCAGG	CAATGCGTGG	2520
CGCAGTATCG	ACAATTATAA	TCCCTTTAAC	CTGAAGCGAT	CGGCCGGTGT	AGGATTGCGT	2580
GTAACGTTAC	CGATGGTCGG	AATGCTCGGT	ATCGATTGGG	GATATGGCTT	TGACCGTCCG	2640
GACAATTCTC	TACAGCGAGG	AGGAAGCAAT	GTCCACTTTG	TGCTCGGACA	GGAGTTC	2697

(2) INFORMATION FOR SEQ ID NO:53

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

```
CAAATAAACA TGAATGGCGA TATGAAACGG TTTTGTATT TGATCGGCTT TGCACTGGCG      60
GTAGCTTTCT CCGGTTTTTC CCAAAAGTTC GCTTTGGTAG ATATGGAATA TATCCTCAGG      120
AATATTCTCG ACTATGAGAT GATGAACGAA CAGCTGGAAC AGGTGTCCAA GAAATGGCAA      180
AATGAAATCG AAGCTCTCGA AAATGAAGCC CAATCTATGT ATAAGAAGTA TCAGAGCGAT      240
CTCGTATTCT TGTCTGCTGC ACAGAAGAAA ACCCAAGAAG AGGCTATCGT AAAGAAAGAG      300
CAGCAAGCAT CCGAGCTCAA GCGGAAGTAT TTCGGCCCGG AGGGGAGCT GTATAAGAAA      360
CGCTCCGATC TGATGAAGCC TATTTCAGAT GAGATTTGGA ATGCTATCAA AGAGATTGCC      420
AAGCGTAACA ACTATCAGAT GTGCTTGAT AGAGGTACGT CCGGAATTAT CTTTGCCAGT      480
CCGTCTATTG ACATTAGCGA CCTTGACTG AGCAAGATGG GCTTTAGCAA G      531
```

(2) INFORMATION FOR SEQ ID NO:54

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

```
CGAATAAATA AACAAACGCA AATGAAGAAA TTTTCTCTCA TGCTTCTGAT GGCTCTTCCT      60
TTGAGCCTCT TGGCACAAAA GGTGGCAGTG GTAAACACTG AGGAGATCAT TTCCAAAATG      120
CCGGAACAAG TAGCTGTAC CAAACAGCTC AACGAATTGG CCGAAAAGTA TCGCCTTGAT      180
CTCAAGAGTA TGGACGATGA GTTTGCCAAA AAGACAGAAG AATTTGTAAA GGAAAAAGAC      240
TCTCTACTGG AGAACATCCG CAATCGTCGT CAGCAGGAAC TTCAGGATAT TCAAACTCGT      300
TATCAGCAGT CATACCAAAC GATGCAGGAG GATTTGCAAA AGCGCCAACA ACAGCTTTT      360
GCTCCTATCC AACAAAAGGT GGCTGATGCC ATCAAGAAAG TGGGTGACGA AGAAAAGTGT      420
GCCTACATCA TGGAGGCCGG TATGATGCTT TACACCGGAG CTACTGCTAT TGAATTGACC      480
GCAAAGGTAA AAGCGAAACT CGGAATCAAG      510
```

(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2484 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

```
ATCATGAAGG AAGCTATTCC CCGAAAGAAC AAGTATATAA AGCTCAACGG TATATACAGA      60
TTGTCATTCA TTCTGCTATG CTGCTCTGCTA TGCTCTCAGG CAGCTATGGC ACAAGGCGTC      120
AGGGTATCGG GCTATGTGCT CGACCGTGGG GAAAAGCCGA TCCCGTTTCGC CGGAGTCAAA      180
GTGCGTGGTA CGGGGACAGG CGCAACGACG AATCTGAAAG GATACTACGA GTTTCGGATG      240
AAGGCCACGA CGGACACGAT CACGATCGAG TTCAGCTCCA TGGGGTACCA AGGGGTAAGT      300
CGCAGCTTTC CGTCTCTGAC CAAGGACACT CGGCTGAATG TTCGTTTGGC AGAGGCCGAG      360
ATGGAGCTTT CGAGCGTGAC GGTACAGGCC ACAAACGCA GACTCAACAC GATGGAGCGC      420
GTCAATACCC GAGACCTTCG TGTCATATGCA GGGCCTACGG GAGGGGTGGA ATCGCTCATC      480
AGTACCTACG CAGGAGTAAC GCAGAACAAAT GAACTAAGCT CGCAATACTC GGTTCGCGGA      540
GGAAGCTACG ATGAGAATAT GGTCTATGTA AACGGAGTGG AGGTTTATCG CCCGCTGCTG      600
GTTCGCTCTG CACAGCAGGA AGGTCTGAGC TTCGTCAATC CGGATCTGAC ACAATCCGTA      660
CAGTTCCTCG CCGGAGGGTT CACGGCCGAC TATGGCGACA AGATGTCTC CGTACTGGAT      720
ATTGCTTACA AGCAACGTAAC GCGGAAGGAA GGAGCGGTAC TCCTCGGGAT GCTACAATCG      780
AGTGCCTACT ATGGCAGCAG TGCCGGAGCC TTCAGCCAAA TCACGGGTGT ACGCTACAAG      840
AGTGCCAAAT CGTCTTGGG CACTACGAC ACGAAAGCCG AATACGATCC GATCTATGCG      900
GACGGACAGA CATTCTGAC GTACCGTTTC AGCCCCAAGC TGTCGGTTAG TTTCTCTCGC      960
AATATTTTCG AACTCTGCTA CAAGTTTGTG CCTCAGACCC GTGAGACGAG CTTCGGTACA      1020
CTGAGCGATG CCAAAAAGTT GAAGATCTTT TTCGACGGTC AGGAACAAGA TCGTTTCCTG      1080
ACCTACTTCG GTGCCTTCAG CATGAAC TTCGCGGACG ACAAACAGCG GCATACGGTT      1140
ACGCTTTCGG CCTTCAACAG TAACGAACGG GAGACCTACG ATATTCAGGG AGAATACTTT      1200
CTGAACGATG TGCAGCTGGG GCGCGACGGA ACTGCTTCGA TGGCTTCGGG CTCAGAGAAC      1260
TCCAACGGCT TGGGCATCGG GCGCAATCAC GAGCATGCGC GCAACAGGCT GAGCTACCGC      1320
GTGCTGAACA TGGGTTACAG AGGGGAGATG AAGCTGAACG AGAAGCATCG CTGCAAGCC      1380
GGCGTATCGG CACAGATGGA GAAAATAGCC GACCATATCA GCGAATGGGA ACGGAGGGAT      1440
TCGGTAGGAT ACAACCTACC TCATCTGGAG ACCGTATTGC TGATGTACAA TAACCTATAT      1500
GCCGATACGC AGATGAGGGG AACGCGCTTG TCGGCATTTC TACAGGATCG ATTCAACTTC      1560
AGCATGGGAG GAGGTACATT TTCTCTCATT CCGGGTATCA GAGCTTCGTG GTGGAGCTTC      1620
AACAAGGAGT TGCTCGTCAG CCCACGTATC AGCGTGGGTT ATTCTCCCGA AAGCAACCCG      1680
GCTTTGGTAC TGCCTGCAGC CGCCGGACTT TATTATCAGG CACCGTTTTC CAAAGAGCTA      1740
AGGCAGACGC ATAAGGATGC CGAAGGCAAT AACGTGGTTG TCCTCAACGA GAAGATCCGC      1800
TCTCAGGGAG CTTTTCACAT TCTCGCAGGA GCAGACTATA CCTTCGAAAT GGGGGGGCGA      1860
AAATACAAGT TTACGGCAGA GGCTTACTAC AAGAGCCTGT TCAACATCAA CCCGTATATA      1920
ATAGAGAACG TGAAGATCCG CTAATCTGGG GAAAACATCG GTTCGGGTTA TGCTGCGGGT      1980
ATCGATCTCA AGCTCTTCGG CGAACTGGTA CCCGGAGTGG ATTCGTGGCT GACGGCTTCC      2040
ATTATAAAG CCCGTACAGAA ACTGGATGGC TACGGTTCTT TACCACTGAT GAACGCACCC      2100
ACTTACAATT TCTCCTTCTT CCTTCAGGAG TACGTGCCGG GCAATAAACG CATCACAGCC      2160
ACCTGCGGG CTGCACTAAG CGGAGGATTG CCCAGCTCA ATCCGAGCAA AGGGCTTAGC      2220
TCGCCGGCCT TTACCGCACC GGCCTATAAG CGTGTGATC TGGGGGTAAT GTACAAATGG      2280
CTCGACCGG ATGACTCTT TGCCGGCCGA AGCAAATGGC TAATGGGAGT AAAAGGGGCC      2340
TACATAGGG CTGACCTCTT CAATCTGTTC GACATGACCA ACGTCAATTC TTACTACTGG      2400
GTGTCGGATG CCTACCAACA GCAATACGCC GTACCGAACT ACCTGACACG CCGCCAATTC      2460
AACCTGCGTC TCCTCGTCGA ATTC
```

(2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2037 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

```
CCTATCCCTT TTCTTCTTAA TATGTACAGC GGACATCATA AAATCCATTA TCCTTTTCTT      60
ATCCTGTTGG TATGCCTTGC TTTTGTGTCG TGCAAGAGCG TGAAGTTGAA AGATGCGGAG      120
AAGGCACATG ATCGCCAAGA GTATACCAAG GCTGCCGATA TGTACAATAC ATTATACAGG      180
CGTACCCGAC GAAAGCAGGT GGAGATGAAA GCTTATACGG CTTTCCGATC CGGTGAAAAC      240
```


TATCGTGCCG	CCGGCAGACA	AGCCAAAGCT	TTGCGTGGCT	ATCTGAATGC	CAGACGCTAC	300
GGGTATCCGG	ATTCTGTGGT	ACTGCTCCGT	TTGGCACAGA	CTTATCAGCA	AGGAGGTAAC	360
TATAAGGAAG	CCGAGGTACT	CTTCCGTGGA	TATCTGGAAG	CTTATCCGAA	AAGTTATTTT	420
GCAGCTATCG	GTTTGGAGGG	GTGTCTCTTT	GCCCCCAGC	AAAAGGAATA	TCCTACACGT	480
TACCGGATAC	GGCGAGCTGC	CGAGTGGAAT	TCGGCACGGG	GCGACTTCGG	CCCGGCCTAT	540
GCACCCGATG	CTTCGGCTCT	CTATTTTACA	TCGAGCAGAA	GCAAAGACGA	CGGTTTGGAT	600
AATAGCAGCA	TAACGGGACT	GAAACCCAAC	GACATTTATA	TCATCAAACG	AGATGCACAA	660
GGACGATGGG	GACGTCCCGA	TAGCGTGTCC	GGAGGAATCA	ACACTCCATG	GGATGAAGGC	720
GTGCCAACGA	TCACGCCCGA	TGGTAGTACC	ATATATTATA	CGTTGGCGCA	GCAAGGAGCC	780
GATTACGACC	GTACGGTACA	GATCTATTCC	GCCGCTCGGA	GCGGAGAAGG	CGGTTGGAGC	840
AACGGTTTCG	TCGTGGACAT	TATGCGCGAT	TCGCTCCGTA	TGGCTGCTCA	TCCCTCTATG	900
TCGGCATCCG	GCGATTACCT	GTATTTTCGTC	AGCAATATAG	GCGGTAGCTA	TGGCGGCAAG	960
GATATTTATC	GTGTCAAGGT	GTGCGATCGT	TCTTATGGTT	CACCGGAGAA	TTTGGGGCCT	1020
GATATCAATA	CGCCGGGGGA	CGAAATGTTT	CCCTTCATAG	ATGGGGATAG	TACCCTTTTC	1080
TTCGCTTCGG	ACGGACACGC	CGGTCTGGGA	GGACTGGATA	TTTTCAAAGC	CACGCTGGAC	1140
TCTACCGGCC	AATGGCATGT	AGTCAATATG	GGACAACCGG	TCAATTCTCT	TGCCGATGAT	1200
TTCCGGCTTGG	CTGTGGAGCC	TAAAGGCCAA	AACAAAGAAG	AAGCTTTGCC	GGACAACGGA	1260
GTCAAAGGTG	TATTTTGTTT	CAACCGAGGC	GATGCACGCG	GATGGCCGCA	CCTCTTCCAT	1320
TTCGAATCTG	AGACCTACTA	CAGGTATGAT	CAAGGTTATG	TGATGGACAG	AGAAGAAAAT	1380
CCCATAGCCG	GAGCCACTGT	CAGGATCGTA	GGCGAACGCG	GCCCCGTAGG	ACAGGGATTTC	1440
GTGACTACTC	GTGACGATGG	CTCCTATAAG	ATGAGCGTGC	AGGGCGATAC	TCGCTATGTA	1500
ATGCTTGCCG	GAGCATCGGG	TTATTTGAAT	CAGTACGTAG	AACTCAAGAC	CGATACCGCC	1560
AAGCAGAGTG	AGACCTACTA	TGTGGACTTT	TTCTTGTCAT	CGCGTGAGAA	AGCCGAGGGC	1620
TTGCAAAATA	TTTTCTATGA	TTTCGATAAA	GCTACTCTTC	GCCCCGAAAG	CATGAAGAGC	1680
TTGGACGAAC	TGATTTCGTAT	CCTCACGGAC	AATCCGGATA	TTCCGATCGA	ATTGGGTTTC	1740
CATGCCGACA	GGAAAGGCC	CGATGCTTAC	AACCTCGGAC	TATCTGACCG	CAGAGCCAAA	1800
TCCGTGTTGG	ATTACCTCAC	GAGTCTGGC	ATAGCGGCCG	ACAGGCTTAC	GTGGAAAGGC	1860
TACGGTAAGT	CTGTCCCCAA	GACGGTGACA	GCCAAAATTG	CCGAACGGCA	CGATTTCTCT	1920
AAGGAAGGCG	ATGTGCTCAC	CGAGGAATTC	GTAGCACCTT	TGACCGAGGA	GCAGCAGTCA	1980
GTCTGCGACC	AACTGAACCG	TCGTACCGAG	TTCCGTGTGA	TCGAAGAAGA	GTTGCGT	2037

(2) INFORMATION FOR SEQ ID NO:57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

CCTGCACAGC	CGAAAACATA	TTGCATACGA	TACTTTCGGA	GAGAGGTATC	TCCGAGGAGG	60
CAAACAGAAA	GGACATTGTA	TGCGGACAAG	ATGCGCCGGC	ATATCGTCAA	GTGCTGTCCC	120
TCTGCCTCCA	TACTCTTGCA	AGAATACTCC	ACAACAGAA	TATTCATTCA	TCACCTTAA	180
ATATCAATAA	TTATGAAAAA	GTTTTTCTTC	GCGCTACTAT	CGATTGGTAT	TTTACGCGAG	240
GCTTTTGCCA	AGACGGACAA	CGTCCCGACA	GATTCGCTAC	GAGTACACAA	TCTTCAGACC	300
GTCACGGTCT	ATTCTACACG	CACGGCCGTA	CCTCTGAAAA	AGATACCGGC	CAAGATGGAA	360
CTCATCTCAT	CGCGCAACAT	CAAGCAGTCC	GGCTTTAAAC	ACATGACCGA	CATCCTCAAG	420
ACGCAAGGTT	CGCTCGATGT	CATCAATATC	CCGGGCTTTA	GTTCGAACAT	CGGTATCCGC	480
GGTTTCAAGC	CCTCCGGCAA	GTATGTAACC	GTATTGGTAA	ACGGCATCCC	TGCGGGAACG	540
GACAATATCT	CTACGCTCAA	CACGAGCAAC	ATCGAACAAA	TCGAGATCCT	CAAAGGCCCG	600
TTCTCTTCCA	TCTACGGCAC	CAATGCCATG	GGCGGTGTGG	TGAACATCAT	CACCCACAAA	660
TCCAAGGACA	AGATCCATGG	CAACGTTTCT	CTCTTCGGCG	GTAGCTACCA	GACCATGGCC	720
GGATCATTCA	ACTTGGGTGG	CCGCTTCGAG	GATATTTTCT	CATTCGATCT	TAGTCTGGGC	780
TTGGACAAGC	AGAACAAGGA	CTATAAGACC	GGATCAAACA	ATTTCCTATC	CCTGAGCAAA	840
CTGGAAGAAG	CTATAGTAGA	TGTAATGCT	ACCAAAAAAC	AGAAAATGAA	GGGGAGCGAC	900
TATACTGTAG	CAACGGGACG	CTGCGTTTC	GGTATCGACT	TCACGCCCGA	ATGGTCGCTG	960
AATCTGTATC	AAAACGTATT	CCTCGGAGAT	GCGATCCCCG	TAGGAGGATC	TATATGGGGC	1020
GTTTACGGAG	AATCCAAAAA	AAATCTGAAT	CGTTCTTCGA	CCTCTTTTCA	GCTGCTCGGC	1080
AAACATGGCT	GCCACACGCT	TCAATTCTCC	CCCTACTTCA	ACATAGAGAA	ATCGGAGAAC	1140
TATAACAATG	CGATCCACAC	CGTTTTCATC	AACACAAAAA	GCGACTACTA	CACCTATGGT	1200
GCCCTACTCC	AGGACAAGAT	TTCTTTTGA	GGACAAAAAT	TCGTACTCGG	TGTCGACAGC	1260
CGAAACATGA	CGATGGAGTC	AGAAAGATTC	GAGCAGGCAG	GAGTGAATAC	AAAGCCATAC	1320

AACCCCGGAT	ATGCCACGAA	CAATATCGGT	TGTTTCGGAC	AGGCCAATTT	CTACCTGCTG	1380
AACGATGCTC	TATCGATATC	TGCCGGTGCA	CGTGCCGACT	TCATGTTCTT	TGACCTGAAA	1440
GCGAACGAGT	ATCTCAACAA	TGAAGCCAAA	CAGGAAACTC	ATAACGTAAT	CAATCCGAAT	1500
GTCCGAATCA	AATATGAGTT	TGTGAAAGGC	CTTACAGCTC	ATGGTACATT	CGGTAGTGCA	1560
TTCAGTGCTC	CCGATGCTTT	CCAAAAAGCA	GGCCAATACG	TAGGCCCGTT	CGGCACGACC	1620
ATAGGCAATC	CTGACCTGAA	ACCCGAAAAG	TCCATGACCT	GGGACTTCGG	TATCGGATAC	1680
AGCAATGCAC	GCTGCGGGAT	CCAAGCCGAC	GTAACCTTAA	CCTATTTCCA	CACCGACCAC	1740
AAAGATCTGA	TCTTGTCAG	CCCTGACTAT	GCTAATAATA	TCACCACATA	CATCAATGCC	1800
GACAAGGCTC	GTATGAGCGG	TATCGAGGCC	CTTTTGTCTT	ATGACTTCGG	CAGCCTCTTT	1860
GCCAACAAGT	TCTCTCTCCG	CGCATTTCGG	AATGCCACGA	TCATGCTCAA	TTCCGAGATG	1920
AAGAAAAGCC	AGACCGATGC	CCCTTGAGC	GAAATGTACT	ACGTTTCGAA	GCAGAACATC	1980
ACCTTCGGTA	TGCAATATCG	TGGCAAAGAA	GGACTTGAAG	TGATGCTCAA	CGGTCGCTTC	2040
ATGGGACGCA	GGATCGAGCA	AAACTGGTAT	GCTTACTACC	CCGAAGTTCG	CCCCGAAGTC	2100
CAGCAACTGC	TGTCAGCAGA	AGAGCCTGAA	TTGGCTGCTC	AGGGACTGCT	CCGTCATCCG	2160
CAAGCAATGG	TGTTCAATGC	CTCTGCTTAC	TACCACATGA	ACAAGTATCT	CACCTTCGGT	2220
GTGAACTTGA	ACAACATCTT	GGATGAGCTT	TATACGGAGA	AAGACGGCTA	CCACATGCCC	2280
GGACGTAACA	TCATGGGTAA	GTTTATGGTC	AAC TTC			2316

(2) INFORMATION FOR SEQ ID NO:58

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1452
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

GGCCGGGCCT	CTTCCCCTTA	CAGGCAAATG	GATGGCATA	TAAACGATGA	ATATAGACAA	60
GCATCTATGA	ACAGGTTTTC	AAATCATTGG	CCCTGCATCC	TCGTGGGGTT	TGTA CTCTGG	120
TTTGTATCGG	CGAGTCGGAC	TGTGGCACAA	AACGCCTCCG	AAACGACGGT	ATCGTACGAT	180
ACGGATACCG	CCGTACTCTC	CGAAGCCGAT	GTGCTTCGGA	TCGCTCTTAG	TGAGAATGCC	240
ACAGTGAAAG	TGGCCGATAT	GGATGTGCGC	AAACAGGAAT	ATGCACGTAG	GGCAGCACGT	300
GCCGATCTCT	TCCCGAAAGT	AGACCTCAAT	GGCGTTTACA	GCCATACGCT	AAAGAAGCAG	360
GTCTTATATA	TAGATATGCC	CGGTTTTCAGC	AGTAGCGAAG	GTATCGAAAT	GGGGCGTACA	420
CACAATACGC	AAGGAGGGGT	GAACGTCTCC	ATGCCATTGG	TGTCGGCACA	GCTTTGGAAA	480
AGCATTGCCA	TGACCGGAGA	ACAGCTCGAT	CTGGCTCTGG	AGAAAGCTCG	CAGCTCCCGA	540
ATCGATTGG	TGGCAGAGGT	GAAGAAGGCT	TACCTCAGTG	TATTGTTGGC	CGAGGACTCT	600
TATGGCGTAT	TCAAGCGCAG	CTATGACAAT	GCTCTGGCCA	ATTATAAGAA	CATATCCGAC	660
AAGTTCGATC	GTGGACTTGT	GGCCGAGTAT	GATAAGATTG	GAGCCAATGT	ACAGGTACGC	720
AACATCGAGC	CTAACCTCTT	GCAAGCGCAG	AACTCCGTAG	CCCTTGCTCT	CTGGCAGCTC	780
AAGGTCCTGA	TGAGCATGGA	AGTGGAAACT	CCGATCAGAC	TCTCCGGTTC	ATTGTCCGAC	840
TATAAAGAAC	AAGTCTATAC	CGGCTATTTT	GCCGCCGATA	CGCTTATTTC	CAACAAC TCC	900
TCCCTGCGTC	AGCTCGATAT	ACAGCGTCGT	CTGGCTGTCA	GTGCAGACAA	GCTGAACAAG	960
TACAGTTTCC	TGCCTACACT	CAATCTGGGA	GGGCAGTACA	CCTATTGCTC	CAACAGCAAC	1020
GACATCAAAT	TCTGGGGCGA	GGGACAACGC	TGGACGCCTT	TCTCCACCAT	ATCGCTCAGC	1080
CTGTACATTC	CTATATTCAA	TGGAGGCAAA	CGTCTGTACA	ACGTGAAGCA	AAGTGCTTTA	1140
TCGATCCGTC	AGATCGATCT	GCAACGACGC	CACATAGAGC	AATCCATCCG	AATGGGAATC	1200
AAGAACCAAA	ATGACCGTCT	GCGTACCTGT	ATGCAGAGAT	TGTGGCCCTC	GGAAGAGGCT	1260
GTCCGAAGTG	CAGAAAAGGG	CTATCAGATA	GCAGAGAAAC	GCTATCAGAC	AGGCGAAGGC	1320
ACTCTCGTCG	AGCTCAACGA	TGCCGATGTG	GCTCTTTTGC	AGGCTCGACT	CAATTATAAT	1380
CAGGCCATAT	TCGACTTTAT	GACCGCAAAG	GCCGAATTGG	ACAAGATGAA	CGGCATGGGG	1440
ATTCCCGAAC	AA					1452

(2) INFORMATION FOR SEQ ID NO:59

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

TTTCATAACT	TTGACTTCCT	AAACGGTATA	AAATTGTTTT	CGATGGCAAA	TAATACTCTT	60
TTGGCGAAGA	CTCGACGTTA	TGTCTGCCTT	GTGCGTTTCT	GTTGGCTCAT	GGCGATGATG	120
CACCTCTCTG	GGCAGGAAGT	CACTATGTGG	GGGGACAGCC	ATGGAGTGGC	GCCGAACCAA	180
GTGCGCCGAA	CGCTGGTGAA	GGTAGCCTTA	AGTGAATCCC	TTCTCCGGG	TGCAAAACAG	240
ATTCTGATCG	GATTCTCTCT	TCCGAAAGAA	ACGGAGGAAA	AAGTACCCGC	CCTATATCTC	300
CTTGTGAGTG	ATTCTTTAGC	GGTGC GCGAC	TTGCCGGACT	ACAAAGGGCG	AGTCTCTTAC	360
GATAGCTTCC	CGATCTCAAA	GGAAGATCGT	ACCACAGCCC	TTTCTGCGGA	TTCCGGTAGCC	420
GGACGCCGCT	TCTTTTATT	GGCTGCGGAT	ATAGGGCCTG	TTGCTTCTTT	TTCCCGATCC	480
GATACGCTGA	CTGCCCGTGT	GGAAGAGGTG	GCTGTGCGATG	GCCGCCCTTT	GCCGTTGAAA	540
GAGCTGTGCG	CTGCCTCCCG	TCGTCTGTAT	AGGGGGTATG	AGGCCCTCTT	TGTACCCGGT	600
GATGGCGGAT	CGCGGAACATA	TCGTATCCCG	GCCATTTTGA	AAACGGCTAA	TGGAACACTC	660
ATACCGATGG	CCGACAGACG	AAAATATAAT	CAGACGGATC	TGCCGGAGGA	TATAGATATA	720
GTCATGCGGC	GCAGTACGGA	CGGAGGGAAA	TCGTGGAGCG	ATCCCAGGAT	TATCGTACAG	780
GGAGAGGGGC	GCAATCATGG	CTTTGGCGAT	GTAGCCCTGG	TGCAAACCCA	AGCAGGAAAG	840
CTCCTGATGA	TCTTTGTCGG	TGGAGTAGGC	CTGTGGCAGT	CTACCCCCGA	TCGTCTCAG	900
CGCACTTATA	TATCGGAAAG	TCGGGACGAA	GGACTGACTT	GGTCGCCTCC	TCGGGATATA	960
ACCCATTTC	TCTTCGGCAA	GGATTGTGCC	GATCCGGGAC	GCAGTCGCTG	GTTGGCCTCC	1020
TTTTGTGCTT	CGGGACAAGG	GCTTGTGCTG	CCATCCGGTC	GTATCACGTT	TGTGGCTGCC	1080
ATCCGCGAAT	CAGGGCAGGA	GTACGTCCTG	AACAACATATG	TCCTCTATAG	CGACGATGAG	1140
GGCGATACAT	GGCAGCTTTC	CGACTGTGCA	TACCGCCGTG	GCGATGAGGC	AAAGCTTTCA	1200
TTGATGCCCG	ATGGCAGGGT	ACTGATGAGC	ATACGCAATC	AGGGACGGCA	GGAGAGCCGA	1260
CAGCGTTTCT	TCGCTCTCTC	CTCCGACGAT	GGCTTACTT	GGGAGAGAGC	CAAGCAGTTC	1320
GAGGGCATCC	ATGACCCCGG	CTGTAATGGA	GCTATGCTTC	AAGTGAAAAG	GAACGGAAGG	1380
GATCAAGTGC	TGCAGTCCCT	GCTCTCGGC	CCGGATGGGC	GTCGCGATGG	AGCTGTCTAT	1440
CTCTTCGATC	ATGTCTCCGG	CCGCTGGTCC	GCTCCCCTTG	TTGTCAATTC	AGGATCGAGT	1500
GCCTACTCGG	ATATGACTCT	GCTGGCGGAT	GGAACGATCG	GTTATTTCTG	CGAAGAGGGC	1560
GATGAGATCT	CATTGGTTTT	CATTGGTTTC	GTCTTGACG	ATCTCTTCGA	TGTCCGGCAA	1620

(2) INFORMATION FOR SEQ ID NO:60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 879 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

AAGTCTCCGA	GCGATTCCGC	TTTGCCGTCG	GTATGGAGCG	CGAATACAAT	ATCTGGACTC	60
GTCGGTGGGA	AACGCATTAC	TTTGCTTATC	CTGTATTCTA	TGGCGATAAG	AAGTAGTAAT	120
ATAGAATCAA	TACAGTGCTT	TGTGATGAAA	AAAGAAAAAC	TTTGGATTGC	GATCGTCCGC	180
GGTTTTGGCTT	TCGTATTGGG	CCTTTATGCT	CTTGCCGCA	GTGTCGCTCA	GCTACGCCGC	240
TCTCAGCCTT	CGGTGACTGT	GACCGGTATG	GCCGAGCGTA	ATTTCAAATC	CGATCTGATC	300
GTTTGGACTG	CTTCGTACCA	GCTCCAGATG	ATGGATCTCG	AATCGGCCTA	CAAGGCTTTG	360
AAGGAAAAAC	AGATATTGGT	AGCAGACTAT	TTGAAAAACA	AGCAGCTGCC	CGATTCTGCT	420
TATATCTTCT	CAAGCGTAGC	CATCTCTAAA	GAATACAAC	ACTATTACGA	TCCTCGGCAG	480
GAACAAAACG	TCAGGACCTT	TGCCGGGTAT	CTGCTCAGCC	AGACAGTTAC	GGTGACCTCA	540
CAGGACATCG	AACATGTGGA	GAAAATATCT	CGCGATATAA	CGGAGCTGAT	CAATCAGGGG	600

GTAGAGATTA CCTCCGACCG TCCGGCCTAT TACTACACCA AGCTCAATGA TCTGAAGGTG	660
GAGATGCTGC GCAATGCCTC CGAAGACGCT TTCAATCGTG CTTGCGTCAT TGCGGAGGGG	720
AGCGGTTTCT CCGTGGGTAA GATGCTATCT TCTTCGATGG GCGTGTTCCTA GATAGTGGGG	780
CTCAACTCGA ACGAAGATTA TAGCTGGGGA GGTTCGTTCA ATACGTCTTC CAAGATGAAG	840
ACGGCAAGCA TAACGGTTAA GGCTTCTTTC GCTTTGAAG	879

(2) INFORMATION FOR SEQ ID NO:61

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

GGGAAACTCC AAATGAAAAA AACAAATTGCA ATTATCGCCT CAGCCCTCTT GGCTTTAGGA	60
GCCGTCGGCT GTAAGAAAAA TGCTGACACT ACCGCTGTCA GTGAAAAGGA TAGCATAGCC	120
TTGTCCATGG GTATTTTGTA CGGACAGGAT TTTGCCAATC AGTTCGAAAT GTCCCGCTTG	180
CAAGGCCAGC CGATTGATTC GGTAGCTTTC TTGGACGGTT TCAAATATGG TATCGATACG	240
ACGCGCTTCT CGTCAATCT GGGAGCCATC TATGCTTCCA ATATAGCTCG TCAGCTGGCT	300
CATGATTCCA TCGATATCGA CAAGTTCTAT GCAGCCATGC GTGCGGCTCT TCTTAAAGAC	360
ACCGTATCTA TCGCCATGAA GCCTGCAGAT GCACAGGCTT TCATGCAACG AATCCAAGCC	420
AAAAAGCAGC GAGAAAAACA TATGAAGCAG TTTGGCCAGA ACATCGAAAA GGGTAATGAA	480
TACATCGATA CCTTTAAAAA AGAAGATGGT GTAACGTGTA CGACAACCTGG TCTGGCATA	540
AAGACTCTTC AGGAAGGTAC GGGAGCTACT CCCTCTTTGG CCGATACTGT ACGTGTCAAG	600
TATGTGGGTA CTCTGGTCGA TGGTAAAGAG TTCGACAAAA ACGAAGAAGG AATCGAATT	660
GCCGTTACCG GTGTGATTAA AGGCTGGACG GAGATGCTCC AACTCATGAA GGTGCGTCAG	720
AAAGTTGCGG TGGTAATCCC ACAGGAGCTG GCTTATGGGG AGACCGGCAA CTATACCATC	780
GAACCGTTCT CTACCCTGAC GTTCGAGATG GAACTTATCG GGATCAAGCC CGGGAAAAAG	840

(2) INFORMATION FOR SEQ ID NO:62

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

TGTCGAAAGC AGAAGCTCTC AAACCCGAAG AGGAGCCGGT ATCCGTGCAG ACGGATATCA	60
TTCCGACAAA GCGATAAGAA TCCGATGAAA GTATTACGGC AAGTATTCTT CCCCATCCTT	120
TTTGTCTTAC TGACAGGTGC CTGCTCCACC ACAAAGAATC TGCCGGAAGG CGAACAGCTG	180
TATATCGGAA TGGGCAAGAC ACAGATACTC CGGCAGGACA AGAGCCACGC CGGCCAACAG	240
GCTCTGACCG AAGTGGAGAG TACACTGAAA GTTACACCCA ATGGAGCTAT TTTCGGCAGT	300
GCAAGTGCCT CCTTACCCAA GATACCATTC GGGCTATGGC TATACAACAG CTTGCTGGGG	360
GATTCCACTG TCATTTCGAA ATGGATATTC GACAAGTTTG CAGCCAAGCC GGTTTTCATC	420
AGTCAGGTCA AATCCGATAG CCGGGCTAAG GTGGCGACGA ACATCCTCCG CGAACACGGG	480

TACTTCGATG	CTAAAGTAAA	AAGCAGTGTG	ACCACTCTGA	AAAAGGACTC	GCTCAAAGCC	540
AAAATCTCCT	ATACGGTGGA	TATGGCCTCT	CCTTATCATT	ACGACAGCAT	CATTCCCTTA	600
CCGATCAGCA	CTTCCCGCA	CAGCATTCTG	GCTTACAGGC	AGACTCCGTC	TTTGATCAGG	660
AAAGGAGACC	AGTTCAATTT	GGCAAAGCTG	CACGAAGAGC	GTCAGACCAT	CAGTGCCCTG	720
CTGAGAGACA	ATGGTTACTA	CTACTTCCGC	CCACAGGATA	TTATCTACGA	AGCCGATACC	780
CTCCTCGTAA	GAGGTGCCGT	ATGCCTGCGA	GCCAAGCTCT	CGGAAGATAC	TCCACCCCAA	840
GCCATGCGCC	CGTGGAGGAT	AGGGAACCGG	ACAGCAGTCC	TGCTCGGAAT	GAACGGAGAA	900
AGCCCCGACAG	ACTCGCTCGA	AGTGGAGGAT	ATGAAAGTCC	TTTACTATCG	TAAAATGCCG	960
GTTCGCCCCA	AGATTTTGGC	CAAACGCTTT	CGTTTCTTCT	CCGGCAATCT	GTATCGGCAG	1020
AAAGACGATG	AGACGACACG	CAAATCCTTG	GCTCGTTTGG	GAGCCTTCTC	CGTTATCGAT	1080
CTCAATTTT	TGCAACGCGA	TTCCATTCC	GGCCTTTTGG	ATGTGCGACT	GCTAACCCACC	1140
CTCGACAAAC	CTTGGGATGC	ATCATTAGAG	ACCTTGTTCA	CGAGCAAAAG	CAATGACTTC	1200
ATCGGTCCCG	GACTGAATTT	TGCTCTTGCT	CGGCGCAATG	TATTCGGCGG	AGGAGAAAAT	1260
CTTTCTTGA	ATATCGGTGG	ATCGTATGAG	TGGGAGACCG	GCAATCGTCC	CGAAAATAGC	1320
AGCAATCGCG	TGATCGATAT	AATTCGTAC	AACATGAATA	CGGCCGTGAA	CCTCTCGTTT	1380
CCCTCGATTG	TATTTCCCGG	TCTGCTGGAT	AAATACTATT	ACTACCCAC	GACTACGACT	1440
TTTCAGGCTT	CTGCCACCGC	GCTGAACAGG	GCACACTACT	TTAGCATGTA	CTCTTTCGGC	1500
TTTTCGACCA	CCTACGAATT	TCAGCCCTCC	AAGGAACACC	GGCATGCTAT	TTTCCCGCTC	1560
AAGCTCAACT	ACGACCTCTT	GGCGCATCAG	ACAGAACTT	TCCAGGCCAT	TACGGCGAAC	1620
AATCCGCCCC	TGCTGCTCAG	CCTTCAGAGT	CAGTTCCTTG	CTCAAATGGG	GTATATCTAT	1680
ACGTTCAACA	AATCCGTTTC	AGAGAAAAGT	CCTCATCATC	TTTGGATGCA	ATTTCGGACTA	1740
TCCGAGGCAG	GCAATCTCCT	GAATCTGATC	TATCTGGCAG	CCGGCAAGAA	GTACAGCGAC	1800
ACCAAGAATT	TGCTCGGCGT	CCCTTCTCT	CAGTTCATCA	AAGCCACGGG	AGAACTGCGC	1860
TATTCCTATA	CCATAGACCG	CAATCAGTCA	CTGGCAACCC	GTTCGGGAC	AGGCGTGATA	1920
TATAGCTATG	GCAATATGCG	AGTGGCACCC	TATAGCGAGC	AGTTCATGT	AGGCGGTGCC	1980
AATAGTATCA	GAGCTTTTAC	CGTCCGTAGC	ATCGGCCCCG	GACGGTTCAA	TCCGGATTCC	2040
GACAATCAGT	ATTCCTATT	GGATCAGGTG	GGCGAATTCA	AACCTGAAGC	CAACGTGGAA	2100
TATAGAGGCA	AGCTTTTCGG	GGATCTCCAC	GCAGCCGTTT	TCCTCGATGC	GGGCAACGTT	2160
TGGCTCTTGA	GGGAGGATTC	TTCCCGTCCG	GGCGGTGCTC	TGTCCGAAGT	GGGATCGGTG	2220
AGCAATTTCC	TGAATAGCAT	CGCTCTCGGC	ACCGGTGTG	GCCTTCGCTA	CGATCTGGCA	2280
TTCTCTGTGG	TTCTGTGCTG	TGTCGGCTTC	GGTCTCCACC	TTCTTTACAA	TACGGGTAAG	2340
AAAGGTTACT	ACAATATCCC	ACGCTTTAAG	GATGCCATCG	GTTTCCATTT	GGCTGTCCGC	2400
TATCCCTTC						2409

(2) INFORMATION FOR SEQ ID NO:63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

TCTCTCTCCC	CGTATATCCG	TTTTCCTATG	TCCTCGCATT	CCGTTGCGTA	TCTAATCGGC	60
ATTGCCGGCT	GCTTGCTCCT	CATGCTTGCT	TCCTCCTGCT	CGGTCACCCG	TTATGTGCCG	120
GACGGTAGCA	GACTATTAGA	CAGGGTAACG	ATCGCAAGCG	AAACGGGCAG	TATCGCTCTG	180
CCGGAAGATA	TTCGGGACTA	TACCCTCCAG	CAACCCAAAT	ACAGACTGTT	CGGGATGACT	240
CGCTGGCTAC	TGCGCGTCTA	TAGCAGCTCG	AATCCGAACA	GCAACAGCTG	GTGGAACCGT	300
TCGCTCCGGA	AAATGGGCGA	ACCGCCTGTC	CTCATCGATT	CTGTCTCTAC	CGATCGTACT	360
GCCAACCGTC	TGCAAAAGGC	GATGGCCGGC	GATGGCTTTC	TCGATGCTAC	TGCTCGTGCC	420
GTGGTAGACA	CCGGCTTGTA	CAAGAAAGCT	CGCATTACTT	ATCTGATTCA	GCCCCGAAGC	480
CGTTATTATA	TACGCAATAT	GGCTTTGGAT	GTGAAGAATC	CACTCCTTCC	TCCCGTTGCG	540
CTTGGCAATT	CGCTTCTTTC	GGCATAACAAG	GTCCGGATCA	GCGAGGGTTC	TCCCTTGTCG	600
CCCATCGTAC	TCGATGAAGA	GAGAAAGGCG	ATAGCTCGTC	ATATGCGCAA	CAACGGCTTC	660
TGGAAGTTCT	CCGCCGAGGA	TGTTTATTAT	GAAGCAGATA	CTACCGTTTC	AGGAGGATCG	720
GGTACGAAAT	CTGCCGATCT	GAAATTAGTG	GTCAATGGCA	TCGGGCGTTA	TCCATATCCG	780
ATCGGCAGGG	TATTCCTTCA	TGCCGATTAT	GATCCTCTCG	AATCGGACTT	CAGAGTTCAG	840
GAGCTGCCAC	GTATCGATTG	GATTTCCGGT	GGCGATTACA	CTGTTTACTA	TGGGAGTAGG	900
GGACGTTATA	TCCGGGCATC	GGCTCTCAGC	CGGTCGGTGT	CCGTTACACC	GGGAGCTTTT	960
TTCTGCGAGG	ATGATGTGGA	ACGCTCTTAT	ATCAAGCTGA	ATGCGCTCCC	TATCGTTTCG	1020
AACGTGAATA	TCCGATTGTG	GGAGCACAAAT	GGTAAGGATG	AGATTGCTCT	GGCGGATAGC	1080
TCTCGCCTTG	TGGACTGCTA	TATTCTTACC	GTTCCGGCCA	AGAGCAAATC	GTTTCAAGCC	1140

GAAGTCCTCG	GCACCAATTC	CGCTGGAGAC	TTCGGGGCGG	CTTTGTCTCT	CGGTTTCACC	1200
GATCGCAATT	TGTTTCGTGG	GGCGGAGATG	TTCAATATCA	AACTCAAGGG	TGCTTACGAA	1260
GCCATTTCGA	AGGGTTCCGA	CAGCTTCATG	GAATATGGGG	TGGAAAGCTC	GCTCCGTTTC	1320
CCTCGTCTCC	TCTTCCCAT	CATTTCTGAC	GAAACGCGCC	GGCGGCTACG	GGCATCCACG	1380
GAATGGAAGA	TCGGGTATAA	TTACCAGACA	CGTCCGGAGT	TTGATCGGGT	GATTCTCTCC	1440
GCTCAACTCA	ATTATTCATG	GCAGACCTAC	CTGCACAATC	GTCTGCGTCA	TACGATCCGC	1500
CTGCTGGATG	TCGATTATCT	CGATCTCCCG	TACATCGATC	CCGACTTCGC	CCAATCCCTT	1560
CCGCCTACGA	CTGCACTGTA	TAACACACG	GAGCAGTTTA	TCCTCGGCTC	GGCATATATA	1620
CTGAACTATA	CCACGGCTTC	GTCCATGGAG	CGTACCGTAT	CCAATCCTTT	TACGGCACGG	1680
TTCAAGTATCC	AGACAGCCGG	CAACCTGCTG	CAAGCCATTT	CTTATCTGAC	CGATTCTCCG	1740
AAAGACGAAC	ACGGGTTGTA	TAAAATGTTC	GGTCTGCACT	ATGCTCAGTT	CGTCAAGCTC	1800
GATCTCGATC	TGGCTAAAAC	CGTTCTTCTC	GAAAAGGACA	ATACTTTGGC	ACTGCATCTG	1860
GGTTTCGGAC	TGGCTTTCCC	TTATGGCAAT	GCTCGCCATA	TACCCTTTGA	GTTACGTTAC	1920
TTTGCCGGAG	GATCGAACAG	CGTTGCGGGC	TGGAGTGTCC	GTACCCTCGG	CCCGGGGAGT	1980
ATGAAGATGA	CTCCGGACAA	GACCTTCTTC	GATCAGATGG	GTGATATTCC	TCTGGATCTG	2040
AATGTGCAAT	ACAGGACAAA	GCTGTTCTGG	AAGTTTCGCG	CAGCAGCTTT	TGTCGATGCC	2100
GGCAATGTCT	GGACGATAAA	GGAGTATGAG	AATCAGGAGG	ACGGTCTCTT	TCGTTTCGAT	2160
CGCTTCTACA	AGGAAATAGC	TTTGGCCTAC	GGTCTGGGGC	TTCGTCTCGA	CTTCGATTAT	2220
TTCCTTGTGC	GGCTGGATCG	CGGACTGAAA	GCCTACGATC	CTCAGCAGAC	AGGGCGTTAC	2280
AAATGGGCTA	TCACACGCCC	AAACCTTTCT	TCCAATTTTCG	CTTGGCACAT	TGCAGTAGGC	2340
TATCCGTTT						2349

(2) INFORMATION FOR SEQ ID NO:64

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2625 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

GTGCAATCTA	AATTGTTATG	TCTTATGAGA	AAAAGAATTC	TACAACTTTT	CCTGACCGCA	60
TTGCTGCTGG	CATTAGGCTC	CTCTCTCGCC	ATAGCGCAAA	CAGTGGTGAC	CGGTAAGGTG	120
ATCGATTGAG	AAACGTCCGA	ACCGCTCATC	GGTGTATCCG	TAAGCACCAG	TCAGGGAGCA	180
TCCTCCCGCG	GTGTAACCA	CGATATGGAT	GGTGGCTTCC	GATTGCAAGT	ACCGGCCAAA	240
TCTGTCTTGA	CTTTCCGTTG	CTTAGGTTAT	GCTACCGTAA	CTCGCTCTAT	AGGCAGAGGT	300
TCTCAAGAAG	ACCTCGGTAC	GATTCTCCTC	GATCCCCAGG	CCATCGGCTT	GGATGAGATT	360
CAGGTAATAG	CCTCTGTGGT	GCCCAAAGAC	CGTATGACGC	CGGTACCCGT	TTCCAATATC	420
CGTGTGGCTG	ATATTCAAGC	AGCATCGTTG	AATGTGCAAT	TTCCCGAACT	GGTTAAATCC	480
ACTCGCTCTA	CTTATACGAC	AAAAGGAAGC	GGAGGTTTCG	GTGATGGTCG	TACCAATGTG	540
CGTGGATTTC	ACACTTACAA	CTTCGGTGTA	CTCATCAACG	GAGTTCCTGT	CAATGGTATG	600
GAAGACGGGA	AAGTATATG	GAGCAATTGG	AGTGGTCTGA	TGAATCAAGC	CAGTACCATT	660
CAGATTGAGC	GCGGACTCGG	AGCCTCCAAG	CTCGGTATCA	GCTCGGTAGG	TGGTACGATG	720
AACATTATCA	CGAAGACTAC	GGACGCCAAC	ACCGGAGGTT	CGGCTTATGT	CGGTATGGGT	780
AATGATGGAT	TGCACAAAGA	ATCGTTCTCC	ATTTCTACGG	GTATGAACGA	CGGTTGGGCT	840
ATCACCATTG	CAGGCTCCCA	TATGACGGGT	CTGGGTTATG	TGAAGGGGCT	GAAGGGACGT	900
GCATTCTCTT	ACTTCTTCAA	CGTTTCGAAG	AAGTTCAATG	AACGTCATAC	CCTCTCTCTT	960
ACCGGATTGC	CTGACACACA	ATGGCACAA	CAACGTTCTT	CCAAATATTC	TGTAGCCGAC	1020
TATGACAAAT	ACGGCATCCG	TCACAATCAA	TCCTTCGGCT	ATCTGCGAGG	CGAACTGACT	1080
CCTACGGGCT	ATGCTTACAA	TACGTACCAC	AAGCCCCAGT	TCTCGCTGAA	CCACTTCTGG	1140
AAGATGGATG	AAAATACCTC	TCTTTATAC	gCANCCTACG	CATCTTTGGC	TACCGGTGGA	1200
GGTCGTCGCG	CTTATGGAAA	GACAGTAAG	TGGGTATTGA	TCAACTACAA	CACCGGACAA	1260
CCCTATGAAC	AAACAAAGGT	GACTCCCAGT	GGACTTATCG	ACTACGATGC	CGTACTGGCT	1320
GCCAATGCTG	CGCGGAGCAA	TGGCTCGGAA	GCAATTTTTC	CCCTTGGCTC	CAACTCTCAC	1380
AAGTGGTTCG	GTCTACTCTC	TTCACTCAAG	AAGAACTTCA	ATAGTTTCGCT	GACTTTGACA	1440
GCCGGATACG	ATGGGCGGTT	CTACCGTGGC	GACCACTATG	ACAAGATCAC	CGATCTGCTC	1500
GGCGGTAGCT	ACTACATAGA	GGATCCCAAG	ACAAAGCTCG	CATACCATGC	GGAAGGTCAG	1560
CAACTGAAAG	TGGGTGACAT	TGTAAATCGG	GACTACACAG	GCGAAATCAT	GTGGCACGGC	1620
CTCTTCGCAC	AGATGGAGCA	TTTCGTCGAA	TGGATCGATG	CATTTCGATC	AGGATCTATC	1680
AACTACGAAC	TATACCGCAA	TCACAACAT	GGCGGTAGCA	AGTCCACCGG	CTACCTGCC	1740
GGCGTATCGC	CGTGAAAAG	CTTCTTCCG	TGGAGTGGCA	AGGCAGGTCT	GAGCTACAAG	1800
TTTCGCACAG	GACACAATGT	ATTCGCCAAT	GGCGGTTTCT	TCACACGTGC	ACCACTCTTT	1860

GGCAATATCT	ATGCTGCGGG	GGCTATCATT	CCCAATGACA	AAGCCAATAT	GGAAAAGGTG	1920
CTTACAGGAG	AGGTCGGCTA	TGGATTACAG	AATCACAAAA	ACTTCGAGTT	CAATATCAAC	1980
GGATACTATA	CGAAGTGAT	GGATCGCGTG	ACCTCGAAGA	GAATCGGAAA	CGAGTATGTT	2040
TATCTCAATG	GCGTTGATGC	TGTTCACTGT	GGGGTAGAGG	CTGAGGTCAG	CTATCGTCCT	2100
ATTCGTACAG	TCGACCTTCG	CGGTATGTTC	TCTCTCGGTG	ACTGGACTTG	GCAAAACAAT	2160
GTAAGTTACA	CTTCTTACGA	CGAAGCCGGC	AATGAGACAG	GGCAGGATAT	AACCTATATC	2220
AAGGGTCTTC	ACGTCCGGAGA	TGCAGCACAG	ATGACGGCTG	CTGTATCGGC	AGACATAGAG	2280
CTGTTCAAGG	GTTTCCATGT	CATAGGTAAG	TACAACTTCC	TTGGCAAGAA	CTATGCAGGA	2340
TTCAACCCCG	CAACGCGTAA	TGCACAGCAG	TACGAAGCGG	ATGGCAAAGA	AATCGTGGAA	2400
TCATGGAAGT	TGCCCCGATG	AGGTCTGTTC	GATCTGTCTG	CATCCTACAA	TTTCAAGCTT	2460
GGTTCACCTA	GCACCACATT	CTATTTCAAC	ATGGACAACG	TAGCCGACAA	GCGATATGTG	2520
AGCGATGCCG	ACGACAATAT	CATCGGTAAG	AAACACGATG	AGGCTTCGGC	TCTCGTATGG	2580
TACGGTTTCG	GCCGCACCTG	GTCTACCGGT	ATTCGTGTAA	ACTTC		2625

(2) INFORMATION FOR SEQ ID NO:65

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1380
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

AACAGATGTA	ATCCCTCGCG	TCAATACTTC	CACCTATCGC	AGAATGACGT	TGGAAGATCT	60
CTCCGAGCTT	TTCTAATCCA	TCTATCTATG	AAGTTTTTCAA	TCCGCCTTTT	CCTCTGCATC	120
ATCTTTTCTCC	TCTCTGCATT	TATCCTGCCT	GCTCTCGGAC	AAAAATCCAA	GCAGGTACAG	180
CGACTTGAGA	AGCAACGTAA	GGAGGCCCTC	AAAGCCATCG	AAAAAACC GA	TCGCGAACTA	240
CGAAATACCA	AGAAAGACAA	GCAAGACAAA	CAAAAGCATC	TCAACCTCCT	GAACAAGCAG	300
GTTGCTCAAC	GCAAGCAGAT	GGTACAACTC	TTGGACAATG	AGGTCAAAGA	GTTGCAATCC	360
GACATTGATT	CCATGACGGG	TGTATGT CAT	CAGCTCTCTG	TAGAAGAGAA	AGCCCGATCC	420
GATGAATATG	CCCAAGCTCT	ACAGTCTATG	CAAAAGCGGA	AACGCTCGTT	GGATCGCATC	480
CTTTTCAATT	CATCGGCCAA	GAGCTTTGAC	GAAGGCATGC	GACGGATGCG	TTTCTTGGA	540
CAATACGCTT	CTGCATACAA	GCTGGCATCT	GTCCGGCTGC	GCGATACACG	TAGCAAGTTG	600
GAGACTGAAC	GTGCGACTGT	AGAAGACGCC	AAAAAGGAGA	AAGGACATCT	CTTAGTCATC	660
AGAGAAGAGG	AAAAAAAGAA	ACTCGAAGGA	CAGCAAGCCG	AGCAACGTCG	GCAGGTGCAG	720
GCCTTTGGGAG	CCAAACAAAA	AGACTTTGAA	GCGCAGCTGC	GAAAGCAGAA	AAAGCAAGCC	780
GAAGCTCTGA	ACAGAAAGAT	CGAGAAACAG	ATTGCCAAGG	AAATAGAAGC	TGCCGAACGT	840
CGTGCTCGAG	AAGAACGTGA	ACGGTTGGCA	CGCGAAGCCA	AAGCCAAGGG	TAAGCCGGTT	900
CCTGCCGAAC	CGGAACGGAA	GGCGGAGACC	AAAGGCGGCT	ATGCTATGGA	TGCTCTGAG	960
CTTGCTCTCT	CGGGCAGCTT	TGCACAGAAC	AAAGGTCGCC	TGCCCGGCC	CGTTCGCGGC	1020
AGATACCGAA	TCGTAAGCGA	CTTTGGCGTG	CATCAGCACA	GTGAGCTGAA	AAAAGTACAA	1080
GTTAATAATG	GAGGTATCGA	CATCGCTGTA	GCAACAGGAT	CCGATGCTAC	CAGCGTATTC	1140
GATGGTGTAG	TGTCCAGTGT	ATTTCGTGATA	CCCGGTTATA	ATTCGGCCGT	AATGGTTCCGT	1200
CACGGTAACT	ATATCACGGT	TTATGCGAAT	CTGAGCAAAG	TGTATGTAAA	TTCCGGCACT	1260
CGTGTTAATA	CGGGTCAGGC	TCTTGGTCGT	GCCTATACGG	ATCCTTCCAA	CAACCAGACC	1320
ATTATTCACT	TCGAAATCTG	GAAAGAACGC	AGCAAACAAA	ACCCAAGACT	ATGGTTACGA	1380

(2) INFORMATION FOR SEQ ID NO:66

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1026 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

```
AGTTTTTATC AAGAAATAGA CAGACTTATG AAAAAGTATT TGTATATGC CTCGTTGCTA      60
ACGAGTGTTC TGCTCTTTTC CTGTTCAAAG AACAAATCCTA ACGAGCCGGT GGAAGACAGA      120
TCCATCGAAA TTTCTATAAG GGTAGATGAT TTCACCAAAA CGGGTGAGGC AGTACGCTAT      180
GAAAGGAATC AAGGAAGTGC TGCCGAAAGG CTCATTACCA ATCTTTACCT CTTGTTGTTC      240
GATCAGTCAG GGGCGAATCC GGCGAAATAC TATATTACCG GTAACACTTT CACCGGAGGG      300
ACCTGGCTTC CTGACGATAT GAAGGTGAAG TTGGATATGA CACAATCCGA GGCCGGAGAG      360
CGCAAAGTAT ATGTCGTAGC CAATGTTGAT AATGCGGTTA AAACGGCTCT TGATGCTGTC      420
GCTAACGAAA GCGATTTGCA GACTGTAAAG AGGACGACTG CAATGCCGTG GTCGACCGAT      480
ATAGCCTCTC CTTTCTGTAT GTCCGGAAGC AAGACACACG ACTTCTTGCG CAATCGTCTT      540
TTGACAAATG TCCTCGTCTT GCGTCCCATG GCCAAGGTGG AGCTGAATAT CTCGCTGAGT      600
GAGAAATTTT AGATTGTGCC GATAATTGTC AATGGTAGTT TGAGTGAGTT CAAGTTCAGA      660
TACGTAAACT TCGACAAGGA GACCTACGTA GTGAAGCCAA CGACCAAGCC GGACAATCTC      720
ATTAGTTCTG CTAATGGTGT TTGGCCTCAG ATTACAGATT GGACTGTATG GGGTGCTTCC      780
TTAAATACTT CTCCTGCTCC GGATGCGGGC ACAGGTTATA CATTGATGTC AAATGGCAAG      840
GTAACGGCAC TACGGATTGT TACCTATCTG AATGAGCGCG ATAGCAAAGG GGCTACGGTA      900
GAGGTCGCAT TGCTCTGTGT GGATGATGCG ACCCTTCCTC CTCGGAATT CGGTCCGGAG      960
CTTTATCGTT TGCCTTTGCC GGACAAGATC CTGCGCAATC ATTGGTACAA GTATGAAGTC     1020
GAGATT                                           1026
```

(2) INFORMATION FOR SEQ ID NO:67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

```
AACCTTAGGA CACAGCCTTT CTTTTTGGTA GATTTGCAAT CTATGATCAG AACGATACTT      60
TCACGATATG TATCCTCGAA CTTTTGGAGT CCGGGAGCTA CCTTTTTCCT CACGATTTTC      120
CCGGCCTTCA TCCTCGCCCG TACTGCTTTG CCGGCTTGTG GAGGGGGTAC TGCTTCAGGC      180
TCCGATCGTA CGCTGGCTGT GACCATCGAG CCACAGAAAT ACTTCATCGA GTCCATTGCG      240
GATAAGTCGG TGCAGTGGT GGCATTGGTA CCGGCCGGCA GCAATCCGGA GGAATACGAC      300
CCTTCGCCTA CCGTGATGAA GCGTTTGTCC GAAGCAGATG CCTACTTCTA TATAGGAGGA      360
CTGGGGTTTC AGCAAAGAAA TCTCGCTGCC ATTCGGGACA ATAACCCTAA GCTCCCTCTT      420
TTCGAAATGG GCAAAGCCTT GGCGGATGCC GGAAGTGCAG ATCTCCACGG CTCCTGCACA      480
GATCATTTCT ATACAGACCT GCATGCCCAT GATCCGCACT ATTGGAGCAG TGTGGTAGGG      540
GCAAAGGCAC TCAGTCGTGC TGCATACGAC GCGCTTGTGG AGCTTTATCC GAACGAGAAA      600
GACAAATGGG ACAAAGGGCA CGACCGTCTC AACGGACGTA TCGACAGCGT GAAGAGACTC      660
GTCGATACCA TGTTTGCCAA TGGCAAAGCA GACAAAGCCT TCGTCATATA TCACCCATCG      720
CTCAGCTTTT TCGCCCAAGA GTTCGGCCTG CCGCAGATCG TCATAGAGGA AGATGGGAAA      780
GAGCCTACGG CTGCCACCTT TCGTCGTGTG ATCGATCAGG CACGTGCCGA TGGTGTGAGA      840
ATCGTATTTA TCCAACCCCG ATTTGAAACG CGTCAGGCGG AGGACATCGC ACGCGAGATC      900
GGTGCTCGTC CGGTAAGGAT CAATCCTCTG CGCAGCTCGT GGGAGGAGGA AATTTTACAT      960
ATTGCTCGCG CTTTGGCTCA TGAACGG                                           987
```

(2) INFORMATION FOR SEQ ID NO:68

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

GCAGATTCTA	TTTGATATCC	TCTTTACTTT	TTTGGGCGGA	ATCGGAAGAA	ATGCTTTAGG	60
GAACCTATTC	CCACCTTATA	CAATAAAAAAC	ATGATCGGAA	AAAAAATCTT	TTTATCCTG	120
CTGGCGCTCA	TTGCGTTTCA	TGGGCTGAAC	GCAGCGACAG	ACACTGAGTT	CAAGTACCCG	180
ACCGATGCCA	ATATCATCGG	TCACGTCAAA	GACAGCAAGA	CGGGTGAACA	CCTGTTCGGT	240
ATCACTATTG	CTATCAAAGG	CACTACCTTT	GGTACATCTA	CAGATGCAAC	CGGGCACTAC	300
TATCTTCGTA	ACTTGCGTCC	GGGTGAGATC	ACTTTGATTA	TGCGTGGCAT	GGGCTATAAG	360
AGCCAGGAGC	GCGTAGTCCG	CGTAGAAAAG	GACAAGACTA	TCGAGGTGAA	TTTCGAAGCA	420
GAAGAGGATG	CCATCAATCT	GGACGAAGTC	GTGATTTCCG	CCAACCGCGA	ACTGACGCTT	480
CGCCGTCTTG	CTCCTACTCT	GGTAAATGTA	TTGAACGAAA	AAGTCTTCTC	GCAAGTCAAT	540
GCTTCTAACC	TGGCTCAAGG	CTTGTCATTC	CAGCCGGGAG	TTCTGTGTA	GAACAACTGT	600
CAGAACTGTG	GTTTCAATCA	AGTTTCGTATC	AATGGACTGG	ATGGTCGTTA	TGCACAGATC	660
CTCATCGACA	GCCGTCCCAT	CATGAGTGCC	CTTGCCGGTG	TTTACGGTCT	GGAGCAGATC	720
CCTGCCAATA	TGATCGAACG	TGTGGAGGTA	GTACGTGGTG	GAGGATCGGC	CTTGTACGGT	780
TCTTCTGCTA	TGCGCGAGT	GGTGAATATC	ATCACCAGG	AACCTTCTCA	CAATTCTTTC	840
ACATTCAATG	AATCTCTGAG	CTTTACCGGT	TTCAAGCAAGC	TGGATAACAA	CACGAACTTC	900
AATGCCTCCA	TCGTACAGCA	TGACAACCGT	GCCGGTGCCA	TGGTATTCCG	GCAGGCTCGT	960
TACCGCAAC	ATTGGGATGC	TAACAATGAC	GGTTATTTCCG	AATTGGGTAA	AATAGATGCC	1020
CGCTCGCTGG	GAGCGGATTC	TTATTTGCGC	TTGAGCGACT	ACAGCAAAT	GACGGGAGAG	1080
TTTCACACGA	TCAGTGAATT	CCGCCGTGGT	GGCGATCGTA	TCGATTTGCC	TCCTCACGTA	1140
GTGGGTGTAG	CTGAACAAAC	TGACCATAGC	GTATTTAGCG	GAAACTTGAA	ATACGATCTC	1200
TTCTCTTTCA	ACTATAAAAC	CCACTTCCAG	GCTTATACTT	CCGGACAGAT	CGTAAATCGC	1260
AAGAGCTATT	ACGGAGGTAT	CGGAGAGATT	GACGTCAATG	GCCACCCGGT	TGGTACGGAA	1320
GGCTACCCCTA	TCCCTCAAGA	TCAATACGGC	AATAATTATG	GCGTGACCAA	AGGCAAGACA	1380
TATATGGGCG	GTATCCAGTA	CAGCTACGAC	TTGGACAAAT	TCCTCCTCAT	GCCTTCGCAA	1440
CTTTTGTTGC	GAGCCGAATA	TACGCGTGAT	GAACCTAATG	ACGTGATGCC	CATCCTTTCA	1500
TGGCAGACCG	GCGAGGATGC	CAATGGGAAT	ACCATTCCCC	TCTATCCCGA	ATTGGATCAG	1560
AATATCAACA	ACTACAGCCT	ATTCGGTCAG	AACGAATGGA	AAAATGACAG	ATGGAGCATC	1620
CTTGTTGGCG	CTCGCTTGGA	CAAGCATAGC	GAAGTCAAGG	ATATGATTCT	GAGTCCTCGT	1680
ACCACACTGC	GTTTCAACGT	GAATCCGGAC	ATCAACCTGC	GCGCTACATA	TGCAAAAGGG	1740
TTCCGCGCAC	GCGATACGAT	CGATGAAGAC	TTGCACGTAG	GGGTGTAGG	CGGTGAGGCA	1800
CAGAAAGTAT	TCAACGATCC	GAACCTCAAG	CCTGAAATTT	CTCATGCATT	CAGTTTGAGT	1860
GCCGATATGT	ATCATCGTTT	CGGTAACGTC	CAGACCAACT	TCCTTGTGGA	AGGCTTCTAT	1920
ACTCGTTTGC	TGGATGTATT	CACCAACGAG	GAGCAGCCTG	ATCAGCACGA	TGGCATCAAA	1980
CGTACACGC	GATCAACCG	TAGCGGAGCC	AAAGTATTCG	GTCTCAATCT	GGAAGGTAAG	2040
GTCGCATACA	AGTCCTTTCA	GCTCCAAGCC	GGTCTTACCC	TGGCCAGCAA	CAAATACGAC	2100
GAAGCAGAGG	AGTGGGGTCT	GAATACGGTG	AAAGACACCA	ACGGAGCTTT	TGTTACCGAG	2160
GCCAATGCAA	ATGGACAACA	GGAATACAAG	AACGAATCCA	TGACGGATAC	GCAGATCACC	2220
CGTACCCCA	GCGTATACGG	TTATTTTACT	TTGGCCTACA	ATCCTGCTCA	CTCATGGAAC	2280
ATAGCCCTTA	CGGGAGCATA	TACCGGTCAG	ATGTATGTAC	CCCACGCTAT	CGAATATGGT	2340
GTGAAGTCTG	CCGAACCTGGA	TATTATGCAG	AACAATCCTG	AGATTACCGA	CGAAACCGGA	2400
AAGGCTCCCC	GTATTGATGA	GCTGAAGAAG	ACACCTGCAT	TCTTCGATTT	GGGCTTGAAA	2460
GTGGGTTATG	ACTTCCACGT	ATTCCAGGCT	ACTGAGGTTT	AACTCTATGT	AGGTATGAAC	2520
AATATCTTCA	ACTCTTTTCA	GAAGGACTTC	GATCGTGGAG	CTGCACGTGA	CAGCGGATAT	2580
ATCTATGGTC	CTACGCAGCC	GCGTACAGGC	TACATGGGCT	TGGTAGTGAA	GTTC	2634

(2) INFORMATION FOR SEQ ID NO:69

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

```
AAACAGATAG TTATGACAGT AAAGCGCGCA GTGCGAATAG CACTTCTCAC GCTGATAGGC      60
ATTCTTTTTT CCTCACCTTC TCTTGTTTCGG GCGCAAAGTC TTTTCAGCAC CGAACATGTC      120
TTGCAACTAT ACAACAAGAT ACTCTATGGA GAGTCGGCGG CGGATACCGT CGCAGAGAAA      180
ACGCGAGGTG AGTCGGCATT TCCTTTTATA GACAAACTCA TCAATCTCGG CCGCACTTTC      240
CTCGGCAAAC CATATCGCTA TCGCGGTCCT TCCCCATGGC CGATGGACTG CTCGGGCTAT      300
GTGTCTTACC TCTACTCCAA AAATCGACAT AAACTCCAC GTGGTGCGGC AGCACAGAGC      360
CAATATACGA ATCCTATCGA GCGCGAGGAT GTTCGTCCGG GCGACCTCCT TTTTTCAAA      420
GGCGCAATG CACGAGCAA CCGTATCGGG CATGTAGCTT TGGTCGTATC TGTCGATGAA      480
GATGATATTA CCATGATGCA CAGCCGCAAT TCGCGAGGGA TCGTGATCGA AAAACTCAAT      540
CGCAGTGCAAT ACTTCTCCCG TCGCTTGGTG AGCTATGGCA GGGTACCCGG AGCCAAGAGA      600
GTGATCCAC GAAAAAGT                                     618
```

(2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

```
AAAGGTACGT GGAATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAAT CCTCCTGACG      60
GCACTGACCG TCCTATCTTC GCTCTCCTTG CTTCGTGCAC AAAATGAATC CGAAGCATCA      120
ACCAATCCGA TGTCAGGCCT CTCCTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC      180
CTGAATCTGC GCAGACAGGA GATCGAACAA GAAAACCGAA TCATTAGTCT CGATGCAGCA      240
CGACACAGTT TCCTGCCTTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTTCGGACGT      300
TCGAAAGACA AAACGGGAGT AACCGTAGAT CGCTCCTCGA TGAATACCAA TCTCAGCATC      360
GGAGCTTCGG TGGAAGTATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG      420
TACAACGTGG AGGATGTAT AGCCCGACTT CAAAAGCGC GTGAAGACCT CAGCCTGCAA      480
ATCGCGGCTC TCTATATCAA TTTGCTCTTC CGTCAGGAAA TGACTCGTAC GGCAGAAACA      540
CAGTTGGCAC TGATTGCGGA GCAACGCAAT CGCACGGCCG AAATGGTTCG CGTAGGTAAA      600
TGGGCAGAGG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC      660
GTACAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAAGC CCTCGAACTG      720
GAGCACCCCG AAAGCATTGC AGTCAAGGCT CCCGACACAG ACGTTCTCGT AGCAGAAAGG      780
TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA      840
CTGCATTCTG GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG      900
GCATACTTCC CGACGCTCAG CCTCTCTGCC GGATACAGCA ACGGTTACTT CCGCGACCTC      960
GGCAAGGAGT ATGCCGCCAT CAACCCCTCC TTCTCCGAAC AGTGGAAGAA CAACGGCAGC     1020
TACAGTATCG GACTCTCTTT GAATATCCCC ATCTTCTCTG CCATGCAAAC GCAAGATCGC     1080
GTTCTGGAGCA GTCGCTGCA AATACGCTCA AGCGAGCTTC GACTCGTCGA AGAGAAAAAA     1140
GCCCTCTATA AAGAGATCAG GCAAGCATAC AGCAATGCCG TGGCAGCCGA TAAGGCCATC     1200
GCAGCAGCCG AAAACAGCAA GGCCGCTACG CTCAAGGCAT ACGAATACGC TCGCGACAGC     1260
TTCGAGGCAG GCGCGTTGTC TGCCTACGAA TATGCCGAGG CAAAAACAAA ATACGCCCTC     1320
AGCCAAGTGG AAGAAGTTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTTGGAT     1380
TTCTATCAGG GCAAAGACTT C                                     1401
```

(2) INFORMATION FOR SEQ ID NO:71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

```
AAAACATCAT ATCGGAATAA TATGCGTTTC CAACATTATC TCATCTGTAC GGCTGCCGTA      60
GCGGCTTTGG CTGCGAATCC CCTTACGGGC CAATCGAATA TGACCCTCGA AGAGTGCATA      120
GACTATGCAC GCCGGCACAG TTCGGCCGTG GCGCTGTCCG CTGCGGAACT GGAGCAGTCC      180
AAGGCCGATT ACCTTCAGGC CGTCGGCAAT TTTCTGCCCC GTGTATCGGC CGGAACCGGT      240
GCTTCGTGGA ATTTCCGACG CGGATTGGAT GCCGAGACGA ATACCTACAC CGACATCAAC      300
AGCTTCAACA ATTCGTACAG CATACATGCC ACGATGACCC TTTTCGACGC TTTGCAGAGT      360
GTCTATCGAC TGCGGATGGC GCATGCACGC CGGGAGGCTT CGCGCCTCTC CGTTCGCGAG      420
CAGCAGGAGC TGGCAGCTCT CGGCACCACG GAGGCCTACT ACGACCTCGT CTATGCGCGC      480
CAAATGCAAG AGCTGGCCAT GCAGAAGTAC GAGGAGAGCA GCCGCCTCCA CCGGCAGACG      540
GCTCGAATGG AAGAGCTGGG GATGAAGAGT CGTCCCGATG TCCTCGAGAT GCAGTCGCGA      600
ATGGCCGGTG ACCGTTTGGC CCTGACTCAA GCGGACAATC AGTGCATCAT CGCTCTGATC      660
CGGCTCAAAG AAAAAATGAA CTTCGCCATC GATGACGAAC TCGTCGTAGA CGATATGCCG      720
GCTGACAGTC TCTCCGCCGA CATGGCCGAA TCGGACAGCT CGGCCGGCGT CTTCGCCCGT      780
GCTGCCCATC ATCATCCCGT CCTCCTCCGT GCCAAACTCG ACGAGCAGGC TGCCACCGAC      840
CGTTTGCGAG CCGCGCGAGG TGCATTCTCG CCGAGTGTGT CGGTATCCGG AGGATGGAAC      900
ACGGGATTCT CACGCTTTT TGAATGGATC GACTATACGC CCTTCAGCGA GCAGTTTCGG      960
AACCCTCGGG GGGAATACGT CAGTCTGAAT CTGAGTATCC CCATCTTTTC GGGATTACAG      1020
CTGTGTAGCC ATCTGCGTCA GCGCGTGCC GAACGCGAGG CGGCAATCGT CCGACGGGGC      1080
GAAGCGGAGC GCAGGCTCTA CAGCGAGATC GCCCAAGCCA TGGCCGACCG GGATGCCGCT      1140
CTGGCTTCCT ACCGCCAGGC GAAGGAGCAT ACCGACGCCA TGCAAACCGC TTACGAAGCC      1200
GTCTTGACGC GTTATGAGGA GGGGCTGAAT ACGGCCATCG ACCTGACCAC TCAGGCCAAT      1260
CGGCTCCTGG ATGCCCGTGT GCAGCGACTG AGAGCGGCCA TGACCTACCG GCTCAAATGC      1320
AAACTCATAG CCTATTACGG CTGCCTTTTC GAC                                     1353
```

(2) INFORMATION FOR SEQ ID NO:72

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2886 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

```
GCCATTTTTC TCGTATCATT GCAAATTGAA AAAATAACAG AGAATAAGTA TAATTACAGAC      60
AAGAGCATGA ACAAATTTTA CAAATCACTT TTGCAGTCAG GACTGGCTGC CTTCGTGTCG      120
ATGGCAACTG CACTGACCGC TTCTGCACAG ATTTCTGTCG GAGGGGAACC CTTGAGTTTC      180
TCTTCAAGAT CCGCCGGAAC GCATTCAATC GACGATGCAA TGACTATCCG CTTACTCCG      240
GATTTCAATC CGGAAGACCT GATCGCACAG AGCCGTGTGG AATCGCAAAG AGATGGCCGG      300
CCGTTCCGGA TAGGACAAGT AATACCGGTG GATGTGACT TTGCATCCAA GGCTTCGCAC      360
ATCTCTTCCA TCGGAGACGT AGATGTATAT CGCCTGCAAT TCAAGTTGGA AGGAGCCAAA      420
GCCATTACGC TTTATTACGA TGCATTCAAT ATTCCGAGG GCGGACGCCT CTATATCTAT      480
ACCCCCGACC ATGAAATTGT GTTGGGAGCA TATACGAACG CCACTCATCG CCGCAACGGA      540
GCTTTTGCCA CAGAGCCGGT ACCGGGGAGT GAGCTTATTA TGGATTATGA AGTGTCTCGC      600
GGAGGGACTT TGCCTGACAT CAAGATCTCC GGTGCGGGTT ATATATTCTGA CAAAGTCGGC      660
GGACGCCCCG TAACGGATAA CCATTACGGG ATCGGTGAGG ACGATTCCGA TTCGATTGCG      720
```

GAGATCAACA	TCAATTGTCC	TGAAGGTGCA	GACTGGCAGG	CAGAGAAGAA	CGGTGTGGTG	780
CAAATGATCA	TGGTAAAGG	ACAGTATATC	TCAATGTGCT	CAGGCAACCT	GCTCAATAAT	840
ACGAAAGGAG	ACTTTACTCC	GCTGATCATT	TCTGCCGGAC	ACTGTGCTTC	CATAACAAACC	900
AATTTCCGTG	TAACGCAATC	CGAGTTGGAT	AAGTGGATCT	TCACTTTCCA	CTATGAAAAA	960
AGAGGATGCA	GCAATGGTAC	ATTGGCCATC	TTCCGTGGCA	ACAGTATCAT	CGGAGCTTCC	1020
ATGAAGGCTT	TCCTCCCGAT	CAAAGGTAAA	TCCGATGGTC	TCTTGCTGCA	ACTCAACGAT	1080
GAAGTCCCTC	TGCGCTATCG	TGCTATTAC	AATGGATGGG	ACAGTACGCC	CGATATTCCC	1140
TCGAGCGGTG	CCGGTATTCA	TCATCCGGCC	GGAGATGCCA	TGAAGATTTC	CATCCTAAAG	1200
AAGACTCCGG	CTCTGAATAC	ATGGATCTCC	TCCAGTGGTT	CCGGAGGGAC	TGACGATCAC	1260
TTCTATTTC	AATACGATCA	AGGTGGTACG	GAAGGAGGAT	CGTCCGGTTC	TTCTCTCTTC	1320
AATCGAATA	AGCACATGGT	CGGCACACTG	ACCGAGGTG	CCGGCAATTG	TGGCGGGACG	1380
GAGTTCTACG	GCAGACTGAA	CAGTCATTGG	AACGAGTATG	CATCCGATGG	CAATACGAGC	1440
CGCATGGACA	TCTATCTGGA	TCCCCAAAAC	AATGGCCAGA	CGACCATCCT	CAACGGAACG	1500
TATCGTGACG	GTTATAAGCC	TTTGCCCTCT	GTGCCCCGGC	TATTGTTGCA	GTCTACAGGC	1560
GATCAGGTCT	AATTGAATTG	GACGGCTGTT	CCTGCCGATC	AATATCCATC	ATCTTACAG	1620
GTGCAATACC	ACATATTCCG	AAATGGAAAG	GAAATAGCTA	CGACAAAGGA	GTGTCTCTAT	1680
TCGGATGCCA	TCGACGAAAG	TATTATCGGT	AGCGGTATCA	TTCGATACGA	AGTAAGCGCA	1740
CGCTTCATTT	ATCCCTCGCC	GTGGATGGA	GTGGAATCTT	ATAAGGATAC	GGACAAGACT	1800
AATCGCCACC	TGCCATAGG	AGACATTGAG	ACCAAGCTGA	AGCCGGACGT	AACACCTCTC	1860
CCCGGAGGAG	GAGTATCATT	AAGCTGGAAA	GTTCTTTTCT	TAAGCCAGTT	GGTTTCCCGA	1920
TTCGGAGAAA	GCCCCAATCC	TGTGTTCAAA	ACCTTTGAAG	TGCCCTATGT	TTCTGCCGCA	1980
GCCGCACAAA	CCCCCAATCC	TCCCGTTGGC	GTAGTCATTG	CAGACAAGTT	TATGGCCGGT	2040
ACATATCCCG	AAAAGGCTGC	TATCGCTGCC	GTTTATGTAA	TGCCATCCGC	TCCGGAATCT	2100
ACTTTCCACC	TCTTCTCAA	GAGCAACACA	AACAGAAGAT	TGCAGAAGGT	GACAACTCCC	2160
TCCGATTGGC	AGCCCGGAAC	ATGGTTGAGG	ATCAATTTGG	ATAAGCCGTT	CCCGGTGAAT	2220
AATGACCATA	TGCTTTTTCG	CGGTATCAGA	ATGCCTAATA	AGTACAAGCT	CAATCGTGCT	2280
ATCCGTTATG	TAAGAAATCC	GATCAACCTT	TTCTCCATTA	CCGTAAGAA	GATTTCATAT	2340
AACAACGGAG	TCTCTTTCGA	AGGCTACGGA	ATACCCTCGC	TCTTGGGCTA	TATGGCTATC	2400
AAATATCTGG	TGGTAAATAC	CGATGCTCCG	AAGATCGATA	TGTCGCTTGT	ACAGGAGCCT	2460
TATGCTAAGG	GAACGAATGT	GGCTCCATTC	CCCGAATTGG	TCGGCATATA	TGTCTATAAG	2520
AACGGAACAT	TTATCGGCAC	ACAGGATCCA	TCCGTCACAA	CTTATTCCGT	TTCAGACGGA	2580
ACAGAGAGCG	ATGAATACGA	AATAAACTG	GTATATAAGG	GATCGGGCAT	TTCGAATGGC	2640
GTTGCTCAGA	TTGAGAATAA	CAATGCTGTC	GTGTCATATC	CGTCTGTTGT	AACAGATCGT	2700
TTGAGCATTA	AGAAGCTCA	TATGGTTCAC	GCTGCCGCC	TCTACTCATT	GGATGGCAAG	2760
CAGGTTCCGT	CTTGGAACAA	CTCCGCAAT	GGCGTGACAT	TCAGTGTTCA	AGGACTTACG	2820
GCCGTTACTT	ATATGCTCGT	TATGCAGACG	GCAAACGGCC	CTGTGAGCCA	AAAGATCGTG	2880
AAGCAG						2886

(2) INFORMATION FOR SEQ ID NO:73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

TGGAAAAAAA	GTAATCCTCA	ATACCGGGGC	AGGACAGCAA	ATTACCGAGA	TCATTATAAT	60
ACAGAAAGCT	ATTTAAGCCT	AAGGAGGAAT	CAACAATGA	AATATCTTAT	CAGACTCTTC	120
TTATCATGTA	TGTTACTCTC	TCTCTGGACG	GGCTGTACAC	ACGAGGAGCT	CTCTATTTGC	180
GATGGCGAGA	ATACGCTTGT	TTTACGCGTA	GAGACCGGTA	AAGCCCCAAA	TGCTCGTGCC	240
ACAGAACCCG	GTGAGGGCAT	ATACAATGAG	AATAAAGTAG	GCTCCATTTC	TGTGCTCTTC	300
TATTTAGAGG	GACAACTTCG	TTGGCAGGTG	AAGTCTACAG	ACTATCAAAT	CCATGAAGGG	360
GCCTATATCA	TTCCGGTCAA	AGAGCAAATG	CGACCACTAT	TCATGGGCAA	CAACAACCTC	420
AGCATCTATG	TAGTGGCCAA	TCTCGATTTC	AATGCTCCGG	CCACAGAAGC	TGCGCTTTCT	480
CAATTTGTGG	TAGAGAAATC	TATTGAAGTC	TCTTCTACGA	CAGCCCCGTC	CGATTTCGTA	540
ATGCTTGCTC	ATGGCAATAA	GCAGATCAAT	ATGGCTACGA	CAGAAGGGAA	ACTGTTGGGG	600
GATTATAAAC	TCAAACGAGT	GGCAGCAAAG	ATTCGCATGA	TAAAACCCAC	CATCAATGTG	660
CAAGGATATG	AAGTGGTCGG	AAATATACAG	GCAAAGTTTC	GCAATTCCGGT	AACGAAGGGG	720
TTCTTTACCA	CAGAAGCTCA	AGAGATCCCA	GCTGCTGCAT	CCTATAAGAC	ATCGGAATAT	780
CTTGATATTG	CAGAGTCGGC	ACCTGCCAAT	TCTATCCATT	TCTATTCTTA	CTATAACAAA	840
TGGACACTCT	CCACACCGGA	GAAGCGACCG	GAATTCTTCA	TCATGGTCAA	ATTCAAAAAG	900

ACAGGACAGC	CGGACAACAC	AGCCAAACCG	TACTACTACA	GAGTGCCCT	CGAATCTCAG	960
GACAATCAGG	TCAAGAGCAA	TGTCCTCTAT	AATCTGAATG	TGAAAATCGA	AATCTTGGGT	1020
TCTTTTCAAG	AGCCGGAAGC	TGTTTCTGTA	AACGGCACAC	TCGCAATAGA	AGAATGGATT	1080
CTCCATCAGG	ATGCATTCAA	TCTGCCTGCC	ACCAATTACT	TGATAGTGGA	ACAGCACGAA	1140
ATCTTCATGA	ATAACGTGAA	CACATACTCG	GTGAAATATC	AAACTTCGCA	GAAACCAATC	1200
AGCATTAGCA	TACAGTCAGT	TACCTTTAGC	TACGTCTCTT	CTGATGGCAC	TCAGCACAAT	1260
GATCTTGTAG	CAAGTAGTAG	CGACCAATAT	CCTACGATTA	CAAGCGATAA	TACAAGCATC	1320
ATAATCACTT	CCAAGATACC	GGTTAATAAC	GTACCAAAGA	AGATCGTTTT	TGAGGTAAC	1380
AATGGGGTAG	CCGGTTTGAA	AGAGACTGTC	ACAGTACTCC	AATATCCTGC	ACAATTTATT	1440
GTCAATACAC	TTGGCACAGC	ATCGGCATGG	AGACCAGACG	GATCTTTGGC	TCCGGGGCTT	1500
AACAATAAAG	CGATTTACCA	TGTCGTAGTA	CTGGTTCCAC	CCGAGAATTT	ATTGAAGAT	1560
GGGACACAGA	CAATCATCGG	TTATCCCCC	ACTGAAACAA	TTTCTTTTCA	TAAGAAAGAG	1620
AACAATACCT	ATCCGATAGT	ATGGTCTGAC	ACAAATACGA	CAAAACAGGA	CCTTGAGACA	1680
TCAAGAATGA	TTTACCTTC	CTTTGAGTTA	GCCTCCCAAC	TTGGGGCTAC	TCTCCCGATG	1740
CCCTATCTCG	AGTATTGGCC	AGGGACATCA	TATCTCCTTG	ACTATTCTGG	AAACTATAAT	1800
AATAAGAGAT	ACGCCTTGTT	TAATTGCGCT	TTTACTGGG	AGAAAAGAAA	AGTTAATAAC	1860
GAAGAAATTA	AATTCGATGA	CTGGCGTTTG	CCGACAGAAG	CTGAGATCAA	ATTGATAGAT	1920
AAGCTGCAAC	ATAATGAGCA	GAGTGCTGTC	CAAGCTATCA	TGACAGGGAA	TTATTATTGG	1980
GATAGTTACT	CTGCAATGG	CTTTATATAA	ATGCAAGGAG	GAGGGGGCCA	AGGAAATTC	2040
TCCAAAGCCT	ATGTTTCGTT	CGTGCGGGAT	GTGAAAAGC	CGATTCTGTA	CAAGAAGTCA	2100
GGTAAG						2106

(2) INFORMATION FOR SEQ ID NO:74

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

AAGAGGGTAG	ATAGCTATGA	ATGCAGACAA	AAAGCTTGCA	AATGTGCAAT	TTGTGTGATA	60
CAAAAATTTA	CTAATGTAAA	ACTAAATGAT	ATGCGAAAAA	TTTTGAGCTT	TTTGATGATG	120
TGCTCTCTGC	ATTTAGGTCT	ACAATCTCAG	ACTTGGCATG	GAGATCCGGA	CTCAGTGCGA	180
GCCTACCTT	CTATCGGTAT	TCAAGAGTCA	AGTTGTACCC	GAATCACGTT	CGAGGTTGTT	240
TTCCCGGAT	TTTATAGTGT	GGAAGAAACGA	GAAGGCAACC	AAGTCTTTCA	GCGCATTTC	300
ATGCCGGGTT	GTGGCTCGTT	TGGGAATCTG	GGCGAAGCTG	AATTGCCTGT	TTTGAAAAAG	360
ATGATAGCCG	TTCCGGAATT	TTCAACAGCT	AACGTTGCTG	TAAAAATCAA	AGAGACGGAG	420
ACATTCGACA	ATTATAATAT	CTATCCTAAT	CCTACCTATG	TCGTAGAGGA	GTTGCCTGAG	480
GGGGGGACTT	ATCTGGTATG	GGCTTTCGCG	ATAAACAAATG	ACTATTATAG	CCAAAATGTA	540
AGCCTCCCTT	CTACTACTA	TGCTATTCT	CAAGACGGGT	ATTTTCGCTC	ACAAAGATTT	600
ATCGAAGTTA	CCCTGTATCC	TTTTCGATAC	AACCTGTGCC	GACAAGAAAT	TCTATTTGCA	660
AAAAAATTCG	AGGTTACAAT	AACTTTTCGAT	AATCCTCAGC	CACCTTTTACA	AAAAACACC	720
GGCATATTTA	ACAAAGTAGC	CTCCTCTGCA	TTTATTAATT	ATGAAGCTGA	TGGCAAATCG	780
GCGATAGAAA	ATGATATGGT	GTTCAAGTCG	GGTACAACAA	CGTACATAAG	CGGAAATGTT	840
GCCAGCAACC	TCCCTCAGAA	CTGTGACTAC	TTGGTTATTT	ACGATGATAT	GTTCACGTA	900
AATCAACAAC	CACACGACGA	AATCAAACGG	CTGTGCGAAC	ATAGAGCCTT	CTACAACGGC	960
TTTGATGTAG	CTCTGTGTAG	TATAAAGGAC	GTATTGAATA	GCTTCCCATC	AAATGCCACC	1020
TCATACATCA	ACGAAACTAA	ACTGAAAAAT	TTCATTTCGCT	CAGTTTACAA	CCAAAGCAAT	1080
GCGAAGAGGA	CTTTAGATGG	CAAACTGGGA	TACGTGCTAC	TGATCGGAAA	ACCATGAGC	1140
AAATATTTGG	CTGACACTGA	TAATACAAAA	GTCCCAACCT	CTTTTATTTCA	TAATGTCTCC	1200
TTAATTTCCA	ATCTGCTCAAT	TTTGTGTTCC	ATATGCGCCT	CCGACTATTT	TTTGTAGTTG	1260
GTTCGCCCC	TTGATACTGT	CGCGGATTTG	TTTATCGGTC	GATTTAGCGT	CACCAATGCT	1320
CATGAATTGC	ACAATCTGAT	TGAAAAGACT	ATCAACAAAG	AAATCTCATA	TAATCCTATT	1380
GCACACAAAA	ATATTCTTTA	CGCAGAAGGG	AAAGGCTGCG	ATGCTCCAAT	CTTACGTTTA	1440
TTCTTAAAAG	AAATCGCCTC	TGGTTACACA	GTCAACTCTA	TCTTAAAAATC	TAATCAGGTC	1500
TCTGCAATAG	ACTCGATATT	TGACTGCTTG	AATAATGGTT	CCCATCATTT	TTATTTTAAC	1560
ACTCATGGAA	TGCCGACTGT	TTGGGGGATA	GGGCAGGGAC	TCGACGTCAA	TACTCTAACA	1620
GCCCGATTGA	ACAATACATC	TTTCGAGGGA	TTATGTACGA	GTCTATCATG	TAGTTCGGCT	1680
GTAGCAGATT	CAACTATTAG	ATCGCTTGGA	GAAGTCTCTG	CCACATACGC	ACCTAACCAAG	1740
GGATTCTCGG	CTTTCTTAGG	AGGAAGCAGA	GCCACCCAAT	ATGCCGTTTA	TTTAGAAGGC	1800
CCCTGTCCTC	CGTCAGAATT	TTATGAATAT	TTACCTTATT	CTTTATATCA	CAATCTCTCG	1860

ACTGTTGTTG	GCGAAATGTT	GCTATCATCC	ATTATCAATA	CTAATTCTGT	TGATACGTAT	1920
TCGAAATTCA	ACTTCAATTT	GCTTGGCGAC	CCTGCACTAA	ACATTATGGC	TCATGGCATG	1980
GAGGTTAGTA	ATTGTATTAC	ACTACCAAAC	AACACCATTA	TAAGCAGTCC	GATAACAATA	2040
AAAAATGGTG	GCTGCCTAAA	AATACCGGAA	AAAGGAGTTT	TGCATTTTAC	TAATAATGGC	2100
TCCATACAAG	TCATGTCCGG	AGGAACTCTG	GAAATAGGCA	ATCAGGCTAA	AATATCCGGA	2160
GAGACCGGTG	CTAACCCAC	CTTTATTACC	GTTTACGGCG	ATGGTCTTGC	GATTAACAAG	2220
CAGGTAGAGA	TAGACAATAT	AGACCGACTT	AACCTTGTTT	CTACGCATTC	GGTCATGCC	2280
AAATTTTCATT	TTGACAGTGT	GAAATTCAAC	AGTGCCCCGC	TGTATACAAC	GAAGTGTATT	2340
GTGGAGATAA	GCAATTGCGA	ATTTACCAAT	CGAAGTGACA	TTATTTCAAA	GAATTGTGAC	2400
CTAAGCGTTG	AAAACAGTAT	GTTTAGCAGT	TCGGGGATAA	CGGTATTCAA	GCCTATGGCT	2460
ACAAGCTCCA	TCACCGGATT	ATCTACAAAA	GCAAAGATTA	CCGACAATAC	TTTTTTTTCG	2520
ACAGGAAACT	TCGCCTACCA	TATCACAAAC	ACGCCAGGCT	TAACAGCAAC	CTCCAATGCT	2580
GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	TACATTTCCG	GTAATAAAAT	AGTCAATTGC	2640
GATGAGGCTC	TTGTACTAAA	TAATAGTGGC	AACAGAACGA	ACAGACTCCA	CAATATCACA	2700
CGGAATGTGA	TAAAAAAGT	TAGGATTGGG	AGCACGCTTT	ATAATTCTTA	TGGTATTTAC	2760
AACCGAAATA	AGATCAGTAA	CAATCATATA	GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	2820
TATTTTCGATA	ATGCTCCTGT	AATCAATGAA	GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	2880
ACTTGGCAGC	TCTATTTCATC	AAACGGTACA	TTCCCTCTCA	ACTTCCATTA	CAACAGCTTG	2940
CAGGGGGGAG	ATCGGATGAT	AACGATTTAC	AACGACACGT	ATACGAATCG	CTATATTGAC	3000
GTTTCAAATA	ATCACTGGGG	CAACAATGAT	TTGTTTGATC	CGAATCAGGT	TTTCAATACG	3060
CCAGACTTGT	TCATTTGGAT	ACCTTTTTTG	GATGGATTGC	CAAATGGGAG	ATCGGGCAAT	3120
AGCTCTGCTG	AAGCAGTAGA	ATTCCAAACA	GCATTGGACT	GTATTGGCAA	TAGCGATTAT	3180
CTTTCGGCAA	AAGTGGTCT	CAAGATGATG	GTGAAACCT	ACCCGGAATC	CGACTTTGCA	3240
ATAGCTGCTT	TGAAGGAATT	GTTCAGGATA	GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	3300
TTGAAAGATT	ATTTAGATC	CAATCCAACC	ATCATCTCTT	CCCAGAACTT	GTCCCGACA	3360
GCTGATTTCC	TGTCTGCGCG	ATGCGATATT	GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	3420
TGGTAGGAAA	ATCGCTTGA	TAGTGAATC	TCCTATCAGG	ACAGTGTTTT	TGCAGTCATT	3480
GACCTTGGTG	ACATTTATTG	GAATATGCAG	TTAGACTCAC	TCAGAGGGAC	TGGTATAGAT	3540
TTGAACATAC	TTTCTGTGA	ACAAAGGAAA	TCGCTCGAAA	GCCATCAAAA	TGTAATAAAT	3600
TATTTGTTGT	CAACTCTTCC	CGAATCAACA	GGTACTCTCC	TGCTCCATT	AGAATGCAAC	3660
AAATCAAGCC	TTGATAAATC	CAAGATAATC	TCTATTTTCG	CCAATCCGGC	GAAAGCTGTT	3720
GTAACAATAA	TCTACTATAC	CGATAACCCT	TCCTGTTCTG	TAATAAATAA	ATATGGAATA	3780
AATGGAGCCT	CGGCTGATAT	AACCGGGTTG	CCCAAACATC	TATCCGAAGG	TTATTACAGC	3840
ATACAGTTCA	ATACATCCAA	CTTTGATCCC	GGTTTCTACC	TGTAACGCT	AAATGTTGAT	3900
CAGAAAATTA	TAGATACGGA	AAAATTACGA	ATCAAA			3936

(2) INFORMATION FOR SEQ ID NO:75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

TCAGAAAATT	ATAGATACGG	AAAAATTACG	AATCAAATAA	TGGCTATCAT	GATGAAAAGT	60
ATTGTTTTTA	GAGCATTTCT	AACGATTTTG	CTCTCGTGGG	CAGCGATCAC	GAATCCGACT	120
GCTCAAGAGA	TCTCAGGCAT	GAATGCATCC	TGTCTGGCTG	CTCCGGCTCA	ACCGGATACT	180
ATCTTATATG	AAAGTTTTGA	GAATGGACCT	GTTCCCAATG	GCTGGCTTGA	GATAGATGCT	240
GATGCTGATG	GTGCCACTTG	GGGAAGCCCA	TCAGGCTCTT	TCTCTGTACC	TTACGGACAC	300
AATGGCCTTT	GCACCTACTC	CCATATACGT	TCCGGTATCT	CAACAGCGGG	CAACTATCTG	360
ATTACACCCA	ATATAGAAGG	AGCCAAACGG	GTCAAGTACT	GGGTATGCAA	TCAGTATAGT	420
ACCAATCCGG	AACATTACGC	AGTAATGGTA	TCGACAACGG	GGACTGCCAT	TGAAGACTTT	480
GTTTTGTTGT	TTGATGATTC	CATAACAGGG	AAACCGACTC	CTCTTGATG	GCGTAGACGA	540
ATCGTGGACT	TACCGGAAGG	GACCAATAT	ATTGCATGGC	GACATTACAA	AGTACCCGAC	600
TCACACACAG	AATTCTTGAA	ATTGGATGAT	GTCACTGTGT	ATAGGTCGAT	CGAAGGGCCC	660
GAACCTGCTA	CCGACTTCAC	AGTAATCAAT	ATTGGTCAGA	ATGTGGGACG	ATTGACTTGG	720
AACTATCCGG	AGGATTATCA	ACCGGAAGGA	AAGGGGAATG	AAGAGTTGCA	GCTTAGCGGC	780
TACAACATCT	ATGCGAACGG	TACACTACTG	GCACAAATAA	AAGATGTCTC	CATACTGGAG	840
TATGTGGACA	GCACTTACTC	TTTGCGAGAC	AATCCCTTGC	AAGTGGAGTA	CTGCGTTACA	900
GCCGTTTACG	ATGAAAGCAT	AGAATCTTCG	ACCGTATGTG	GCACGCTGCA	TTACGCCACG	960
GATGCCATCC	TTTATGAAAA	TTTTGAGAAT	GGACCTGTTC	CCAATGGTTG	GCTTGTGATA	1020

GACGCTGATG	GAGATGGATT	TAGCTGGGGA	CACTATTTGA	ATGCATACGA	CGCTTTTCCC	1080
GGCCATAATG	GAGGCCATTG	CTCCTTGTCG	GCTTCTTATG	TTCCGGGTAT	AGGCCCGGTG	1140
ACTCCCAGCA	ACTATCTGAT	TACCCCCAAG	GTGGAAGGAG	CCAAACGTGT	CAAGTACTGG	1200
GTAAGCACGC	AGGATGCCAA	TTGGGCAGCG	GAACATTACG	CGGTGATGGC	TTGACAACG	1260
GGGACTGCTG	TCGGAGATTT	CGTCATATTG	TTCGAAGAAA	CCATGACAGC	GAAGCCGACC	1320
GGCGCATGGT	ATGAAAGAAC	CATCAACTTA	CCTGAAGGGA	CTAAATACAT	CGCATGGCGG	1380
CATTACAAC	GTACCGATAT	ATATTTCTTG	AAGTTGGACG	ATATCACTGT	ATTGCGGACT	1440
CCTGCATCAG	AGCCCGAACC	TGTTACCGAT	TTCGTTGTCT	CGCTTATTGA	AAACAACAAG	1500
GGACGATTAA	AGTGGAATTA	TCCTAACGGC	TACGAACCCG	ATAAGACTGA	TGATAAAGAC	1560
CCATTGCAGC	TTGCCGGCTA	CAATATCTAT	GCAAACGGCT	CGCTCCTTGT	TCACATACAA	1620
GACCCGACTG	TTTGGAGTAT	TATCGATGAG	ACTTATTCTT	CACGAGACGA	TCAGGTGGAA	1680
GTGGAATATT	GTGTCACTGC	CGTTTATAAC	GACAATATCG	AGTCCCAATC	GGTTTGCGAT	1740
AAGCTGATTT	ATGATTCTCA	ATCGGACATT	ATCTTATATG	AAGGCTTTGA	GGCCGGAAGT	1800
ATTCTGAAG	GCTGGTTGTT	GATTGATGCT	GATGGCGACA	ATGTTAATTG	GGACTATTAT	1860
CCTTGGACTA	TGATGGACA	TGACAGTGAG	AAGTGTATTG	CATCCCCTTC	GTACTTACCG	1920
ATGATTGGCG	TTTAACTCC	GGATAACTAT	TTGGTTACAC	CCAGACTCGA	AGGAGCCAAG	1980
CTTGTCAGT	ATTGGGTAA	TGCGCAAGAT	GCTGTTTATT	CGGCTGAGCA	TTATGCTGTG	2040
ATGGTTTCTA	CTACGGGAAC	TGCTGTTGAA	GATTTTGTCC	TCTTGTTCTGA	AGAGACAATG	2100
ACCGCTAAGG	CTAACGGTGC	TATGGTATGAG	CGAATATTA	CATTGCCTGC	AGGAACAAAA	2160
TATATTGCCT	GGCGGCATTA	TGATTGCACC	GATATGTTTT	TCTTGCTCTT	GGATGACATT	2220
ACGGTTTATC	GTTCTACTGA	GACTGTTCCC	GAGCCTGTTA	CTGATTTTCG	TGTCCTCGCTT	2280
ATTGAGAATA	ACAAGGGTCG	CCTGAAATGG	AATTATCCTA	ACGGCTACGA	ACCCGATAAG	2340
ACTGATGATA	AAAAACGATT	GCAGCTTACC	GGCTACAACA	TCTATGCAAA	TGGCTCGCTC	2400
CTTGTTTACA	TACAAGACCC	GACTGTTTTG	GAGTATATCG	ATGAGACTTA	TTCTTCACGA	2460
GACGGTCAGG	TGGAAATGGA	ATATTGTGTC	ACTGCCGTTT	ATAACGACAA	TATCGAGTCC	2520
CAATCGGTTT	GCGATAAGCT	GAACATACT	ATCACATCCT	TGGATAATAT	TCAATCTGAT	2580
ACAAGCTTGA	AAATATATCC	TAAATCCGCA	TCGTATGTGG	TAAGGATAGA	GGGATTGAGT	2640
CGGAGCAAGT	CGACAATCGA	GTTGTATAAT	GCGCTGGGAA	TTTGCATATT	AAGGGAAGAG	2700
ACTCATTCAG	AGAAAACCGA	AATCGATGTT	TCACGTCTCA	ATGACGGAGT	CTACTTGATT	2760
AAAGTAGTCG	GTGGAATAAA	AACAACAACC	GAAAAGGTAG	AGATAAAGAG	GCCG	2814

(2) INFORMATION FOR SEQ ID NO:76

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

ATAATCTTCT	GTACGATTCA	TCACTCTGAG	TTGGAAATAA	TGAACAGCAT	CATGAAATAT	60
CAATTATATA	CGGCCGTCAT	AATGGCTCTC	TCTGTATCAT	CCGTTTGCGG	TCAAACCCCA	120
CGAAATACAG	AAACCAAACG	CCCCGACACG	CTGCGCAGGG	AGCTTACTAT	CGTTAATGAC	180
CAGACTGTGG	AGATGGAGCA	TGCGGATCCG	CTTCCGGCTG	CATACAAGGC	CATCGAACCT	240
CGATTAAAAC	CTTTCGCTCC	GGAATATAAC	AAGCGTACAT	TCGGATTTGT	CCCTGAAGTT	300
TCCTCTTCAG	GCAGGAACAA	TCTTCCGAAT	ATCCTGCCGA	CGGAAGGTCA	TATGAAGCAC	360
CGGGGGTACC	TGAATATCGG	TATCGGCCAT	ACGCTAAACC	AGCGAATGCA	TGCCGGCTAT	420
CGTCTGATAG	ATGCAGAGCA	GGAGAGACTG	AATCTTTTCC	TCTCCTATCG	TGGGATGAAA	480
TCGGCTTTCA	ATACCGGTGA	CTTCGACGGC	GACAGAAAGG	ATAGACGAAT	GATGGCAGGA	540
GTGGACTACG	AGCAGCGCAG	GCCTTCCTTT	GTGCTTGCTA	CCGGCTTGTA	TTATTCTGAAC	600
CATTATTTCA	ATAACTACGG	ACGGGGAGCT	ACCACCAATG	TGGGCAGCAT	CCCTCAGCTA	660
TCGACACCTG	TTACTCTCTA	GATGACAAC	GGGACCCACA	ACGTCCGTGT	ATACTTGGGT	720
GCAAAAAATG	ATGTGATCGA	TGCCAGGATC	GACTATCGTT	TCTTCCGTTC	TATTCCCTAT	780
CTGGGTACCG	ATCCGATGAA	GGCTCTCACA	GAACATACGC	CTGAACGTAA	CGTGACGATG	840
AGTAATGAGT	TGTCCGATGA	TATTAAGCTC	GGTGTCTGAAG	TTCTGACGGG	AGGATTGTTT	900
TTTGCCAAAA	ACAGCGAAAT	GATTCAAACG	GGCGTTCTGT	CCGAAACCGA	CCGCAACCTG	960
TATTATGTGG	AGGGCGCGCC	CACAATCGGA	TTTGTCTGGAG	ACTCGGACAA	TATGCAATGG	1020
AACATACAGG	CCGGAGTAGG	GATTTCTTCC	CATTTCTGGAG	CCAAAGGGAG	GTGTTTTC	1080
TGGCCTAAAC	TGGATGCTTC	GCTTAGTATC	TTCCCTTCAT	GGCGTGTGTA	TGCGAAAGCC	1140
TTCCGGCGGTG	TGATTCGAAA	TGGTCTCGCC	GATGTTATGC	AAGAGGAGAT	GCCCTACCTG	1200
ATGCCCAATA	CGATTGTACT	CCCTTCGCGC	AATGCTTTGA	CCGCCCAATT	AGGGGTGAAG	1260
GGGAATATAG	CCGATGTGGT	ACGTATGGAG	GTTTATGGCG	ACTTCTCCAA	GCTGACAGGT	1320

GTGCCTTTCT	ATACTCCGAC	TCTACCCTTA	TATAATCCAT	CCGACTTGTA	TCAGTATAAT	1380
GTGAGTTTCT	TGCCGATATA	TGCCGACGGC	AGCCGCTGGC	GCGCAGGTGG	TAAGCTGGAA	1440
TACTCTTATC	GCGATATGCT	CCGCTTTCTG	GTAGACGCAT	CCTATGGCAA	GTGGAATTG	1500
GATGGAGGAC	TTGTCGCCTC	CATGCAGCCC	GATCTTATAT	TGAAGGCAGA	AGTAGGTGTT	1560
CATCCCATTG	CCCCATTGGA	TGTCAGACTC	CGGTATACAC	AGCTGAACGG	ACGGTATCGG	1620
TATTCTTTTCG	GCTCGGCTGG	CTCGGAAGCC	TTGGGTATCG	GTAATGTACA	TCTTCTTAGT	1680
GCGGATGTTT	CATACAAGCT	GAAAAAGAAC	TTGAGCCTTT	ATCTCAAAAT	CGATAATATG	1740
CTGGCGGAAA	CGACAGAGCT	TATCGGTTAT	TATCCTATGC	AGCCGTTCCA	TTGTTTCGCC	1800
GGTTTTAGCT	GGACTTTC					1818

(2) INFORMATION FOR SEQ ID NO:77

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1071 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1071
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

AACTCCCATG	CAACAGTCTC	CGTTATATGT	TCAATGATGG	AAAAATGTAT	CTTGCTCAC	60
TATCCACATA	ACCTTGTTG	CATGATTCGC	AAGCATTTTCG	GTATCATTTT	GGGATTTCTT	120
TCTCTTGTGT	TTTCGGCAGG	TGCTCAACAA	GAGAAGCAGG	TGTTTCATTT	TCTGAACCTT	180
CCGGCTACTG	CACAGGCTTT	GGCTGCCGGA	GGCAAAGCTA	TCACCATCGT	AGACGACAA	240
CCCGGACTGG	CTTTTGAGAA	TCCGGCTCTG	CTCGGATATG	AATCCGGTGG	CCGCGCCTTT	300
CTTTCCTATT	TATATTATAT	GAGTGGTTTCG	CATATGGGCA	ATGCCTGTTA	TGCTCGTCC	360
GTCCGAGAGC	GTGGCATGTG	GGGTGTTGGC	ATGCGTTTCC	TGAACTACGG	GTCTATGCAA	420
GGATACGATC	AGAATGCGAT	TGCCACCGGC	TCTTTTAGTG	CTTCGGATAT	AGCTGTACAA	480
GGATTTTACA	GCCATGAACT	GAGCAACCAC	TTCCGCGGTG	GAGTCAGCCT	AAAAGCATTG	540
TATTCTTTCTA	TCGAGACGTA	TAGTTCCCTT	GGCCTTGGTG	TGGATGTCGG	TATCAGTTAT	600
TACGACGATG	ACAAAGGATA	TTCCGCTTCC	GCTCTGTTCA	AGAACGTAGG	GGCGCAACTG	660
AAAGGCTATA	ATGAAGAACG	GGAACCGCTC	GATTGGGATT	TCCAGCTCGG	CTTTTCCCGC	720
AGTTTTATCA	ATGCTCCGTT	TCGCTTGAC	ATCACGTTGT	TCAATCTGAA	TCCGCACTAT	780
TTCAAGCGTC	TTGTACCACG	CGATCTGTCC	AAGATGCAAA	AGTTCTCTCG	ACACTTCTCG	840
ATAGGAGCAG	AATTTACTCC	TTCCGAGAGG	TTTGGGTCG	GGCTGGGATA	TACGCCACAG	900
ATTGCACAGG	ATTTTCGAGG	GGAAGGCGGC	AACAAATGGG	GAGGTCTTTC	GGCCGGCGTC	960
GGTTTCACTT	CAGGTGTAGT	ACGTGTAGGC	GTATCTGCTG	CCACCTATCA	TCCTGCAGCT	1020
CTTTCGTTCA	TGTGTTCCGT	AGGTATCCGT	TTGGACGATA	AGAGCATCTT	C	1071

(2) INFORMATION FOR SEQ ID NO:78

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1011
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

CCTCAGCCCG	TCGGCCTTAA	AGAAATAACC	ATTAAACCCA	TGTGCCTCGA	ACCCATAATT	60
GCTCCGATTT	CATCCGAGTT	GCTCGAGCAG	GAGCTGACTG	CCGATCGTTT	TCTGCGGATG	120
ACAAACAAG	CCGGCAATGA	GATCTATGTT	TTTACGGCCG	AAGAAGCTCC	GCATTGCATG	180
AAAGAAGTAG	GCCGACTGCG	AGAAGAAGCC	TTTCGGCATT	ATGGCGGAGG	TACTGGCAAG	240
GCGATCGATA	TAGACGAGTT	CGACACCATG	CCCGGGAGCT	ACAAACAGCT	GATCGTATGG	300
GATCCGCAAA	ACAAGGCTAT	ACTCGGAGGC	TACCGCTTTA	TCTATGGGCG	GGACGTTGCT	360
TTCGATACCG	ATGGCAAGCC	TTTGCTGGCA	ACGGCAGAGA	TGTTTCGCTT	CAGTGATGCT	420
TTTTTGCACG	ATTATCTCCC	CTACACAGTC	GAATTGGGAC	GTTCTGTTCTG	GTCGCTCCAG	480
TACCAATCGA	CACGGATGGG	CACAAAGGCC	ATTTTGTGTC	TGGACAATCT	TTGGGACGGT	540
ATCGGAGCAC	TCACTGTAGT	CAATCCAGAG	GCACTCTATT	TCTATGGCAA	GGTGACCATG	600
TACAAAGACT	ATGATCGGCG	AGCTCGCAAT	CTGATCCTGT	ATTTTCTTCG	CAAGCACTTC	660
TCCGATCCGG	AAGGCTTGGT	CAAGCCTATT	CATCCCCTAC	CGATAGAGAT	CAGTGCGGAG	720
GACGAAGCCT	TGTTCTCCTC	ATCCGACTTT	GACACCAATT	ACAAGACTCT	CAATATAGAA	780
GTGCGCAAGC	TGGGTATCAA	TATCCCTCCT	CTCGTGAGTG	CATATATAGC	TTTGTCTCCG	840
GAGATGCGTG	TTTTCGGCAC	TGCAGTGAAT	GAGTCTTTTCG	GAGAGGTGGA	GGAAACCGGC	900
ATATTCATTG	CTGTGGGTAA	GATCCTGGAA	GAGAAAAAAC	AACGGCACAT	AGAGAGCTTC	960
ATCCTCAGCC	GGAACGAAAA	AAAAGGTCTC	GACAGTAGCA	ATGGCCGATC	A	1011

(2) INFORMATION FOR SEQ ID NO:79

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1698 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1698
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

TACGACGGAG	CGAGACTGGT	CTATACCCTA	TTTCGGAATA	GAAACGACAT	TCACCCCTATG	60
AAAACCATTG	TAAGATACAG	CCGCCCTCCG	GTCGCTCTCT	TCTTTTGCCT	TTTGGGAGCT	120
GTGCACCTGT	CTGTCGAGGC	GCAGATGCTC	AATACTCCTT	TCGAGCTGTC	GGATCAGATC	180
GTCTGTCTC	CCACCGAAAG	GCAATACAGG	GAGATTTGTG	TGCAAACGAA	AGAAAAAAGG	240
GGGGCCGATC	TTTTCCCGTT	GAGCGATAAG	CTGCGCGATT	CGGCCTATGT	TCGTTTCGGC	300
TCGGCCTATG	GCGATATTGC	GGGCGACTAT	CTTCCGTACA	ACGGCAATAA	CTACTCCTCG	360
CTCTCGCTCG	AATCGGGTGG	TCCGATCAGT	GTCGTAAC	ATGGCACATT	GCAGGGCAGT	420
GCTTCCTACT	CACGTGGCAT	GCACAAACGC	ATCGGCTGGA	ATGCTCTGCG	CAACGCCGAA	480
GCCTACTATC	CCTATTTGGT	GTCCGATTCT	ACCGGCGGAG	ACTATCATT	CGAAGACTAT	540
CGGCTTGCCG	GCTACTATTC	TTTTCGCGCC	GGCCGCTTGC	CCCTCGGTAT	AGGCTTCTCA	600
TACAGGGGCG	AAGTTGCTTA	TCCGCTGACC	GATCCGCGTA	CGACCAATAC	GACCGGTGCA	660
TTGGAGCTTT	CTTGTGCTAC	CTCTTTGACG	CTGCCTCGAG	AGAACAGGCT	ATCGCTTTTC	720
GCTGCGTATC	TCTATCATAG	ACAACACCTC	ACACAGTACA	ACTGGCGTCC	CGGGCAGCAG	780
GACAAATTCT	TCGTCAGCTA	CGGTTTCGGT	CAGGTGGATG	TCAGCAACAG	CCCTATCTGG	840
TTCGGTATCT	CCAGAATGAA	CTACGTCAAC	GGATGGAAGC	TTAGCTCCCG	TCTGGATACC	900
CGTAGGGGCG	ATGCCATCGG	TCTCGACTAC	AGCGGCTACT	TCCTCGATAC	CGAAGAGAGG	960
TCGTCCATCA	ATCTCTTTTG	TTTGCTTTAC	AATCGCCTGC	GACTCTATGG	TAGCTGGCAT	1020
CTGTCCGACT	TCGATTTTTC	ATTTTCAGCC	GACTATGCTC	TGCGCCAAGG	GATAGAGCGG	1080
ATATACGAAG	ACTACAAGCC	GGATGATAAT	TATCATATCT	ACGACCTCCG	TATCTTGGCC	1140
ATTCGCCGCT	GGTATATGCT	CAATGAGTTT	TCTGCCCAAG	CCCAAGCCTC	CTACCGTATT	1200
CGCACGGATA	GAGGTTGTGC	CCTGAGAGTG	AGTGCCGGTA	GTGATTTCTA	CGGCTATGAT	1260
GAGACGTATC	GCAAGCATGG	ACATCATACC	ATGAGCGGAA	TGCTACGTCC	TTTTGCCGGT	1320
ATAGCCTATG	ACCATGCCGG	ATCCAAATTG	GATTTTGGAC	TTTCGCTTTC	GGCTGCTTAT	1380
CGAATGGTGC	TGACGCATT	GTATAAGATT	CGTACCATCC	AGAAAGAGCA	GCTCGACTAT	1440
CAGCTGGCCT	ATTTGCCCTA	TGCTATCGT	AATAGAGAAG	GCGTGGAGGT	GCGTTCTCT	1500
CTGTACGTCT	CGATTCCGAT	GCAGAATACC	CACCGCCTGA	TGACAGAGCT	GCGGTTGTAT	1560
GGCGACCTGA	TGAAAAGAAA	GGACGGTATA	GCCTATGGCA	AAACGCCCGG	TGTCATCTCA	1620
CATATCTCTG	CCGATCCGCA	AGCCGAACGA	ACGTCCGGCC	ATACCATCGG	GGCTATCTGC	1680
AATATCTCTC	ACCTCTTC					1698

(2) INFORMATION FOR SEQ ID NO:80

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2457 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

AGGACGAACG	TTTTCTTATC	TTTGTCCCAT	AAAATTGGGA	GAAGGGGTGC	TTCCTGTAGC	60
AATCGGAATG	CGTGGATGGC	TGAGAACAAA	CCCTCATCAC	CTGAACCGGA	TAATACCGGC	120
GTAGGAAACT	CTCCGCTGTA	CTATCTTCAC	GGCGAAGCAA	TCATTCCCCC	TCTCTCTTCT	180
TTGTCCAACT	TCAATGATAA	GAGATTTATG	AAAAAACTTC	ACATGATTGC	CGCCTTAGCC	240
GTCCCTGCCTT	TCTGCCCTGAC	GGCACAAGCA	CCCGTCTCCA	ACAGCGAGAT	AGATAGTCTT	300
AGCAATGTGC	AGCTCCAGAC	CGTACAGGTC	GTAGCTACTC	GCGCCACGGC	GAAAACCCCT	360
GTGCGTTACA	CCAACGTTCTG	CAAGGCCGAA	CTTTCCAAGT	CCAATTATGG	TCGTGACATC	420
CCCTATCTGC	TGATGCTGAC	TCCCTCCGTG	GTAGCCACCA	GCGATGCCGG	TACGGGTATC	480
GGATATTCCG	GCTTTCCGCT	GCGTGGCACC	GATGCCAATC	GCATCAACAT	AACTACCAAT	540
GGAGTACCCC	TCAACGACTC	CGAATCTCAG	TCCGTCTTTT	GGGTGAATAT	GCCCCGACTTC	600
GCCTCTTCCA	TGAAGACCTT	TCAGGTGCAG	CGAGGTGTGG	GTACTTCCAC	CAATGGTGCC	660
GGAGCTTTTG	GGGCAAGTGT	CAATATGCGT	ACGATAAATT	TGGGACTGGC	TCCTTATGGC	720
CGTGTCGATT	TGAGCGGAGG	TTGTTCCGGC	ACATTCCGCC	GATCGGTCAA	ACTCGGTAGC	780
GGACGCATCG	GTGCCCATTG	GGCAGTGGAT	GCCGCGCTGT	CCAAAATCGG	TTCGGACGGC	840
TACGTGGATA	GAGGAAGCGT	GGATCTGAAA	TCCTATTTTCG	CACAGGTGGG	CTATTTCCGT	900
AGCAACACGG	CTCTCAGGTT	CATCACTTTC	GGAGGAAAAG	AAGTTACGGG	TATCGCATGG	960
AACGGTCTTT	CCAAGGAGGA	TGAAGCCAAA	TATGGCCGCC	GATACAACAG	TGCCGGTCTT	1020
ATGTACGTGG	ACGCGCAAGG	AGTACCGCAC	TACTACCACA	ATACCGACAA	TTACGAGCAG	1080
CGTCACTACC	ATGCCATCAT	GACGCACAGC	TTCTCTCCTT	CCGTTATCCT	CAACCTCACG	1140
GCACACTACA	CGGCCGGATA	TGGCTATACG	GAGCAATATC	GTACCGGACG	TAAACTAAAG	1200
GAATATGCAC	TGCAGCCCTA	TGTGGAATAA	AGTGTGACCG	TGAAGAAAAC	GGATCTCATC	1260
CGTCAGAAAGT	ATCTGGACAA	TGACTTCGGA	GGACTCATCG	GTTGCTTAA	CTGGCACACC	1320
GGTGCAATGG	ATTTGCAGTT	CGGGGCCCTCG	GGCAATATCT	ATAAAGGAGA	CCACTTCGGC	1380
CGTATCACTT	ACATCAAAAA	GTACAATCAG	CCCTTAGCTC	CCGACTTCGA	ATATTATCGG	1440
AACAGGGCAG	ACAAAAGAGA	AGGTGCAGCC	TTTGCCAAAG	CCAAGTGGCA	GATCACTCCG	1500
GAAGTGAACA	TGTATGCCGA	CCTCCAGTAT	CGTACCATCG	GCTACACGAT	AAACGGCATC	1560
ACGGACGAAT	ATGATGAGGT	ACAGGGAGT	ATGCAGCACA	TCGATTTGGA	CAAGACCTTC	1620
CGCTTCCTCT	ATCCGAAGGC	CGGTCTTACC	TATAGTTTCG	ACGATGCTCA	TACTGCCTAT	1680
GCTTCTGTTG	CGGTAGCACA	CCGCGAGCCT	AACAGAACCA	ATTACACCGA	AGCCGGAATA	1740
GGACAGTATC	CTACGCCTGA	GCGACTGATC	GACTATGAGC	TGGGCTACCG	CTATGCTTCG	1800
CCCCTCTGTT	CGGCCGGAGT	AGGTCTCTAT	TATATGCAAT	ACAAGGACCA	ACTCGTGTCTG	1860
GATGGCCGTT	TGAGCGATGT	GGGACAGATG	CTCACAAGCA	ACGTCCCCGA	CAGCTACCGT	1920
ATGGGACTGG	AGCTGACTCT	CGGTTGGCAG	ATCCTTCCTC	GTTTGCTGCG	TTGGGATGCT	1980
TCTTTCTACTA	TGAGTCGCAA	CAAAATCGAC	CGCTACGTAC	AATATACATC	CGTATATGAT	2040
GCGGACTACA	ACTGGCTCGA	ACTCAAGGAG	GAGACCCCTG	AAAGCACGGA	TATAGCCTAC	2100
TCGCCCAATG	TCAATTGCCGG	CAGCATGCTT	ACCCTCTCTC	ATGCCGGTTT	CGAAATGGCT	2160
TGGACGAGCC	GCTTCGTCAG	CAAGCAATAT	CTGGACAATA	CACAGCGCAG	CGATCGCATG	2220
CTTTCCTCCT	ATTGGGTGAA	CGACCTCCGC	CTCGGCTATG	TGCTGCCGGT	TCACTTCGTT	2280
AAGAGAGTGG	CACTGGGCGT	ACAGCTCAAT	AATCTCTTCA	ACCTCATGTA	TGCGTCCAAT	2340
GCCTACATCT	ACGATGCCGG	TTACGTACAG	GCATCCGGAG	AACTAAGTGC	ATATGCCGAT	2400
CTGCGTTATT	ATCCTCAGGC	CGGATTTAAT	GCACTGGGTA	GTCTGACAAT	CGATTTTC	2457

(2) INFORMATION FOR SEQ ID NO:81

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

```
TACAGGCGAT CGGGAAGGGT TTGTCCTCGT ATCCTCCGGA ACAAACGTTC CTACGCAGAT      60
ACTCGGTAC AGCCGAGAAG AGCGGTTCTGA CTACGAGCCG GCACCAGAAC AAAGATGAAA      120
AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG      180
CGGTTTCCGA TGGTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TCTGCCCAAG      240
CGTCCTTGGC GGCACATCGG TAAACGATA GCGTCAATC TGGCCGTATG GGGCTTCGAT      300
CATTTTCATCA TGAACGAGGA CTTTGCAGAC ATCAGTTGGC AGACTATCAA GAGCAATTTT      360
CAAACAGGCT TTGGCTGGGA CAATGACAAG TTGTCAACCA ACCTTTTCGC ACATCCTTAT      420
CACGGATCGC TCTATTTCOA TGCAGCGAGG TCGAACGGTT TGAGCTTCAG GCACTCTGCT      480
CCGTTTGCCCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT      540
ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG      600
CTGTCCGACC TGCTCGGACC CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG      660
GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT      720
TCTGTGCGGA GTGCGAGCGG ACAGATATTT CAGTCTGTCC CCATAACAT AGTCGTCGAT      780
GCCGGCTTTC GCTTTTTGGC AGACAAGCGG CATGCCCCGA CCGGTGCCAC GGCTCTGACC      840
CTGAATCTGA GATTCTGATA CGCGGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT      900
TTCTTCCAAT TCAAAGCCGG ATTGAGTTTC TCCGAATCGC AACCTCTGCT GAGCCAGATC      960
AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTTGGTG     1020
GGAGGTCTCT TTCAGCACTT CGACTACTAC AATTCGGAAA AACGAATAAG CAAAAATTCG     1080
GAGGAGGTAC TCTTGGAAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG     1140
ATCTTCCAGC ACCACGGAAA ATTTGACGCA CGTCCTCTGG AGCTATATGC CGAGACCTAC     1200
CTGAATGTCG TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC     1260
TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG     1320
TGGAGCTGGC TCTTGGGAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG     1380
CCGCACCAGA AAAATACCGA TGTCAGCTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG     1440
CGCCTACTGG TGACGAGTTC CGAGTTTCGA TTTCATCCTG GCCCCTGGCA TGTAGCCATC     1500
GTGCTCGGCC GTTTCATCCG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTTCGAT     1560
ACCGGCGACA TACAGCTGCG TGTCGGATTT CACTTC                                     1596
```

(2) INFORMATION FOR SEQ ID NO:82

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

```
AAAAGAAGAA AAAACAGAT GAAACGACTG ATTGTTTTTC TGGCAATGGG TGGCTTGCTG      60
TTCACCTTTC CGAACGCACA AGAAGCAAAC ACTGCATCTG ACCTCCCAA AAAGGACTGG      120
ACTATAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC      180
GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA      240
GATAAATGGA GTTGGGACAA CGGTTTGCGT ACAGACTTCG GTCTGACCTA CACAACAGCC      300
AACAAGTGGA ACAAAGTGT AGACAAGATC GAACTCTTCA CGAAGGCCCG CTATGAGATC      360
GGCAAACATT GTTACGGAAG TGCGCTTTTC ACTTTCCTCT CACAGTATGC CAAAGGATAT      420
GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA      480
TATCTCACTC TCGGTATTGG TCGGACTAT AAGCCCAATG AGAAGTTCTC TCTTACCTC      540
TCTCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTGGGGAGCC      600
TTCGGGGTGA AAGTTGGTGA AAAGACAATG TTGGAACCTG GTGCTTTGGT AGTGGGTTTC      660
GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTCTCGGCT      720
TATACGCACG ACTTTGGCAA CATTGACATC AATTGGGAGG CTATGCTGGC CATGAAGATC      780
AACAAGTTCC TCACGGCTAC GATAGCCACC AATCTTATCT ACGACGATGA TGTGAAGATC      840
AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC      900
```

(2) INFORMATION FOR SEQ ID NO:83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

ACGAGAGAGA	GTGTGTTACA	TTGTAGAACA	AAACTCAAAA	AAGAACGAAA	AATGAAGAAA	60
ATGATTTTGG	CAGCTACTAT	GCTGCTCGCA	ACAATCGGTT	TTGCAAATGC	TCAGAGTCGT	120
CCTGCTCTTA	GACTGGATGC	TAACTTTGTC	GGTAGTAACT	TAATGCAAAA	AGTCGCAAAC	180
ACGAGCGTGA	ACAATAAGAT	GATCGTAGGC	TTACGTGTTG	GTGCTGCTGC	TGAGTTTCGCT	240
CTTAGCAATG	ATGGATTCTA	TCTCGCCCCC	GGATTGGCCT	ATACGATGAG	AGGTGCTAAG	300
ATGGAATCAC	TAAGTGAAC	GACAACTCGC	TTGCATTATC	TGCAAATACC	GGTGAATGCC	360
GGTATGAGAT	TTAGCTTTGC	TGACAACATG	GCTATTTTCAT	TGGAAGCAGG	TCCCTATTTC	420
GCATATGGTG	TCGCCGGAAC	GATTAAGACT	AAAGTTGCAG	GC GTTACGGC	TTCTGTAGAT	480
GCCTTTGGTG	ATAACGATA	TAACCGTTTC	GACTTGGGCT	TGGGCTTGTC	TGCTGCCTTG	540
AGCTACGACC	GTTATTACGT	ACAAATTGGA	TATGAGCATG	GATTGCTTAA	TATGTTGAAG	600
GATGCTCCGG	ATAAGACTTC	TTTGCCTAAT	CATGACTTCT	TTGTGGGTCT	CGGTGTTCCG	660
TTC						663

(2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

ATCAAACGAA	TAGAAATGAA	AAGGATTTTT	ACTGTAGCCC	TTGTGCTACT	TGCTTCGGTC	60
ACTATGGCCA	TCGGACAAAG	CCGCCCGGCA	CTTCGCGTAG	ATGCCAACTT	CGTAGGCAGC	120
AATCAGAGCA	TGAAAAGAGA	CGGATATGTG	TGGGACACCA	AAATGAATGT	CGCCTGCGG	180
GTCGGTGCCG	TCGCCGAATT	CATGATCGGA	TCAAGAGGAT	TCTACTTGGC	TCCGGGTCTG	240
AACTATACGA	TGAAGGGCTC	CAAAACCGAA	TGGGATATAC	CCGAAATGGT	TCCTGGTACC	300
TATATTACGA	TGGTTTCCAC	TCGCTTGAC	TATCTGCAAC	TGCCGATCAA	TGCCGGCATG	360
CGGTTTGACC	TGATGAATGA	CATGGCGGTT	TCGATCGAAG	CGGGTCCTTT	CCTTGCAATC	420
GGTATATATG	GTACATATCG	GCAGAAGTTG	GAAGGATGGA	AGCCGAACAA	CTACAGCACA	480
GAGTTTTTTG	GCCCAACGCT	TGGTGGCCCA	ACAAATATCC	GCTGGGACAT	CGGGGCAAAC	540
ATAATAGCCG	CATTCCACTA	TAAGCGTTAT	TATATACAGA	TAGGCTATGA	ACATGGATTT	600
GTGGATATTG	TGTCAGGTGG	AGGTTCTGAT	ATTCCCCGAC	TGAACGACAA	TAGGCAATCC	660
TCTTCGACGA	CCGCTCTAAG	AGAAAAGGGA	AATAACGAAT	ACGCTTATAA	TCGTGACTTC	720
TTCGTGGGCA	TAGGTTACCG	CTTT				744

(2) INFORMATION FOR SEQ ID NO:85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

AAAAGAAAGA	GTATGAAAAG	AATGCTGCTG	CTTCTCGTTG	TATTATTATA	TGGAATTGCA	60
GGCCGATTGG	GTGCACAAGA	CGTTATCAGA	CCATGGTCAT	TGCAGGTCGG	AGCGGGATAC	120
TCCGATACGG	AGAACATCCC	GGGAGGATTC	ACCTATGGTT	TCTATTGGGG	AAAGCGTATG	180
GGGAGCTTTC	TGGAAGTGGG	GCTGTCCATG	TACAACTCCA	CACGTCAAAC	AGCCAACAAT	240
GCAGACTCCT	TTGCATCGAA	CGAAGGAGAC	GGATCTTTTC	AGGTAAATAT	GTCTTCTCCG	300
AATGAGAAGT	GCTCATTTCT	CGATGCAGGC	AGTGCCAACT	GCTATATGAT	CGTCGTCGGA	360
GTCAATCCTC	TCCATCTGTT	TTGGCAGAAT	AGCCGGCACA	ATTTGTTTCT	GGCAGTACAA	420
GCCGGCTGT	CCAATAAGCA	CAATATTCAT	TTCATCTATG	GAGACAAGGG	AGCCAAAGTC	480
AGTATCTACA	CCAATTCGAA	TACCTACATC	GGTTACGGAG	CACGTGTAGC	CTACGAATAT	540
CAAATTCATA	AAAACGTGGG	GGCGGGTGCC	GCTGTAATGT	ACGACCACGG	CAATAAGATG	600
CTTACGGCCA	TGGCCACGCT	CTCCACTCAT	TTT			633

(2) INFORMATION FOR SEQ ID NO:86

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2859 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

ATCCGAATGA	GAGTATCCGA	TCTCTGTTCC	AGACTTTCAT	GGTTATTACC	CGTAATCCTT	60
GTCGGATTGC	TCTGTGCTAC	TTTGGTGCCT	GCGGAACGTC	CTATGGCCGG	AGCAGTCGGA	120
TTGCACCACC	GTCGGCATGC	TGCGTGCTCT	GATTCTACAG	CGAAAGACAC	GGTGCCTCTC	180
GCAAAACCTA	TTCCTGACAG	TGCTTTTCGA	GATTCCCTTC	CTGCCGATTC	CACCGGATCG	240
ATGCGGCAAG	ATAGCGTGTA	TGACGATGAA	TTCGAATTGG	AAGATATAGT	GGAGTACGAA	300
GCTGCCGATT	CCATCGTTTT	GCTCGGACAG	AATCGTGCCT	ATCTTTTCGG	CAAGAGCTAT	360
GTGAGCTATC	AAAAGAGTCG	CTTGGAGGCA	AACCTCATGT	ATCTCAATAC	CGACAGCAGT	420
ACGGTTTATA	CTCGCTATGT	CCTCGATACG	GCCGGTTATC	CGATGGCCTT	TCCTGTTTTC	480
AAGGATGGAG	AGCAGTCGTT	CGAAGCCAAG	AACCTTACCT	ACAACCTCCG	CACGGAGAAG	540
GGGATTATCA	GCGGAGTGAT	CACGCAGCAG	GGCGAAGGCT	ATCTGACTGC	CGGTAAGACC	600
AAGAAGATGC	CCGACAATAT	CATGTTTATG	CAAGGAGGGC	GTTATACGAC	CTGCGACAAT	660
CACGATCATC	CTCACTTCTA	TATCAATCTT	TCCAAGGCAA	AGGTGCATCC	GGAGAAAGAC	720
ATCGTCACAG	GTCCGGTCAA	TCTGGTTATC	GCCGATATGC	CGCTGCCGAT	AGGTCTTCTT	780
TTCGGCTATT	TTCCCTTTTC	CAACAAATAC	TCTTCCGGTA	TATTGATGCC	CACGTACGGA	840
GAGGACAATC	GCTATGAGG	TTATTTGAGG	AATGGTGGAT	ATTATTTTGC	CTTCAGCGAC	900
TATATCGATT	TGGCATTGCG	TGGGGAGATC	TTTTCCAAAG	GGTCATGGGG	CATTTCAGCC	960
CAATCGAAAT	ATAAGAAGAG	GTATAAGTAC	AACGGCTCGT	TGGAAGCCAA	TTATCTGGTA	1020
TGGAAGTCCG	GCGACAAATA	CGTGCCCGGA	GACTACAGCA	AGACCACCAG	TCTGAATATC	1080
CGATGGACAC	ACAGTCAGGA	TCCGAAGGCC	AATCCTTTGC	AAACGTGTGC	GGCCAATGTC	1140
AATTTTGCCA	CCGGGAGCTA	TTTCCAGAAT	TCGCTGAATA	CCACCTATGA	TGTCAATGCC	1200

CGTACTGCTA	CGACACGAAG	TTCGGCCGTG	AGCTATTTCG	GCAAGTTTCC	GGGTACTCCT	1260
TTTTCGATTA	CGGGTAGCAT	GGATATCAGC	CAGAACATGC	GCGATACGAC	GGTGAGCCTT	1320
ACCTTGCCGA	ATCTTTTCGAT	TAATATGTCC	ACGCGTTATC	CTTTCAAGCG	GAAGACCCGT	1380
GTAGGACCGG	AGCGATGGTA	CGAGAAGTTG	AGTGTGGGCT	ATTCCGGTCA	GCTTCGCAAT	1440
AGTATCTTGA	CAAAAGAGAA	AGATTTGCTC	CAGAGCAATC	TCGTGCGCGA	TTGGAAGAAT	1500
GGTATGCGTC	ATTCCGTACC	GATCAGTTTG	ACTGTCCCTT	TGTTGGATTA	TATCAATCTG	1560
ACTATGGGGG	TTAACTACAA	TGAGTGGTGG	TACACGAAAG	GCATACGGAA	GTCTGTGGAAT	1620
GAGGATAAGA	AAACATTTCCT	GCCTTCGGAC	ACGACCTATA	AATTCCGCAG	ACTGTACGAT	1680
TACAGTCTGT	CGGCAGGCTT	ATCTACCACA	TTGTACGGTA	TGTTCAAGCC	TTGGAAACCT	1740
TTTTCCTTCG	GAGGCAATCT	CATTATGATC	CGTCATCGCT	TCACGCCAC	TGTCAGTTTC	1800
TCCTATATGC	CGAAGTTCAC	GAAACGCCGA	TATGGCTTTT	GGGAGCTTCT	TGAGCATACG	1860
GATCAGAACG	GCAAGCTGCA	TACGCTGCTC	TACTCTCCTT	ATTTTCGAGCA	GATATTTCGGT	1920
GCTCCCTCCA	TGGGCAATGC	AGGATCTGTC	AATTTCTCTT	TTGACAACAA	CTTAGAGGCC	1980
AAGATCAAAT	CCAAATCGGA	TTGACAGGG	ATCAAGAAGA	TCAGCCTGAT	AGATCAGTTC	2040
ACATGGTCTA	CATCTTACAA	TATGTTTGGC	GATTCGATCC	GATGGAGCAA	TATCTCGGCT	2100
TCGCTGGCAC	TTGCGCTCTC	CAAGAGCTTT	ACCTTGCGCT	TGTCCGGTCT	GTTTCGATCC	2160
TATTTGACGA	AGTATTATGA	GGGAGAAGAT	GGGAAGATCA	TTCCCTATAA	GAGCAACGAC	2220
CTGCGCATTT	TTAACGGCAA	GGGATTGGCA	CGCTGATCA	GTACGGGTAC	TTCTTTCAGC	2280
TATACGCTCA	CGAAGAGATC	GCTCAGCGGA	TTGATAGCTC	TTTTCAGTGG	CAAAAAGGAG	2340
CGGAGAGATG	AAAAGAAAAA	CACAGGGGCT	ACTCCTCATG	AAGGAGACGA	TGCTGCCGAT	2400
ATACTTGAGG	GAGGAAGACC	GCAAAATGAA	AGTGGGGGGT	CGTCTCTCGA	GCGCAACCGT	2460
CAGGGCGGAG	CAGTGGATCA	GGATGGTTAC	TTGCGCATAT	CGATCCCATG	GAGCCTGTCC	2520
TTGACTATA	GTTCGAATAT	TGCTACCGAC	TACAATAGGT	ACAAATGTCAA	TAAGATGGAG	2580
CACTACTACC	GGGTAACGCA	GAATCTGAGC	TTTCGCGGCA	ATATCCAGCC	TACACCGAAC	2640
TGGAGCTTCG	GATTCAATGC	GAATCTGAGC	TTTCGCGGCA	ATATCCAGCC	TACACCGAAC	2640
TGCAACGTCA	CTGCGGACAT	GCACTGCTGG	GCTATCTCGG	CCAGTTTTCAT	CCCTATAGGA	2700
GCATACAAAGT	CCTATAATTT	CGTCATATCG	GTGAAGAGTT	CACCTTTGCA	GGATCTGAAG	2760
TATCAGCAGA	GCAATCGTCC	CATCACGAAT	ACTTGGTAT			2820
						2859

(2) INFORMATION FOR SEQ ID NO:87

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

AAATGGAAAT	TGGCATGCGC	TTTTGATTGC	GCGTGTGTGT	TCGATCCATT	TGTAGTAACT	60
AACGAGGTAA	TAATAATGAT	GAAACGATAT	ACAATAATTC	TTGCAGTTT	TCTTTTATTC	120
TGCACGGTAT	TTACCTTTCA	AATAAAAGCT	CGCCCTTATG	AAAGATTGTC	AGATGTAGAG	180
AAGCCTTGGA	TTCAGAAACA	TCAATGGAT	TCTAAATTGG	TGCCTGCAAA	TAAGGGTAAC	240
TTAATTCAAG	CTGAAATGT	ATACCAATCT	GTTTCTGAAC	ATAGTGACTT	AGTTATTTCA	300
CCTGTGAACG	AAATAAGGCC	TGCAAAATCGT	TTCCCTTCGC	ATAGGAAGTC	TTTTTTTGCA	360
GAAAATCTAC	GGGCATCTCC	CCCCGTAGTT	CCCGTTGCCG	TCGACAAGTA	TGCGGTACCG	420
GTTGCCAATC	CAATGGATCC	TGAAAAATCCC	AATGCCTGGG	ATGTGACGCT	AAAAATCACT	480
ACTAAAGCGG	TAACAGTACC	TGTCGATGTG	GTGATGGTTA	TCGACCAGTC	TTCGTCAATG	540
GGAGGGCAAA	ACATTGCCAG	ATTAAAGTCT	GCCATTGCAT	CGGGACAGCG	TTTTGTGAAA	600
AAAATGTTGC	CTAAGGGGAC	GGCTACAGAA	GGGGTGCGTA	TCGCTCTTGT	GAGTTATGAC	660
CATGAGCTC	ATCGTTATC	TGATTTTACC	AAAGACACTG	CTTTTCTCTG	TCAAAAAATC	720
CGGGCTTTGA	CTCCTATTTG	GGGAACACAT	ACCCAGGGGG	GGCTTAAAT	GGCGAGAAAC	780
ATTATGGCCA	CTTCTACTCG	TGTGGATAAG	CATATCATAT	TGATGTCTGA	CGGGTTAGCG	840
ACGGAGCAGT	ATCCTGTAA	AAATGTAACT	ACTGCAGACT	TCATTGGCAA	AACTGGAAAT	900
GCGAATGATC	CCATTGATTT	GGTTATACAA	GGAGCAATTA	ATTTCCCTAC	AAATTATGTT	960
TCCAACAATC	CATCTACACC	TCTTACCCCA	AATTATCCAA	CTCATCTTTC	TAAAGTTGGA	1020
CGGAGAAATC	TGCCGGAATC	CAAATTCGAT	TATAGTAATC	TGAGTGCAAG	GATTACTTTT	1080
GATGGTGTG	CTGGCGCATT	GGTCTATGAA	CCGAGGTTTC	CTCATCCCTA	TTATTATTAT	1140
TTCCCTTGTA	ACGCTGCTAT	CAATGAGGCT	CAGTTTGCGA	AAAACCTCTG	TTATACAATC	1200
CATACTATTG	GCTATGACCT	GGGAGATTTT	GCCTTGGCCA	ACAATTCGTT	GAAACTAACC	1260
GCTACAGACG	AGAAATCACT	CTTTACGGCG	ACACCGGCCA	ATTTAGCTGT	AGCGTTTGAT	1320
AATATTGCC	AAACTATTAA	TATAGGTATA	CAGAGGGGGG	AGGTGACGGA	CTTTGTAGCT	1380
CCTGGTTTCA	TCGTTAAAAA	TCTGACGCAA	TCGGGAGATG	TTACTCATTT	GCTAAATGTT	1440

TCAAATGGAA	CGGTGCACTA	TGATGTCTCT	ACTAAAAAAC	TGACATGGAC	TACTGGTACT	1500
ATCCTGAGCT	CATCAGAAGC	TACCATAACT	TATCGTATTT	ATGCCGATTT	GGATTATATA	1560
CAGAACAATG	ATATTCCGGT	AAATACTACT	TCTGCTATCG	GCCCGGATCT	TGGTGGATTC	1620
GATACCAATA	CCGAGGCCAA	ATTGACCTAT	ACCAATTCCA	ATGGCGAACC	GAATCAGCAG	1680
TTAATTTTCC	CACGTCCGAC	GGTTAAGTTA	GGTTATGGTG	TTATTAAGCG	GCACTATGTA	1740
TTGGTAAATA	AAGACGGTCA	ACCCATACAG	GCAAATGGAA	CAGTTGTCTAG	TTCCCTAAGC	1800
GAGGCATTAG	TTCTACAGTC	ACAAGATTTC	TTTTTGCCCT	CAGGTGGAGG	TCATATTGTT	1860
CCCAAATGGA	TAAAGTTGGA	CAAAACGACC	GAAGCATTAC	AGTACTATTC	CGTACCGCCG	1920
ACTAACACGG	TCATCACTAC	TGCCGATGGT	AAACGTTATC	GTTTTGTCTGA	AGTCCCAGGC	1980
TCCACGCCGA	ATCCGGGCCA	AATCGGTATC	AGTTGGAAAA	AACCGGCAGG	AAACGCTTAC	2040
TTCGCTTACA	AGCTCCTCAA	TTATTGGATG	GGAGGAACAA	CAGACCAACA	GAGTGAATGG	2100
GATGTGACGT	CCAATTGGAC	AGGAGCCCAA	GTACCGCTCA	CAGGAGAAGA	TGTAGAGTTT	2160
GCAACGACAG	AAAATTTCCG	TTCTCCGGCG	GTAGCCGATT	TGCATGTCCC	GACAACCAAC	2220
CCCCAAATTA	TCGGTAACCT	TATCAATAAT	TCCGACAAGG	ATTTAGTTGT	TACCACAAGC	2280
AGTCAATTGA	CGATCAACGG	CGTGGTTGAG	GATAACAATC	CGAATGTCTG	TACGATCGTC	2340
GTGAAGTCGT	CGAAAGACAA	TCCTACGGGG	ACATTGCTTT	TTGCCAATCC	GGGCTATAAT	2400
CAAAATGTAG	GGGGGACCGT	CGAGTTTATC	AATCAGGGAT	ATGATTGTGC	CGATTGTGGT	2460
ATGTATCGCA	GGAGCTGGCA	GTATTTCCGT	ATCCCTGTCA	ATGAATCAGG	TTTTCCAATT	2520
AATCGATGG	CGCGAAACGA	CAATGCTCAAC	CAATGGGTTG	AGCCTTTCAA	TGGCGATAAG	2580
TGGCGGCCAG	CACCTTATGC	ACCTGATACA	GAGCTTCAAA	AATTCAAGGG	CTACCAGATC	2640
ACGAATGACG	TGCAGGCACA	GCCTACGGGA	GTTCACAGCT	TCAAGGGTAT	GATTTGTGTG	2700
TGCGATGCCT	TCCTGAATCT	GACACGCACG	TCCGGTGTCA	ACTACTCGGG	CGCCAACTTG	2760
ATCGGCAACT	CATCACTGG	ATCAAGCAGG	GTATTGTCTT	CCCGCCGGAA		2820
GTCGAGCAGA	CGGTGTATCT	GTTCAACACG	GGAACACGCG	ACCAGTGGCG	TAAGCTTAAT	2880
GGAAGCACGG	TTTCAGGCTA	TCGAGCCGGT	CAGTACCTCT	CTGTACCTAA	GAATACAGCG	2940
GGTCAGGACA	ATCTTCCGGA	TCGTATTCCA	TCGATGCATT	CCTTCTTGGT	GAAGATGCAG	3000
AACGGAGCGT	CTTGTAACGT	GACCATCTTG	TACGATAAGC	TGCTCAAGAA	CACGACTGTA	3060
AACAACGGTA	ATGGTACGCA	GATCACATGG	CGATCCGGCA	ACTCCGGATC	GGCGAATATG	3120
CCGTCACTTG	TGATGGATGT	TCTTGGTAAC	GAGTCGGCCG	ACCGTTTGTG	GATCTTTACC	3180
GATGGGGGTC	TTTCTTTCGG	ATTCGACAAC	GGCTGGGATG	GTCGCAAGCT	GAAGTAAAAA	3240
GGTTTGTTCAC	AACCTTATGC	GATGTCCTGAC	ATCGGTAATG	ATAAATTCCA	GGTTGCAGGG	3300
GTTCCGGAGT	TGAATAACCT	GCTGATCGGC	TTCGATGCGG	ATAAGGATGG	TCAATACACG	3360
TTGGAGTTTG	CTCTTTCCGA	TCATTTTTCG	AAAGGGGCTG	TTTACCTGCA	CGATCTTCAG	3420
TCAGGAGCCA	AACACCGTAT	TACGAATTCT	ACGTCGTATT	CATTTCGATG	CAAGCGGGGA	3480
GATTCGGGG	CTCGTTTCCG	CCTGTCTAT	GGATGTGATG	AGAACGTAGA	TGATTTCGCAT	3540
GTCGTGAGTA	CAAATGGCCG	TGAAATTATA	ATTCTGAATC	AAGATGCTCT	TGACTGCACT	3600
GTAACCTTAT	TCACAATAGA	AGGTAAGCTT	CTTCGCCGCT	TGAAAGTATT	AGCTGGTCAT	3660
AGAGAAGTCA	TGAAAGTGCA	GACCGGAGGG	GCCTATATTG	TGCATCTTCA	AAATGCTTTC	3720
ACTAATGATG	TGCATAAGGT	GCTTGTGAG	TAT			3753

(2) INFORMATION FOR SEQ ID NO:88

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ACTATGGAAG	TGAAGAAAAA	CACAGTGGTG	CTACGCCCTC	TGATTTGGTT	CGTGGCCATT	60
CTTCTCTTCC	ACTCCTCACG	GCTGTGGGGA	CAGGAAGGGG	AGGGGAGTGC	CCGATACAGA	120
TTCAAAGGAT	TCGTGGATAC	CTACCATGCC	GTACGCAGCT	CTTCTCCTTT	TGATTTTATG	180
AGCTCGCGTA	CGAGAGTGAG	AGGTGAGCTG	GAGAGTCTGT	TCGGTAATTC	GAAAGTAGCC	240
GTATCGGTCA	ATGCCACCTA	CAATGTCTTA	CTGAAAGACG	AGACCGGCTT	ACGTTTACGT	300
GAAGCCTTCT	TCGAGCATCA	GGAAGAGCAT	TGGGGGTTGC	GCCTCGGACG	ACAGATTGTC	360
ATTTGGGGGG	CTGCCGACGG	TGTGCGCATC	ACGGATCTGA	TCTCCCGGAT	GGATATGACC	420
GAGTTTCTGG	CACAGGATTA	CGATGATATT	CGTATGCCGG	TCAATGCATT	GCGTTTCTCT	480
GTCTTCAACG	AATCGATGAA	AGTGGAAATC	GTGGTACTGC	CTGTATTCGA	GGGGTACCGT	540
CTGCCCTGTG	ATCCTCGCAA	TCCTTGGAAAT	ATCTTCTCCC	TTTCGCCCCAT	TGCTCAGGGG	600
ATGAATATCG	TCTGGAAAGA	AGAAGCCGGC	AAACCGGCCT	TCAAGGTTGC	CAATATCGAG	660
TACGGTGC	GATGGAGCAC	TACGCTCTCC	GGTATCGACT	TCGCTTTGGC	TGCATTGCAT	720
ACATGGAACA	AGATGCCCGT	CATCGAAGTA	CAGGGCATTG	TGCCGACGGA	AATCATCGTT	780

AGCCCTCGCT	ATTATCGTAT	GGGATTTGTC	GGCGGCGACC	TCTCCGTACC	CGTCGGACAG	840
TTTGTTTTCA	GGGGAGAGGC	TGCGTTCAAT	ATCGACAAAC	ACTTCACCTA	TAAGAGTCAT	900
GGCGAGCAAG	AGGGTTTCCA	AACAATCAAT	TGGTTGGCCG	GAGCCGATTG	GTATGCTCCC	960
GGTGAATGGA	TGATCTCAGG	ACAATTCTCA	ATGGAAAGCA	TATTCAGGTA	TAGGGATTTC	1020
ATCTCCCAAA	GACAACATTC	TACCCTGATT	ACTCTCAATG	TTTCCAAGAA	ATTCTTCGGC	1080
AGTACACTCC	AACTTTTCGA	CTTCACCTAC	TACGACCTTA	CGGGCAAAGG	ATGGTTTCAGT	1140
CGCTTTGCAG	CTGACTATGC	CTTGAACGAT	CAGATACATC	TGATGGCCGG	ATATGACTGG	1200
TTCAGTAGTA	AGGGCAGCGG	TATATTTCAT	CGCTACAAAG	ACAATTCCGA	ACTCTGGTTC	1260
AAAGCCCGCT	ACAGCTTC					1278

(2) INFORMATION FOR SEQ ID NO:89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

TACGGCAAAA	GAAGAAAGCT	CGGAACCTCC	GTCCGACCTT	CCGTTCTAAC	CCAAATCAGA	60
TTTATTTTGG	ACTTACACCT	TATTACTGAT	TTTTTTGAAG	GGCTTCGGGT	CAATCCTATC	120
GGTGCAGCAG	CCATAGTGGC	TTTCATTATC	GACCTGCTTC	TTCTTTGCTG	TTCGGCTTTT	180
ATGTCCTCCT	GTGAGGTGGC	TTATTTTTC	CTAAAGCCGA	TCGATCTGCA	GAACATCCGC	240
GAACGGAATC	ACTCTTCCGA	CATCGCGCTT	TCCAATTTAT	TAGACAATTC	GAATCAGCTA	300
TTAGCTACTA	TTCTGATCGG	GAATAATGTG	ATTAATGTAG	CCATCGTTAT	CCTTTCCAAT	360
TATGCCATCG	AGCAGACATT	CGTTTTCTCT	TCTCCGATCA	TTGGATTTCT	GATCCAGACG	420
ATACTCCTGA	CACTGTCTCT	TTTGCTGTTC	GGAGAGATTC	TGCCGAAAGT	GTATGCGCGG	480
AAGAATCCGC	TGCAATACTC	CGCCTTTTCT	GCTGCAGCTA	TGTCCGTTAT	CTATAAGATA	540
TTGTCACCGT	TTTCAAAATT	GCTGGTCAAA	AGTACCGGCA	TCGTTACCAG	AGGTATCAGC	600
AAGAAGAAAT	ACGATATGTC	CGTGGATGAG	CTCTCGAAAG	CGGTAGCCCT	CACCACTACG	660
GAGGGAGAGC	CGGAGGAGAA	AGAAATGATT	AACGAAATCA	TCAAATTC	TAATAAGACA	720
GCCTGCGAAA	TCATGGTTCC	CGGTATCGAT	ATTGTGGATG	TGGATCTGAG	CTGGCCATT	780
CGTAAGATGC	TTGACTTCGT	TGTTTCGTCG	GGTTATTCCA	GACTTCCCGT	TTGAGAGGGG	840
TCAGAAGACA	ATATCAAAGG	GGTGATTTAC	ATCAAAGATC	TAATCCCACA	CATGGATAAA	900
GGCGATGAAT	TGACTGGCA	TCCTCTGATT	CGTAAAGCAT	ATTTTGTCCC	CGAAAACAAG	960
CGCATAGATG	ATTTGCTCGA	GGAGTTTACA	GCCAATAAGG	TGCATGTCTC	CATCGTTGTG	1020
GATGAGTTTC	TGGCACTTGG	CGGACTGATC	ACAATGGAGG	ACATATTGGA	AGAGATCGTC	1080
GGCGAGATTA	CGGACGAGTA	CGATGAGGAA	GAACCTCCCT	TTAAGGTTT	GGGGGATGGC	1140
AGTTATCTTT	TCAAGGAAA	AACGTCTCTC	TCCGATGTTC	GACACTATCT	TGACCTTCCG	1200
GAAAATGCTT	TCGGTGAATT	GGGGGACGAG	GTAGATACGC	TAAGTGGGCT	CTTCTTGGA	1260
ATCAAGCAGG	AACTCCCCCA	TGTGGCGCAT	ACAGCAGTGT	ACGAGCCATT	CCGCTTTCAA	1320
GTGACCCAAA	TGGACAAGCG	CCGAATCATC	GAAATCAAGA	TTTTCCCTTT	CGAGCGCACT	1380
TGGAGGTCG	AA					1392

(2) INFORMATION FOR SEQ ID NO:90

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

ATAATTTATA	GATCAACAAT	GAAACTATTA	CTTTATCTCC	TATTGGTCTT	GTCGACTCTA	60
TCCCCGATGT	ATTGCGAAAT	GCTCTTCTCA	GAGAATCTCA	CAATGAATAT	AGACAGCACC	120
AAAACCATAC	AAGGAACGAT	ATTGCCCGTA	CTGGATTTCA	AAACCGAAAA	GGAAAATGTG	180
TTACACTTCA	AAAATACTGC	CAATCTCAAT	CTGCTGATAA	AGCACGGTCA	AGTAATCAAC	240
TTAATTAATA	AGCTTGAGTT	TTCTACCTAT	GGCAATAAAG	TAACCGTAAG	TGGAGGATAT	300
GTACACACCG	AATACCGCTA	TTTGTGTCAT	CATGTTTTTG	AGGTTTATCC	TTATGTCGAG	360
TCGCAATGGG	CAGAAAGTAG	AGGAATGAAA	TATAAGGTTT	CTACGGGATT	ACAGTCGCGT	420
TATCGGCTGG	TAAATAGTGA	TAACTGTCTC	ATGTTTGCAA	CATTGGGGGT	ATTTTTCGAA	480
TTCGAAAAAGT	GGGAACAGCC	AGCCACTAGC	CTCTTTGCAG	GAACGTATGC	ATACAGCCGA	540
AGTATCAAAA	GCCACCTGTC	TATCAGTTTC	AGACATCGGT	TGGGTGAACA	TTGGGAATT	600
ACAACTACGG	CTATTCACCA	GGGAAAGCCT	GACAGTTATT	TTAAGAAGGC	ACGTTTGGGA	660
GGAGCTATCG	ACCTCAAATA	CCATATCACA	CCTACGATAG	GAATACGCGG	GGCCTATCGG	720
ATCATCTACG	ATACTGCCCC	TATTGTACCT	GTGCGGAAAG	ATTACAACAC	CGTTGATGTT	780
GGTATCGATA	TTTCGTTT					798

(2) INFORMATION FOR SEQ ID NO:91

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2721 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

ACTATATGCG	TTGCCTTCTT	ATCCGCTCCC	GTTCGGGCAT	TGCGCGAGTC	GCCGCCAATG	60
GGGGCGGAGC	GGAAGACTCC	CTCTCTCCTA	CCCCTTCTTT	TCGAGCATTC	TGATAAAGGA	120
AAGGGGTTTC	ACTACAGACT	ATTCACAAGC	AATAAACTTA	AAGTGTTTGC	CACAGGTAAC	180
AGCCGATACA	TACACAATAA	ACCAACAATC	ATCCAAGCAA	TGAAACGAAT	CGTTTTATCA	240
TCTTTCCTGT	TCGTTCTGTC	CATACTTTCT	TTGATGGCAC	AGAACAATAC	CCTCGATGTA	300
CACATATCCG	GTACGATCAA	GGATGCCTCC	TCCGGCGAAC	CAGTGCCCTA	TGCCACTGTA	360
AGCATCCGGC	TGACAGGAGC	AGATACCACA	CAGGTGTTCC	GACAAGTGAC	TGACGGCAAC	420
GGCTACTTCG	TCATAGGCCT	GCGGCGAGCT	CCCTCCTATC	ACCTGACAGC	TTCGTTTCGT	480
GGTATGAAAA	CCCATACCAT	GCAGATTAGT	CGGGGAAATG	GACAGCACGA	CATCAAAATCC	540
ATCGACATTT	CTCTCGAATC	CGAGGACAAA	CAACTCTCCA	CCGTCACCGT	ATCGGCAGCA	600
CGACCACTGG	TGAAGATGGA	GATAGACCGC	CTGTCCTATA	ATATGAAAGA	TGACCCCGCA	660
GCCAAGACGA	ACAACCTGCT	CGAAATGCTG	CGCAACGTTT	CTTTGGTAAC	GGTGGATGGT	720
CAGGGCAATA	TCCAGGTGAA	AGGATCTTCC	AACTTCAAAA	TCCACCTCAA	TGGCAGGCCC	780
TCGACCATGG	TGAGCAGCAA	CCCGAAGGAG	GTCTTTCGCT	CCATTCTCTG	CCATACGATC	840
AAACGGGTGG	AGGTCATCAC	CGATCCGGGT	GTAAAGTACG	ATGCGGAAGG	CACAAGTGCC	900
ATCCTGGACA	TCGTACCGGA	AGAAGGTAAG	AAGCTGGAAG	GATATTTCAG	TTCCATCACG	960
GCCAGTGTC	GCAACAATCC	CACAGCCAAC	GGTAGTATCT	TTCTGACGGC	AAAGTCCGGC	1020
AAAGTCGGGC	TGACTACCAA	CTATAACTAC	TACGGTGGCA	AAAACAAGGG	CTCTCGTAC	1080
TTTACCGAAC	TGACTACATC	CATGCTCCAA	ACGATAGAAG	AAGGCAAAGG	GCAAGAAACC	1140
TTTGGCGGAC	ACTTCGGCAA	TGCCCTCCTC	TCATTGAGTA	TAGATTGCGT	CAATCTCTTT	1200
ACGGTGGGCG	GCAATGTACG	CCTTTGGGAG	ATGACCACCG	ACCGGAACAG	CGTAGAAAAA	1260
AGCTTTGCCC	CGAGCAACCT	CATGTCCTAC	ATAGACAGAA	AACTCAAAAC	ACAGATGGAT	1320
GCCGGATCAT	ACGAGCTCAA	TGCCGACTAT	CAGCACAGCA	CTCGCCTGCC	GGGCGAATTG	1380
CTCACCGTTT	CCTACCGCTT	CACTCACAAT	CCTAATAATA	GCGAGACCTT	CATTGACCAA	1440
TGGAAGCGCG	ATCCGCTCAA	CACAGCTAAT	ACGATCCAGT	ACGCCGGCCA	GCACTCCAAA	1500
TCCGATGCGG	GCATGGACGA	ACATACGGCA	CAAGTGGACT	ATACACGTCC	CTTAGGACAA	1560
GCACATTCTT	TGGAAGCAGG	GCTGAAGTAC	ATCTATCGTC	ATGCCACGAG	CGATCCTCTC	1620
TATGAGATAC	GACCATCCGA	AGATGCTCCG	TGGCAGCCCG	GCTCTCTATA	TGCACAGAAT	1680
CCGTGGAACG	GAAAGTTCGG	CCACGATCAA	TACATCGGAG	CAGCCTATGC	CGGCTACAAC	1740
TATCGTAAGG	ATCAGTATTC	TTTGCAAACC	GGCCTCGAG	TGGAAAGCAG	CAGGCTGAAA	1800
GCACTCTTTC	CCGAAAACGC	AGCAGCAGAT	TTCTCCACAC	ACTCGTTCGA	CTGGGTGCCA	1860
CAGCTCACGC	TCGGCTATAC	CCCCTCGCCC	ATGAAGCAGC	TTAAGCTGGC	CTATAACTTC	1920

CGAATCCAAC	GTCTTGCAAT	CGGCCAACTG	AATCCCTACC	GGCTACAGAC	CAACGATTAT	1980
CAAGTACAGT	ATGGTAATCC	CGACCTAAAG	TCGGAGAAGC	GTCACCACGT	CGGTCTCTCC	2040
TATAATCAAT	ACGGAGCCAA	GGTCATGCTT	ACAGCATCGC	TCGACTACGA	CTTCTGCAAC	2100
AACGCCATCC	AGAAATTACAC	CTTCTCCGAC	CCGGCCAATC	CCAATCTGTT	CCACCAGACC	2160
TATGGCAATA	TCGGACGAGA	GCATTCTTTC	AGCTTGAATA	CCTATGCCAT	GTACACGCCG	2220
GCCGTATGGG	TCAGGATTAT	GCTCAACGGA	AATATCGATC	GCACATTCCA	AAAGAGCGAA	2280
GCACTCGGCA	TTGATGTCAA	TTCATGGTCC	GGCATGGTAT	ACTCAGGCCT	GATGTTCCAC	2340
CTGCCGAAGG	ATTGGACTGT	GAATCTCTTC	GGAGTTTATT	ATCATGGGGG	AAGAAGCTAC	2400
CAGACGAAGT	ATGATGGCAA	TGTATTCAAC	AATATCGGTA	TAGCCAAACA	GCTTTTCGAC	2460
AAAAAATTGA	GAGTCTCGCT	GAGCGCAAAC	AACATTCATG	CGAAGTATTC	GACATGGAAG	2520
AGCCGGACCA	TCGGCAATGG	ATTTACTATT	TATTCGGAAA	ATGCCGGTAT	ACAACGGAGT	2580
GTTTCCCTCA	GCCTCACCTA	CAGCTTCGGT	AAGATGAATA	CACAAGTTCG	CAAGGTAGAG	2640
CGTACGATCG	TCAACGACGA	CCTCAAGCAA	ACCTCATCCC	AAGGACAGCA	GGGTGGCGGA	2700
CAAGGAAATC	CTACCGGCAA	T				2721

(2) INFORMATION FOR SEQ ID NO:92

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1350
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

TGGTGCCAAT	CCGACCCAAT	ACCTCATTGC	CATGCAGTAT	ATCGAAACGC	TCAAGGACAT	60
CAACAAGGGC	GATCAGACCA	AGACCGTTTA	CCTCCCGTTC	GAGGCTACCG	GTATGCTCGG	120
TGCCTTGGGC	GGTATGAAGG	ATTTGGTGAA	AGGATGAGAC	TCTCTGCCAT	TCTTATCGCT	180
TTGATTGTGA	TGCTGCCTGC	TGTGCTTAGC	GGGCAGCATT	ATTATTCCAT	GGCGGGAGAG	240
CGACTGGAGA	CGGACAGCAT	TCGTCCGAAC	GAACCTCTCG	CATCGATCCG	AAGTGCCTT	300
TTCTTTCGGA	ACAAATGAATA	CAATGCACGT	TCGGTCAAAG	GTTATACGTT	GCCGGGTGCA	360
CGGGTTTCCG	CTTTTGCCTC	TTACTCGCTG	CCGGCAGCAC	ATGGTGTGAA	GCTTTCGCTC	420
GGAGTATCTA	CCCTGAACCTA	CTGGGGGGCA	AGTCGCTATC	CGGCCGGTAT	CGTTTATTCC	480
GATTTACCTT	ATTGGACGGA	CTATAACGAC	TATGTACGCT	TGCGTATCCT	GCCTTATGTA	540
CAGGCCATGC	TGAAGCCGAC	GGCCACGACT	GCTCTCATGC	TGGGCAATAT	AGCCGGTGGT	600
ACGGCTCAGC	GACTGATCGA	ACCGATCTAC	AATCCTGAGT	TGGATTTGAC	GGCTGATCCT	660
GAAGCCGGTG	TGCAATTTTCG	GGGTGATTGG	ACACGTTTCC	GAATGGATGT	TTGGGTCAAT	720
TGGATGAGCA	TGATTTTCAA	AAATGACAAAT	CATCAGGAGT	CGTTTGTCTT	TGGCTTGTCC	780
ACTACTTCGA	AATTGTTATC	GGGTGAAGGC	AAATGGCGAC	TCGAACTGCC	CTTGCAGGCT	840
ATTGCCACGC	ATCGCGGCGG	GGAAATACAA	TGGGCGCAGC	AGGATACCGT	GCATACATGG	900
GTCAATGGAG	CTGTCGGACT	TAAGCTTTTCG	TATCGCCCTC	GTACCGACAA	ACCCATGCAG	960
ATTTGGGGAT	CTGCTTATGG	TGTGGCAGCC	TTGTCAAGCG	GAGGATACTT	CCCTTACGAA	1020
AGAGGGTGGG	GCGGTTATCT	TTCTCTCGGA	ATGGACTTGG	AGCACTTCGC	TTTTCGTACC	1080
GACTATTGGT	ACGGCAGGCA	TTACGTTTCT	CCCTTTGCTG	CACCTTTCGC	CAATTCCCTG	1140
ACGTATGACA	AACAGCCTCT	TACGAACGGT	TGGGCGGATT	ATATTCGTCT	CTATGCCGAC	1200
TATTCGTGGC	GGATGGCAGC	AAGTGTTTCG	TTGGCGGCTG	TTGCTCGGGT	ATGGTTCCAG	1260
CCTTCGGATC	GTTTTGCGAT	GAGCCACGCC	TTGGAAGTGA	CGATGCGTAT	CGATCCCAAA	1320
TTCCCAATAG	CTTTTCTGAA	AGGCAATCAT				1350

(2) INFORMATION FOR SEQ ID NO:93

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

```
CCGTTTTTCAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC      60
TCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG      120
GACTCGTCGC CGGCATATTC GCCCATGGGC TCTTTGTCTT CATCTCACATC ATTTGATTCG      180
ATACCCGACC AACGTATGAA CAAATCGCTA TTATCATTTG CATGCCTCAT CCTGTGCGGT      240
ATGCCGGCCA TCGCCCAACA GACAGGACCG GCCGAACGCA GCGGCGAGCC TTCTCTGGCC      300
GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAAGCTGA AGGTGTACTT AGGCATACAG      360
TCGTTCTACG ACCAGCCGCT TGTCGATGAC GAATCCCATC TCGGACACTT CAAGGTACAG      420
GAGCTGCGGA TGTCTGCTCA TGGCGAACTG AACCGCCACC TCAGCTTCGA CTGGCGACAA      480
CGTCTCAACC GTGCCGCCGA CGGCACTTCG TTTGCCGACA ATCTCTCCAA TGCCATCGAC      540
ATCGCAGGTG TGGACTGGCA CCGGAACGAC AAGGTGTCTT TCTTCTTCGG ACGTCAGTAC      600
GCGCGTTTCG GAGGGATAGA ATACGACATG AACCCCGTAG AGATCTACCA GTACAGCGAC      660
CTTGTGGATT ACATGACCTG CTATACTTCG GCGGTGAAGT TCGCATGGAA CTTCACCCC      720
GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC      780
CACGTGACAC CCGATGTCGC TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG      840
AACGGTACCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTTCGAT GGCTCATCAG      900
GCCCAAGAGC GTAATATGTG GTACTTCACT GCGGGCAACC GTTTCAATCC GGGCAAACGG      960
ATCAACGGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG     1020
ACTGCTCGCT ACGGCAAGGG CAAGACCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG     1080
AAGTGGAATC TCCGATTTT CGATCAGGTC AATCTCTTCC TCAAAGGCAT GTACGAGAAC     1140
GGCTATGCGC CTGCCCAATA CGGCGAGAGC AGCCACACGC GCCACTCCTA CGGCTATATG     1200
GGAGGGGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTCTGTAC CTACATAGGA     1260
CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CGCCGGTCTG     1320
ATCTATCAGA TACCTTTCTT A                                     1341
```

(2) INFORMATION FOR SEQ ID NO:94

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

```
TATAAGCAAG CTATAATGAA ACATTTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT      60
TCTTTTTTCCG GTACCTATAC CTTTGACAAA GAAAATAATA CAGAAAAGTC ACGATTTGAT      120
TTTTCTGTGA GGCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG      180
TATACATCTG CTAACGATAG ACTTTTGTCT GGTGCAATTT ATCTGGGCTT GACACCAAGT      240
AAGAAAGAAA ATGCAACCGG CGTAGCATTT CGTTTCTTAT CNCCCTCTCC GGGTTATTAT      300
GTCGATATAT CCGGCAAAGA AAATACCTTG AATTATGCGT TTTACGTTGT CGGAGCATAT      360
AATAGAATAG CCATTTCCTAT ACGCCCTATC AAAAATTTTA ATTTTCATCTT CTCTACAGAA      420
GTCGGAATGG CTTGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTTC GCAGACTTGG      480
GATAAGCAGC GCAAGTCGAG GTCCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATNC      540
CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTCTTG CATGTTTCGA      600
AAAAGGATCA ATGACTACCA GCAAAAGGAT CGAACCTTCA TTGCACTTAT CGACAACAGT      660
ATTGGCATAG GATTAAACCT C                                     681
```

(2) INFORMATION FOR SEQ ID NO:95

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1218 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

```
ATATTCATAG ACCCCGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA      60
ATGCTGAAAA ATAAATTGGC CCCCTTGGCC ATACTGTTCC TTTTGTCTCC AAAGGCTATG     120
AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG     180
GATGCACGTG CGGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TCGGTATTCA     240
CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA     300
TATACACCTT GGCTGTCCAA GCTGGTCAAT GATATTGCCC TGATGCAGAT GACCGGTTTC     360
TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA     420
GGAAAGTTGG AGACTTTTCA CGAATTGGGC GAATCCATGG GAGAGGCCCA TCCCAATGAA     480
TTTGCTGTCG ATTTGGGCTA TAGCCGCCAG TTGTCGGAGA ACTTCTCCAT GGCTGTTGCA     540
CTGCGTTACA TCCGCTCAGA CCAAAGCACT CACAACACCG GAGAGAATCA GGCCGGAAAT     600
GCCTTTGCGG CGGATATAGC CGGTTATTTG CAGAAGTATG TGCTACTGGG TAATGCGGAG     660
AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA     720
GGTGTCACGA GTTTTTTCAT CCCTACTTCG TTGAATCTCG GGACGGGGCT GTTGTATCCG     780
ATCGATGACT ATAACAGCAT CAATTTCAAC CTGAACTTA GCAAGCTGCT TGTACCCACT     840
CCTCCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG     900
GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG     960
GAAGAATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAAATT    1020
TTTGTTTCGT CCGGATATTC ATACCTGCAC CCCACCAAAG GCAATTTGCA GTACTTCACG    1080
GCCGGTGCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCTACCT GTTGTCTACG    1140
ATCCAGAGTA ATCCGTTTGA TCAGACTCTG CGGTTTACGC TTGCTTTCGA TATGGATGGA    1200
TTGCGCAATT TGTTCAC
```

(2) INFORMATION FOR SEQ ID NO:96

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

```
CTAATAATCG AAAAGGAAAT GAAAACAACA GTTCAACAAA TTATCTGTG CCTGGCTTTA      60
ATGATGTCAG GTGTATTGGG CGGAAACGCA CAGAGCTTTT GGGGAAGAAAT AGCTCCTCCT     120
TTTATCAGTA ATGAGCCTAA CGTCAAGTAT ATAATTCCCA ATATGGGGAT TGATTCAAAG     180
GGAACAATCT ATGTAACCGT GACAAAAAGG ATTCAGCAGG GAGCAAATTA TACTTCTGAG     240
CAATTGGGTA TGTACTATCG ACCATTAGGT GATAATGAAC AGTGGTGGAA ACATGATCCG     300
TATTTTGATG ACAAGATAGT TGCGGATATT CAGACAGATG CATATGGCAG AGTTTATGTA     360
TGTACGACTT CTCTCGAGA TCAAGAGTAT CAACTTTATA TAAACGAGCA GAACGAATGG     420
AGGTGTATAT TCAAAACTTC TGTGTCTACA TATGAGCATG GTATGGCTGT TTTTCGCTCT     480
TCGACAGGGG TGACTTATAT AGGTACCAGG CATCACATCT TCGCATCAGG TGTAATATGAT     540
TTCGAGTTCA AACTATCTA TGAAGACTCT ACACCTATGA GCTGTCGCTT TGCAGAGGCT     600
ACGAATAGTG GCACCATCTA TCTGGCATTG ATGCATGAAA CCACAATGTC TACGACTATC     660
CTTACTTATC AAAACGGTGA GTTCGTGATC ATCTCGGAAA GTGAATTGAG TAACTCGATT     720
ATTGCATCCA TGTGCTCTAA TAAAGAAGGT GATATAATAG CTCTTGTTAC TTCATATACA     780
```

GGATTTATGA	GTGGAACCCT	TGCGATCAGA	AAAGCAGATG	AAGGCAAATG	GCAACTTGTT	840
GGCGGAGATA	TACAGAAATG	GATCGTTCAA	AATATATGCA	TGATGGACGA	CAACAAGATT	900
GCTTGTGAAG	TCTTCGGGAC	TCCTAACGGA	GTAGATGGTC	GGACAAGGGT	TGTGTTTCT	960
GACGCATCTG	TCTTTGATTT	TSAGTGGTAT	GAAGATGAAA	TATACGGAGG	CCTGATATTT	1020
GACACTTTCT	TCTATAGCCC	TGGGACAAA	CTTCTTTATG	CGAAATTG	TGGGATTATG	1080
CTCAGGAGTA	AAGAGTCTTT	TATAACCTCT	TTCATTTCTC	CGACAGTTGT	ACAAGGAGTG	1140
GATGTCATA	CTTTGGCCGG	GAAGATAAGG	ATCGAAAGTG	AAACTCCGGT	GTCTGAGGTG	1200
TTGCTTTTCG	ACCTGGCTGG	CAGGATGGTA	CTTCGGCAAA	CCATTGATAA	TAAAATCTAT	1260
TCGGACATAG	ATACTAACGG	ACTAAAGCGA	AGCGGTATTT	ACGTAGTCTC	GGTGC GGCTC	1320
TCTTCCGGAC	AGGTATTGAG	TCATAAGGTG	CAGGTA			1356

(2) INFORMATION FOR SEQ ID NO:97

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 993 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...993
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

GGCCTGTACG	GTATGTCTGT	TGTACCTATA	ATAATTTATC	TTTGGCGGTAT	ATCAAATTAT	60
GCAAGACTCA	TGATAATCCG	GTGTCTTATC	CGTCGTCCGA	GAACCGTCCT	GTTCGGGTTG	120
ATATTCGTGG	TAGGTCTTTT	CTCTGCGATG	GCGCAAGAGA	AAAAGGATAG	TCTCTCTACG	180
GTTCAGCCAG	TGCCGAATAG	CAGCATGGTG	GAGCAGACCC	CTCTTCTCTC	CATTGATCAC	240
CCCGTCCTGC	CCGCTTCTTT	TCAGAATACC	CGTACACTGA	AAAGGTTTAG	AGACAAACAT	300
CTTTCCGATG	CTTTGCTCAA	TGGATTGAAG	CCTCATCGCT	CATCTTTGCA	ATTGAATGAG	360
GAACCTCAACT	TCGCGGCAGA	GCGTCGGGAT	TTCGTTTCTC	CCCTCTTGCA	AACTCGCCAC	420
GCTGCCGGTG	TCCTTTTCATG	GCGACCGACC	GATAGGATGC	ATTTTATAC	ATCGGGCAAT	480
ATCGGTCTTG	GCCATGATT	ATTGACCGGT	GTGCGCAAGG	ACTTCGGATG	GAATGCTGGT	540
GCCGACTTCT	TGCTGAGTCA	AAATCTTACG	GCACATGTCC	AAGGCGGTTG	GCAGCAGAAT	600
TTCGGCTTTA	TACCTATGAC	GGCTGTCAAT	GGCCAACCTGC	GTTGGCAAGC	CACCGAGAGA	660
TTGAGTTTAA	CCACCGGTAT	CGATTATCGA	CAGGTACAGT	GGAATGCTTT	CGATAATAGA	720
ACGTTCTCG	TTAAAGGAAG	TGCTCGATAC	GAAGTGATGG	ACAATGTCTT	TGTCAATGGA	780
TTTGGCAGCT	ATCTCTCTA	CAGCAGTACG	CGCTCAGGAC	TCAATATGGC	TGTTCCGATG	840
CATGGATTTC	GCCCTCAGTA	CGGTGGATCG	CTTGAGCTGA	AAGTCTCCGA	GCGATTCCGC	900
TTTGCCGTCG	GTATGGAGCG	CGAATACAAT	ATCTGGACTC	GTGCGTGGA	AACGCATTAC	960
TTTGCTTATC	CTGTATTCTA	TGGCGATAAG	AAG			993

(2) INFORMATION FOR SEQ ID NO:98

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GAGACGAACT	CTTGGGTATC	CAGCGATTGC	AATTCGACGA	CGATGAAAAC	GAATAGACGA	60
TACGCATTTG	TTTGTCCGCT	TCTGCTACTC	ACCGGATTGT	TGGCATGGGG	GCAGGATTCT	120
TCCCACGGTA	GCAATACAGC	GTTTGCAACT	GATTCTTCGA	GTAGAGAGTT	GCCCCACGGAG	180
CAGTCCGGCT	ACCGCATTCA	TTCTGCCTAT	ATGGTCGGTG	GTGGCGGAAG	CATAACGCGC	240
GACACCTATT	TGTCACCCCT	TCGTTATGGA	GGATGGACAC	TGAATTTGTT	GGGAGAGAAG	300
ACGTTCCCTC	TCAAAGCCTC	CGATTCCCGT	TGGATGATCC	GTACCGGGCA	TGAGCTGGAT	360
TTTGCCCTGA	TGGACAATCC	GGCCAATAAT	GCTCATTTCT	ATTCCCTGCT	GTATAACGGT	420
TCCGCTGCGG	CTCTTTACCG	CCTTGGCGCT	AAGCATCTGC	GAGCCGCGTG	GATGGACAAT	480
CTGCGCTTGG	CATTCGGCCC	GGGCTTGGAA	ATCGGGCTTG	GAGGAATTTA	TAGTACACGC	540
AACGGCAATA	ATCCTGCGAC	ATTGAAGCTC	TACACCAATG	CCATCGCCCA	AGCCTCGATA	600
GGATACTACG	TCCCCTCCGA	AACTTTTCCC	CTGTATTTTC	GGTGTCTCTC	CCAGATCAAT	660
CTCTTCGGTA	TAGCCTATGG	AAATGGTTT	GGTGAGAGCT	ATTACGAGAA	TTTTTTGCTC	720
AATAACGGCA	TTGCAGGCTC	CCTGCATTTC	ACTTATCCGG	GCAAGTTTAC	TCGGTTCACG	780
ACACTCATAA	CGGCGGATAT	TCCCATTCCG	AACTTCTGTA	CGCTTCGTGT	CGGTTATCGC	840
TATTCCCATT	TGGGCTCTTC	GCTTAACGCA	TTGGATACTC	GAATCCACAG	TCATACGGCT	900
TTTATCGGTT	TCGTACGGA	GTTTTACGGA	TTCCGTGGGC	GCAAAGCCAT	GAATACCGGT	960
CGGAGAACCA	GTCTTTACTA	TCATGAT				987

(2) INFORMATION FOR SEQ ID NO:99

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...957
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

TTTACGTCCG	GTACGATATT	CGTCCGTATA	GCCATATCCG	GCCGTGTAGT	GTGCCGTGAG	60
GTTGAGGATA	ACGGAAGGAG	AGAAGCTGTG	CGTCATGATG	GCATGGTAGT	GACGCTGCTC	120
GTAATTGTCT	GTATTGTGGT	AGTAGTGC	TACTCCTTGC	GCGTCCACGT	ACATAAGACC	180
GGCACTGTTG	TATCGGCGGC	CATATTTGGC	TTTCATCCTC	TTGGAAAGAC	CGTTCCATGC	240
GATACCCGTA	ACTTCTTTTC	CTCCGAAAGT	GATGAACCTG	AGAGCCGTGT	TGCTACCGAA	300
ATAGCCCACC	TGTGCGAAAT	AGGATTTTCA	ATCCACGCTT	CCTCTATCCA	CGTAGCCGTC	360
CGAACCGATT	TTGGACAGGC	GGGCATCCAC	TGCCCAATGG	CGACCGATGC	GTCCGCTACC	420
GAGTTTGACC	GATCGGCGGA	ATGTGCCGAA	CGAACCTCCG	CTCAAATCGA	CACGGCCATA	480
AGGAGCCAGT	CCCAAATTAT	CCGTACGCAT	ATTGACACTT	GCCCCAAAAG	CTCCGGCACC	540
ATTGGTGGAA	GTATCCACAC	CTCGCTGCAC	CTGAAGGTCT	TCGATGGAAG	AGGCGAAGTC	600
GGGCATATTC	ACCCAAAAGA	CGGACTGAGA	TTCGGAGTCG	TTGAGGGGTA	CTCCATTGGT	660
AGTTATGTTG	ATGCGATTGG	CATCGGTGCC	ACGCACGCGA	AAGCCGGAAT	ATCCGATACC	720
CGTACCGGCA	TCGCTGGTGG	CTACCACGGA	GGGAGTCAGC	ATCAGCAGAT	AGGGGATGTC	780
ACGACCATAA	TTGGACTTGG	AAAGTTTCGGC	CTTGCGAACG	TTGGTGTAAG	CGACAGGGGT	840
TTTCGCCGTG	GCGCGAGTAG	CTACGACCTG	TACGGTCTGG	AGCTGCACAT	TGCTAAGACT	900
ATCTATCTCG	CTGTGGGAGA	CGGGTGCTTG	TGCCGTCAGG	CAGAAAGGCA	GGACGGC	957

(2) INFORMATION FOR SEQ ID NO:100

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1842 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```
CCATATAATG  TCCAATCTAT  TAGCAACAAG  ACGATTAAAA  AACAAATGGA  AAACCTTAAAG      60
AACATTACAGC  CCAGAGAGGA  TTTCAACTGG  GAAGAGTTTG  AGGCCGGTGG  CGTCCATGCT      120
GCCGTGAGTC  GTCAGGAGCA  GGAAGCTGCT  TATGACAAAA  CGCTCAATAC  CATCAAGGAA      180
AAGGAAGTGG  TAATGGGTAG  GGTAACTGCT  ATCAACAAGC  GTGAAGTGGT  TATCAATGTA      240
GGGTACAAAT  CGGAAGGTGT  GGTACCTGCA  ACAGAATTCC  GCTACAATCC  CGAACTCAAA      300
GTGGGAGACG  AAGTGGAGT  TTATATCGAG  AATCAGGAAG  ATAAGAAGGG  CCAGCTCGTC      360
TTGTCTCACC  GCAAGGGTCG  TGCCGCTCGC  TCTTGGGAGC  GCGTGAACGA  GGCTCTCGAA      420
AAAGACGAAA  TCGTAAAGGG  CTATGTGAAG  TGTCGTACCA  AGGGTGGTAT  GATCGTCGAT      480
GTATTCGGTA  TCGAGGCTTT  CCTCCCGGGA  TCACAGATCG  ACGTGCGCC  CATTCGCGAC      540
TACGATGCAT  TCGTTGAGAA  GACGATGGAG  TTCAAGATTG  TGAATATCAA  TCAAGAATAT      600
AAGAATGTAG  TTGTTTCCCA  CAAGGTGCTC  ATCGAAGCAG  AGCTCGAACA  ACAGAAGAAA      660
GAAATCATCG  GCAAGCTCGA  AAAAGGGCAG  GTACTCGAAG  GTATCGTCAA  GAATATTACT      720
TCTTACGGAG  TATTTATCGA  CGTGGTGGG  GTGGATGGTC  TTATCCATAT  CACTGACCTT      780
TCATGGGGTC  GTGTGGCTCA  TCCGGAAGAA  ATCGTACAGC  TGGATCAGAA  GATCAATGTC      840
GTTATCCTCG  ACTTTGATGA  AGATCGCAAG  CGTATCGCTC  TCGGACTCAA  ACAGCTGATG      900
CCTCATCCTT  GGGATGCTCT  CGACAGCGAG  CTTAAGGTAG  GCGATAAGGT  GAAGGGTAAA      960
GTTGTGGTGA  TGGCAGATTA  CGTGCTTTC  GTTGAGATTG  CACAGGGCGT  TGAGGGTCTT     1020
ATCCACGTAA  GCGAAATGTC  ATGGACACAG  CACTTGCGTT  CTGCTCAGGA  CTTCTGTCAT     1080
GTAGGCGACG  AAGTGGAGC  CGTGATCCTG  ACGCTCGACC  GCGAAGAACG  CAAAATGTCTG     1140
CTCGGTCTGA  AGCAACTCAA  GCCGATCCT  TGGGCTGATA  TCGAAACTCG  TTTCCCTGTA     1200
GGCTCTCTGC  ACCATGCTCG  TGTTCGCAAC  TTCACCAATT  TCGGTGTATT  CGTTGAGATC     1260
GAAGAGGGCG  TAGATGGCCT  TATCCATATT  TCCGACCTTT  CTTGGACGAA  GAAGATCAAA     1320
CACCCAGCG  AGTTTACGGA  AGTAGGTGCT  GATATCGAAG  TTCAGGTAAT  CGAGATCGAC     1380
AAGGAAAACC  GTCGTCTCAG  CTTGGGTGAC  AAACAGTTGG  AAGAGAATCC  TTGGGATGTA     1440
TTGAGACGG  TATTCAGTGT  AGGATCTATC  CACGAAGGAA  CGGTAATCGA  AGTGATGGAC     1500
AAGGGTGTCT  TCGTTTCTCT  GCCTTACGGT  GTGGAAGGTT  TTGCCACTCC  GAAGCACATG     1560
GTGAAGGAAG  ATGGCTCACA  GGTGTACTC  GAAGAGAAGT  TACCTTTCAA  GGTATTGAG      1620
TTCAATAAGG  ATGCCAAGCG  AATCATTGTA  TCTCATAGCC  GTGTATTCTG  AGATGAGCAG     1680
AAAATGGCTC  AGCGTGAAGC  CAATGCAGAG  CGTAAGGCTG  AAGCCAAAGC  GGCTCAGAAA     1740
GAAGCTGTCT  CCGAAGCTGC  CAATCCTGCA  CAGGCTGTAG  AGAAAGCCAC  TCTCGGAGAC     1800
CTCGGCGAGC  TGGCCGCTTT  GAAAGAAAAG  CTTTCAGAAA  AC                                     1842
```

(2) INFORMATION FOR SEQ ID NO:101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

```
TCGACAATAA  TGAAAAAAGC  TATTCTTTCC  GGAGCGGCCT  TGCTCCTCGG  CCTATGTGCC      60
AACGCACAAA  ACGTGCAATT  GCACTACGAT  TTCGGTCATT  CCATCTACGA  CGAACTAGAT     120
GGACGTCCCA  AACTGACTAC  CACAGTGGAA  AACTTCACAC  CCGACAAATG  GGGGAAGCACC     180
TTCTTCTTCA  TCGACATGGA  TTACACGGGC  AAGGGTATCC  AGTCGGCCTA  TTGGGAGATT     240
TCGCGCGAAC  TGAAGTTTTG  GCAAGCTCCC  GTTCCATTCC  ATTTGGAGTA  CAACGGAGGC     300
CTCTCCACAA  GCTTTACTTT  CGGACACGAT  GCTCTAATCG  GTGCCACCTA  CACCTACAAC     360
AACCCCTCCT  TTACACGTGG  ATTTACGATC  ACGCCCATGT  ACAAGCATCT  GGGTGCAC      420
GACTTCCACA  CCTATCAGAT  CACCGGCACT  TGGTACATGC  ACTTTCTGGA  CGGTCTGCTT     480
ACCTTCAACG  GCTTCCTCGA  TCTTTGGGGT  TTCCCCCAAG  AGAACCCAAT  CGGGGGCCCT     540
GTGCTCAAAG  AAGGGGATAA  GTTCGTATTC  CTGTCCGAAC  CGCAGTTCTG  GATCAACCTC     600
AATCGCATCA  AAGGCATCGA  CAAGGATTTC  AATCTCAGCA  TAGGGACAGA  GATGGAAATC     660
AGCAGGAACT  TCCTCGCAT  GGACAAATTC  TCCTGCATCC  CTACTCTTGC  GGTCAAATGG     720
ACTTTCAAC                                     729
```

(2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

```
ATGAAAACAA TTAGTAAGAA CCATGCGGCA CGGATCTGTG CCGCCATTGC TTTGTTTGCA      60
GTGTGTAACG GCCGGATAGC TGCTCAGGAT TTTCTCTATG AAATAGGAGG AGGTTTGTGGT      120
GCTGCTCAGT ATTTTGGCGA TGCAAAACAGA GGCTTGTTCG GTTCATCCGG AGTAGGTTTG      180
GAGTTGGTCG GACGTTACAA TTATAATTTT CGCTGGGCTT TCAGTACCAT GTTGATTTGG      240
CGTACATTGA GAGGCGATAC CGATAAGTCC GGGAATGTCT TCCCCGATTT TGCTCAAGCG      300
GATTTTAAGG TCGGCTTGAC TCAGCTCCAC GTTAGAAGCG AATTTAACTT TCTCCCTTAT      360
AGCGATGGCT ATAAGTATCT TGGTACAGCT CGGCTGTCTC CTTATGTAGC GGCCGGGGTTG      420
TCTTTGGGTT TTGCTTCGGG TGCTAAAGGT TCGGCTTTTG CTCCCAGGAT TACTGCGGGA      480
ATGGGAGTGA AGTATAAGCT TAAACCGCGG ATCAATGTCG GTATCGAGTA TTCTTTCACG      540
GGGTTACTTA CCGATGCTTT GGATGCGCTG ACGGATAAAA GTGTTTGGCT CGAGGATCCA      600
TATAAGATCA ATGACTCCTG GGTCAAAAAC AAGGATGCTA CAGGGGCCTT AGTGCTTAGG      660
ATTACGTATG ACTTCGGCTT GCGTAAGACT TTTTGAATA AACAA                      705
```

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

```
AATATAATGT ATAAAGACTA TAAGGGTTTG TATGCGTCGC TTCGGTGGTA TGCCCTGATC      60
ATTGGGTTGC TATTGTCAGC AGACGGTATA CAGGCTCAGA ACAACAACTT TACCGAGTCG      120
CCTTACACTC GCTTCGGCCT TGGCCGTCTC GGAGAACGGA CGACTATTAG TGGGCATTCC      180
ATGGGAGGAC TCGGCGTCCG TCTGCGTCAG GGCACATACG TCAATGCCGT CAATCCTGCT      240
TCATACTCGG CTGTGGATTC GATGACGTTT ATCTTCGATT TCGGTGCATC TACCGGAATT      300
ACGTGGTATG CCGAGAACGG GAAAAAGGAC AATAGGAAAA TGGGAAACAT TGAGTATTTT      360
GCCATGCTTT TTCCTATTTT CAAATCCATT GCTATGAGTG CGGGAGTGCT TCCTTACTCC      420
GCATCCGGGT ACCAGTTCGG ATCCGTTGAT CAAGTGGAAG GAGGCAGCGT CCAGTACACC      480
CGTAAATACT TGGGGACAGG CAATCTGAAC GATCTCTATG TCGGTATAGG TGCAACCCCG      540
TTCAAAAACT TCTCAATAGG AGCCAATGCT TCATCCCTTT TTGGGCGATT CACACACAGC      600
AGGCAGGTAA TCTTCTCCAC GGAGGCTCCT TACAATCCCG TACATCTCTC GACGCTGTAC      660
TTGAAGGCTG CCAAGTTCGA CTTGCGTATG CAGTATCACC TTCTTCTCAA ATCAGATCGT      720
TCGCTCGTTA TCGGTGCCGT CTATTCTCCG CGGGTGAAGA TGCATAGCGA GCTGACTCAG      780
ATAAAGAATC AGGTTTCAGAA CGGTGTAGTA GTGGAGAGCG AAACCCAAGA ATATATCAAG      840
GGAATGGACT ATTATACCTT GCCTCATACA TTGGGGATAG GTTTTCTT TAAGAAAGAAA      900
GATAAACTTC TCTTAGGAGC AGACGTCCAA TATAGTAAAT GGAAAGGCGA GAAATTTTAT      960
AAATCCGATT GCAAATCCA GGACAGAATA CGGGTATCTC TCGCGGAGA GATCATACCG      1020
```


GATATAAATG	CCGTTGGGAT	GTGGCCTAAA	GTTCGCTATC	GCTTCGGTTT	ACATGGTGAA	1080
AATTCTTACC	TGAAAGTGCC	GACTAAAGGC	GGTGTATATC	AAGGATACCA	TATCGTAGGT	1140
GCTGTATTCC	GTATAGGAAT	CCCCTCAAT	GACAGACGTT	CGTTCGTAAA	TGTCTCTCTT	1200
GAATATGACC	GATTGATCCC	GAAGGAGGGT	ATGATCAAAG	AAAATGCTCT	GAAATTGACC	1260
TTCGGCCTCA	CGTTCAACGA	GTCATGGTTT	AAAAAGCTGA	AACTGAAC		1308

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

AATACCATTT	CGGAGAATGG	GAACGATAGC	ACCTATTTTT	CTTTTCAAAC	TTTCTTATG	60
CGATCGATTT	ATCAATTACT	GTGTGCAATA	CTCCTTGCTT	CTCTTGTTT	CGTCGGGCTG	120
GAAGCCCAAC	AAGCCGGAGT	AGCAGGTAGA	GTATTGGACG	AAGAAGGCAA	CCCCATGATT	180
CAAGCCAACG	TACAGCTTGT	ACAGAGTACC	GGCCAAGTAG	CCGTTGCCGC	AGGTGCCACT	240
AATGAAAAAG	GGTTGTTTAC	CCTGAAAAAG	TCACAGGAGG	GTGACTACAT	TCTGCGGTTT	300
TCATATGTAG	GTTCACACTAC	CCACGACGAA	AAAATATCTC	TTAGAAACGG	GCAAACCATT	360
ACGCTCAAAG	ATATATCCAT	GAACGAAGAT	GCCCGTCTTC	TACAGAGTGT	GACGGTGCAG	420
GCTAAAGCGG	CAGAGGTCGT	GGTACGCAAC	GATACGCTCG	AATTCAATGC	CGGATCCTAT	480
ACCGTAGCAC	AGGGAGCTTC	TATCGAGGAA	CTGATCAAGA	AGCTACCCGG	AGCAGAGATC	540
GGATCCGATG	GGAGATCAC	CCATCAACGG	AAGGACATTA	GCAAGATCCT	TGTCGATGGC	600
AAAGAGTTTT	TCTCCAAAGA	TCCACAGGTG	GCAATAAAGA	ATCTTCCGGC	CGATATGGTC	660
AATAAAGTAC	AGTACTGAA	CAAACAGAGC	GAGCTGTGCG	GGATGAGCGG	TTTCGATGAT	720
GGAGAAGAGG	AGACCGTAAT	CAACCTGACG	GTGAAGCCCG	AAAAAAGAA	AGGCCTCTTC	780
GGAACGCTTC	AGGCCGGCTA	CGGTACCGAC	CAACGCTATA	TGGCCGGAGG	GAACGTCAT	840
CGGTTCGATG	GAAATAAGCA	ATGGACATTC	ATCGGTAGTG	CGAACAATAC	GAACAATATG	900
GGCTTTAGCG	AGATGGACAG	CGAGATGGGA	TCCATGACCT	TCTTCTCTCC	CCAAGGCGGT	960
GGTCGACGCG	GCTTCGGCAA	TAGTGGAGGT	GTTACGTCTT	CGTCGATGCT	GGGCGGCAAC	1020
TTCAAGTGTG	AATTCTCTCT	TGCCCTTAAT	ACAGGAGGCG	ATGCACGCTA	CGGATACAA	1080
GACAAGGCCA	TAGAGACGAC	CAAACGCGTG	GAAAATATCC	TCGCCGAAGG	GAATACTTAT	1140
ATGGACGAAA	ATATATTGGA	ACGCTCTTTC	TCTCACAATG	GTCAGGCGCG	ATTAGGATG	1200
CAATGGAAAC	CGTCCGAACG	TACCGAAGTG	GTATTCGAGC	CGGATCTTTC	GATATCCAAG	1260
ATCGATGGGT	TCTTTAACGA	CACATACGAG	ACGAAAGATG	CCACCGGAAT	CTCTATCAAC	1320
AAAGGTTCTA	TCCACCAAAC	TACACAAGGA	AACAACCTCA	GACTGAACGG	AGAATTGGAT	1380
ATCAGTCACA	AGTCAACGAA	CGAAGGCCGT	ACGATCAGTG	CCTCCGTCAG	TGGCGGTCTG	1440
ACCGACGAAG	ACGGAGATGG	CATATATCAG	GCTGTGCTCC	AAAGCGTGGA	GACGAATCAA	1500
AAGCAATTCA	ACGACAACCT	CAACCTGCAA	TATCGGCTTC	GCCTCTCGTA	TGTGGAACCG	1560
TTGGGTAAAA	ACTACTTCGC	ACAAGCGATT	CTGAACAGAC	GTTTCTCCCG	TCGCAATTCT	1620
GATCGTGAGG	TGTACCGACT	GGGCGATGAC	GGGCAATACT	CCATATTAGA	CAGTCAGTAC	1680
GGACTCTCCT	ACAGTAACGA	GTTCAACCCG	TATCGCATCG	GACTCAACCT	CAAGAAGATT	1740
GCCAAAACGT	GGGACTACAC	CGTAGGATTC	AATGTGGATC	CCAACAGAAC	TGTCAGCTAT	1800
CGGAGCGTAG	CCGGAGTAGA	GCAGGACAAA	CTGGCTTTCA	ATCGTGTCAA	TCTCTCCCG	1860
ATGCTCCGAA	TCAACTACAA	ACCGAGCAGG	ACTACCAACC	TCCGAGTGGA	CTACCGAGGA	1920
CGCACGACAC	AACCATCCAT	CAATCAGATC	GCTCCCGTTC	AGGACATCAC	GAATCCGCTA	1980
TTCTGTGACG	AAGCAATATC	CGGTCTGAAG	CCGAGCTATT	CCAACAATGT	GATGGCCATG	2040
TTCTCGGACT	TGATGCCCAA	AAGTCAGCGA	GCTTTCAACA	TTGTTTCTCT	CGGCAACTAT	2100
ACATTCGACG	ACATCGTCCC	CAATACGCAC	TACGATCCGT	CTACAGGGAT	CGGTACCACT	2160
CGTTACGAAA	ACGCCTCCGG	TACGTGGCAA	GCGAATCTTC	ATGGGACACT	ATCGCTTCCA	2220
CTCAAGAACCA	GGGCATTTC	TTTCAGGATG	TCCTTGTTCA	ACAGGTGGCC	CGAAGGACAA	2280
AGCTTCATCA	ATGACGATAA	GAACAAAGCT	CTCTCTTTCC	GAACGAGGGA	ACGCCTGACG	2340
CTGACCTATC	GCAACAATTC	GATCGATACG	AGTATCGGTG	GCAATATCCG	ATTCTATATG	2400
GCGAATAATA	GTCTGAGCGG	ACAGAAAGAT	TCTCGCACAT	ACGATTTTGG	CGGCAATTAT	2460
CAAGTTGCC	TAAACGCTTC	CTATGGATTG	CGTATCGACA	CGGATGTTGA	ATACAATACG	2520
AACTCCGGTT	ACAGCGGAGG	ATTGAGTCTG	GACGAATGGC	TTTGGAATGC	TTGCTTTTCA	2580
TACAGCTTCC	TCCGTGACAA	GGCCGGTACA	CTGCGTGTCA	ATGGCTATGA	CATCCTCGGT	2640
CAGCGGTCAA	GTATCAGCCG	TTCTGCTTCG	GCCATCAATA	TAGAAGAGAG	CATGTCCAAT	2700
ACGATCGGAC	GCTACGTGAT	GGTGGACTTT	ATCTACCGAT	TCAACGCCTT	CAGTGGTGGT	2760
GGATCTCGCA	GCGATCATCA	GCGTGGCAAT	ATGAATCGTC	CGGGCCCAAC	TTTCGGCGGT	2820

(2) INFORMATION FOR SEQ ID NO:105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GGAGAGTATC CTGCAAACAG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA	60
AGTTTGCTCC TGCTTGGAGC GGTACTGCTG ATTACGCTTC CTGCGTACTC GCAGAATGAT	120
GACATCTTCG AAGATGACAT CTATACATCG CGAAAAGAAA TACGTAAACA AAACCAAGTT	180
AAAGACTGCG AAAACCAAGA GGACGGATAC GGCGACGATA CGGAATATAC AGTGGCTTCC	240
GATCGGGACA TTGACGCCCTA CAATCGTAGA GATGGCCAGT CCTACGATGG GAAAAAGTTG	300
TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTCGCTA TAGTCGCCGC	360
TTGGCTCGAT TCTATAAGCC GAATACGATC GTCATTTTCAG GTGCCGACAA TGTATATGTA	420
ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA	480
AACATTTACA TCAACAGTCC TTGGTGCGAT CCGTTCCTT ATACGTCATG GTATCCATCT	540
TTCTCCGGCT GGTACAACTA TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC	600
GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC	660
TACAATCCCT ATGGAATCGG TATGGGTTGG GGATATCCTT ATGGCTGGGG CAGCTATTAC	720
GGTTGGGGTG GCTATCCGGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGACCTAT	780
TCCAATGGTC AGCATTCCGG AGCTTACTAT TCTTATGGCC GACCGAATCG TATCAAAGGT	840
GGAACGTCGG GTGCCAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCGTCTTCG	900
CAAAAAATA AGTTCGGATT GCAGTCGAAC AAACCCAATA ATAATCTGCA AAATGTCAAG	960
TCGGGACGTA CCGGCCGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAAC	1020
GGGCAAAAGC AGAATCGTCC CGTATTCCAG CAGAATCAGT CCGGCAATGA CCGACCGACC	1080
GGACGGAATA TCCGACGCGA GAGACAGGGG GAAATAACG ATAGGACATT TTCGACTCCT	1140
TCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GCTCTTCTTC CGGCTCTATG	1200
AGCGGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT	1236

(2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

AGTAATAGCA GCTCCACAA GTGGTTAATT TATTATCATA TAGAAAAGAC TAAAAGTATT	60
ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG	120
GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC	180
TCTTTGAATA GGGATGATGC TCCGATAAA TGGCAACCTA TGCAATGCCA TTTCAGTATT	240
CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC	300

TATATCATGG	GTATAATCAA	GAACAATTAT	CTGGAGTTTG	GTGCCCCTTT	CGAGGATCTC	360
TATAAGCCCC	TGCCCCGACA	TGAACCCGAG	ATGGGGCGTG	CGGTTCTCTCA	CATGTATGTG	420
AAGGGAAGCT	ATCATTTGGG	GGAGCTGACT	ATGGGAGACT	TCTACGATCA	GTTCGGTAGC	480
GGTATGGTAT	TCCGCACCTA	TGAAGAGCGC	AACCTCGGTA	TAGACAACGC	GGTTCGCGGC	540
GGACGTATAG	TACTCACTCC	TTTTGATGGA	GTGCGTGTC	AGGGTATTGC	AGGACAGCAG	600
CGTAACTACT	TCGACCGCAC	GGGCAAGGTA	TTCAATTCCG	CGCGAGGCTA	CCTACTGGGT	660
TCTGATCTGG	AGCTGAATGT	AGAGCGTTGG	AGCAGTGCCA	TGCGCGACAA	TGACTATCAT	720
TTGGGTATCG	GGGGATCGTT	CGTTTCCAAA	CACGAAGCAG	ACGAAGATAT	ATTTGTGGGT	780
GTAGGCGAAG	ATCGCAAGCG	ACTCAACCTG	CCGCTCAATG	TCCCGATTAT	GGGCCTGCGC	840
ACCAACTTTC	AAAAAGGAGG	TCTCGCCCTC	TACGCAGAGT	ATGGATACAA	ATACAACGAT	900
CCCTCGGCAG	ACAATGACTA	TATCTACCAC	GACGGACAGG	CTGCACTCCT	CTCTGCCTCA	960
TACTCCAAAA	AAGGAGTAGT	TATCTGTTG	CAGGCCAAAC	GTGTGTGAGAA	CTTTGCTTTC	1020
CGCAGCAAGC	GAAGTGCCCA	GCTCACACCG	CTTATGATCA	ACTATATGCC	GGCTTTTACC	1080
CAAGCTCACA	CTTATACGCT	GGCGGCCATC	TACCCCTATG	CTACTCAGCC	TCAGGGAGAA	1140
TGGGCTTTCC	AAGGTGAACT	CGGTTACAAC	TTTGCTCGCC	GGACAGCTCT	CGGTGGACGC	1200
TACGGTACCG	GCTTGCGTAT	CAACGTTTCG	CATGTGCGTG	GTCTGGACAA	AAAGATGCTC	1260
AAAGAGAATC	CCGACGAACT	GATCGGAACG	GATGGCTACA	CCGTTTCTTT	CTTCGGCATG	1320
GGCGACCTCT	ATTATTCCGA	TATAGATGTG	GAGATTACTA	AAAAGGTAAG	CCCAGGATTC	1380
AACTTTACGC	TCACCTACTT	GAATCAGATC	TACAATAACA	AGGTACTGCA	CGGTGCAGCC	1440
GGAGAGAAGC	CTTGGAAGAT	ATCTGCCAAT	ATCTTCGTCT	ATGATGGTAA	GTATAAGCTG	1500
AGTAATAAGG	TAGCCCTCCG	TACCGAATCG	CAATATTTGC	ACACGAAGCA	GGATCAGGGT	1560
GACTGGATCT	ACGGCATGGC	CGAGCTCTCT	ATCCTGCCTT	CTCTGATGCT	TTCCCTCTCG	1620
GAGCAGTATA	ATATCGGAGA	GACCAAGAAA	CATTATGTCA	TGGGGTCTGT	CACCTATACT	1680
CACGGAGCAC	ATCGAGTAGC	TTTCTCTGCA	GGCAAAACCC	GTGCAGGGAT	GAAGTGTCTG	1740
GGAGGTGTAT	GTCTGTGGT	CCCTGAGACT	CAGGGATTCT	ACCTTTCTTA	TAGCACCAAT	1800
CTG						1803

(2) INFORMATION FOR SEQ ID NO:107

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...756
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

AGGGGGTCGA	GTTCGGGCAT	TTCAGCCCGT	GGACGCGACA	TGCGTTCTTT	ATTTTGTAGC	60
GCGTTGCGCA	GCTCCTCTCT	CCATGGTTCA	GAGCGACGCA	GTCGGATAAG	TTCTTCTGTA	120
GTCATGTCAA	TAAGGCAGAA	AATAAGGTTA	TTCCATCTCT	CGGTATGCGC	CCAAACGCAT	180
GATCATCTCA	TCGAAATCCA	CTTGGTGTGC	ATCGAATTCT	GGGCCATCGA	CACAGACGAA	240
TTTCGTCTGT	CCTCCACACG	TTATACGACA	AGCCCCACAC	ATACCGGTGC	CATCCACCAT	300
AATTGTATTG	AGAGAAGCTA	TGGTCGGTAT	CTCGTAACGT	TTGGTCAGGA	GAGAAACGAA	360
CTTCATCATC	ACAGCCGGCC	CGATCGTAAC	GCAGAGGTCT	ACCGTTTCCC	GTTTGATAAC	420
GCTTTCCACT	CCATCCGTTA	CGAGGCCCTT	CGTCCCATAA	GACCCATCGT	CTGTCATGAT	480
GATCACTTCA	TCGCTATTGG	CTCGCATTGG	TTCTTCAAGG	ATAACCAGAT	CTTTAGTTCT	540
GGCAGCCAAT	ACGACAATTA	CACGGTTGCC	TGCTTTGTGG	AAAGCCTCCA	CGATCGGGAG	600
CAAAGGAGCC	ACACCCACAC	CGCCTCCGGC	ACAAACCACT	GTGCCGACCT	TTTCGATATG	660
CGTACTCTGT	CCCAGCGGAC	CTACCACATC	CGTGATATAG	TCGCCGACTT	CGAGTTCGGC	720
CAATTTCTTG	GAAGATTGTC	CCACGGCCTG	AACCAC			756

(2) INFORMATION FOR SEQ ID NO:108

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

```
CTCTTGTTTT CTCTCCTTT ACCCCGAATG GATCGTCTTA AGCCTTCATA TATTGTTCTGA      60
ATAGCAGCCA TTCTCTGCTT GTTTGTCGGC AGGCCTTTGT TTGCGCAGAG CTATGTGGAC      120
TACGTCGATC CGCTGATCGG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT      180
CCGGTGATCG GTTTACCGTG GGAATGAAT AGCTGGACAC CGATGACCGG TGTACCCGGT      240
GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTCGCG GATTCAAACA GACCCACCAA      300
CCGAGTCCTT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCCTTAC GGCACCGCAG      360
AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAAATGGT GCAAGCAACT CTTTTCGGAC      420
GAACAGACCT CGTGGTTCTC GCACAAAGCG GAGACGGCGA CGCCATACTA TTATAGTGTC      480
TATTTGGCCG ATTACGACAC ACGCGTGGAG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT      540
CGCATACGTT ATTCCGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTCG TCTTGATGCC      600
TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTCACA CCGTAGTGGG CATATCTCGC      660
AAGAATAGCG GAGGTGTGTC GTCGTAAGT GCCTGTTATT TCATCCTGCA GTCCGATACT      720
CCTATGGCCG ATGTCCTGCT TGAGACAGAT ACCGGCAAGT CAGACGAAGG CACAAGGGCA      780
TGGGCAGCCT GTCGCTTCGA TTCGAAGAA GTTACCGTCC GGTGGGCATC TTCTTTTATC      840
AGTGTGCGAG AGGCCGAAA AATCTTGCG GAAGTCAAAG GGCAGAGTTT CGACCGGATC      900
AGACTTGCCG GTCGCAAGG TTGGGAGTGG TACCACTCCT TAGGTTATGT TCCGGCTGAT      960
ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTGTCTGCT TTTCCCCCGT     1020
CGCTTCTATG AGGAGGATGC TTCGGGCAAT TTGTGTCATT ACAGCCCCTA CAATGGAGAG     1080
GTACTTCCCG GTTATCTCTA TACCGATACC GGATTTTGGG ACACTTTTCG AGCCCTTTTC     1140
CCCTGCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT     1200
GTATATCGCG AGAGTGGCTT TTTCCCCGAA TGGGCCAGTC CGGGCCATCG GGATTGTATG     1260
ATAGGCAACA ACTCTGCTTC TGTCTGGCG GATGCCTACC TCAAGGGTGT TCGGGTAGAA     1320
GATACCCGTA CACTGATGAA CGGACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAAATC     1380
TCCTCCACGG GTCGCAAGG TTGGGAGTGG TACCACTCCT TAGGTTATGT TCCGGCTGAT     1440
GCAGGCATCG ACGAAAGTGC TGCCCGTACG CTCGAATATG CTTATAACGA TTGGTGCATC     1500
CTCCGACTGG GCGGCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT     1560
TCGATGAAC ATCGTCATCT GTTCGATCCG GAAACCAAAC TCATGCGCGG TAGAAATCAG     1620
GATGGTAGTT TCCGGACACC TTTTCCCCCT TTCAAATGGG GAGATGTATT CACGGAGGGC     1680
AATGCCTGGC ACTACACTTG GTCGGTCTTT CATGATGTGC AGGGGCTTAT CGACCTGATG     1740
GGAGGAGATC GCCCGTTCTG GTCTATGCTC GATTCGGTAT TCAATACTCC TCCTATGTTC     1800
GATGAGAGCT ATTACGGATT TGTCATCCAC GAAATCAGAG AGATGCAAAT AGCGGATATG     1860
GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATATGA TATATCTGTA TAATCATGCC     1920
GGTCATCCAT GGAAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT     1980
ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTT     2040
TCTGCTTTAG GCTTCTATCC TGTACACCC GCTACGGATC AGTATGTGCT CGGTTTCGCCG     2100
ATTTTTCCTA AGGTAATACT CTCCTTTCCC GACGGACACA AAACGGTGTT GCATGCTCCG     2160
GCCAACAGTG CCGATACGCC TTACATCCGC TCGATCAGCG TAGAAGGAAA AGAATGGAGC     2220
TGCAATTACC TGACTCACGA ACAGCTTCGC TCTTCTGCAT CCATTCAATG GATGATGGAC     2280
ACGAAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTCTCCACG     2340
GAGCAACAGC GTCGCGCTAA TCACAGTAAT     2370
```

(2) INFORMATION FOR SEQ ID NO:109

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

ATTGTGGCA	GTAAATGAA	TCTATCGGA	TTACAATCTT	TCACTATGAT	GAAATCCATG	60
CGCAGCGTG	TGTTGCTACT	CTTTCCATTG	TCTTTGATCA	CTGCTTTGGG	CTGTAGCAAT	120
AACAAAGCTG	CCGAATCGAA	GTCTGTCTCT	TTCGATTGGG	CCTATCTCGA	ACGCTACATC	180
CCTCTGCGGG	CAGACATAGA	TACGCCATCG	CTGCATGTGA	TGATCAGCTA	CGTCTATCCT	240
TCGGGAGATG	ATATGCTCAC	AGAGATTTTC	AACGGTTTGC	TCTTCGGCGA	CAGCCTGATG	300
GATTCTCTTT	CGCCGAGAA	TGCCATGGAA	GGCTATGCAC	AGATGCTGGG	AGAAGACTAT	360
CGCTCTAACA	ATGCCGAAGC	CAATCTGCAA	GGGCTTCCTT	CTGACCTTTT	GGACTATATC	420
TACAAGCAGG	AAAATACCAT	CGCTTATTGC	GATACGGGAT	TGATCTCCAC	GCGCATCAAT	480
ACATATACTT	ACGAAGGCGG	TGCACATACG	GAGAATACAG	TCCGGTTTGC	CAACATCCTT	540
CGCACCACCG	GCAAGGTGCT	CGAAGAGCGA	GATATATTCA	AGATCGACTA	TGCGGAAAGG	600
CTGTCCGCAC	TCATCATAGG	ACAATTGGTG	CACGATTTCG	GCAAGACCAC	ACCTGCCGAA	660
TTGGATGCAA	TAGGTTTCTT	CAACGCAGAA	GAAATACAGC	CCAATGGCAA	TTTTATGATC	720
GATGACAAAG	GTCTCACATA	CTGTTTCAAT	GAGTATCAGA	TAGCTGCTTA	TGCCAGAGGT	780
GCTGTCTATG	TCCGTCTCGG	ATATGACGTA	TTGGCTCCTT	TGCTAAGGGA	TGATTCCCCA	840
CTAAAGCGTT	ACTTGCCG					858

(2) INFORMATION FOR SEQ ID NO:110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

GGGATAATAT	CTGTTCTTTC	ACATGTGGTT	GACCGTCCAC	AATGGGGTGC	TTCTCCCGAA	60
GCTGCTGGCA	CGCATAGTGT	GTATTCGATT	CTACATCCCT	CCGCCGGTAT	TATCCGGATC	120
AGGTCTATGG	GTATTATCTC	AGCCTGCCGT	ATCGCAATTC	TTGCCGGCAA	GCACCCCGT	180
AGCGGTCTGT	CGAGGGCAAA	TGTAGGTATT	CTTTCGTACA	ATCCAGAAAA	CACGCCCCGAG	240
AAAAAGAGAA	AACTGCAAGA	AAAAAATGTT	TTCCTCCAAA	TCCGGCTCCG	TCAATCATTT	300
AATAATTTGA	TACCTTCGCT	CCCATTTAGA	ATCGATAACA	CAAAAAAAT	CACTGAAATG	360
AAAAAACTA	CTTTGACAGG	ATCGATATGT	GCTTTACTCC	TGTTTTTGGG	TCTCTCGGCC	420
AATGCCCAAT	CGAAGTTAAA	GATCAAGAGC	ATTGAGGCAG	CTACCACTTT	CAGTTCGGCC	480
ACGGCCGGAA	ATGGTTTTGG	TGGCAATATC	TTCGGCATGG	ACATGAGCAT	ACGGATGAGG	540
GTACACCACA	GCATTCTGCC	CGAAGGGTTG	GATTTTTTCG	TAGGAATACA	TGAAAGAAGA	600
GCACACTGGG	AAGAGGCCGG	AAGTCCGAAG	CTCATGTATA	CGAATGTCCC	AAGTATCATT	660
GGTATTGTTG	AAAAGTTAA	AGTCTTCGAA	GACGCAGAAG	ACTTTTTTGA	CAAAAAAGCT	720
CTCGGCCGCT	TCCTCATCAG	TTTGGGGATA	TCCTATACCA	AGCATCTGGG	AGCGTATTGG	780
GGATGGACCA	ATGACGCCCA	TATTCTTTTC	TCACCGATAC	CCAAGAGCAA	GGTCCACTAT	840
GACACCTACA	CAAGAGCTGG	CAGTGACCTT	GTACTTCAGT	CCGAAGATGT	TGCCACAGTG	900
AGCAATGGCT	TTTACCCGGG	GATCGGACTC	AAAAGTTCTA	TTTGGTGGAA	AATGCCCCATC	960
AAGAGCAAAT	ATGATTTTCG	CCTCGGTTTC	AGCCTGGGCT	ATGAGTATCT	GAACCTGCTA	1020
TATCCGTATC	GTAATTTCAA	GCTGGATGGA	AATAAGCCGC	TTTCAGCACT	ATCTCCTCGC	1080
ATGAACCACA	TCGGCCATGT	GGGCTTCAAC	TTTACCGTGG	GTCTTTGGAC	TAAT	1134

(2) INFORMATION FOR SEQ ID NO:111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...3807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

GTAAATGTGA	TGGGCAAGTA	TAAAAGAGCT	AAGTACCGCT	ATTGGCTTTT	TCCTTTCTGT	60
TCGGATTATT	ATACCTTTGA	GGGAGTTACT	TTTTTATGCG	CATCTGACGA	TATGACAACC	120
AAGAAACCCC	AAGCCATTTT	AGACTTAGAG	AAGGCCTATA	ACATTGAAAT	TCCTGATCTC	180
TCCTCACAA	AAGGGATAAG	CTGGTCGGTA	AATAGATATT	TCAAGCAAGA	TTCTCCCGT	240
GCAGTCGTTG	AGCTTTGCTT	GCGAGAATGT	CAGATAGAAA	GCATGACTTG	GCTTATTGAT	300
TTTCCTGCTC	TAAAAAAGCT	TGATCTATCG	TATAACCAAA	TCAGTAAGCT	AGAGGGTCTA	360
GAACTCTTA	CTTCGTTAAG	AAAACTTCGT	CTAAGAAGTA	ACCAAATCCG	TAACTAGAG	420
GGCCTGGATA	GTCTCACCTC	GCTTAACAAA	CTTCTCTCT	CCGATAACCA	AATCAGTAAG	480
CTAGAGGGTC	TGGAACGTCT	CACCTCGTTA	GCGGAGCTTT	ATCTTTTGGA	TAACCAAATC	540
AGTAACTAG	AGGGTCTGGA	ACGTCTCAG	TCCTTAGCAA	CGCTTGAAC	ATCGGGTAAC	600
CAAATCCGTA	AGCTGGAGGG	TCTGGAACGT	CTCACGTCCT	TAGCAACGCT	TGAACTATCG	660
GGTAACCAA	TCCGTAAGCT	AGAGGGCTG	GAACGTCTCA	CTTCGTTAAC	AAAGCTTCGT	720
CTAAGAAGTA	ACCAAATCAG	TAAAGCTAG	GGTCTGGAAC	GTCTCACGTC	CTTAGCAACG	780
CTTGAACAT	CGGGTAACCA	AATCCGTAAG	CTGGAGGGTC	TGGAACGCT	CACGTCCTTA	840
GCAACGCTTG	AACTGTCGGG	TAACCAAATC	AGTAAGCTAG	AGGGTCTGGA	ACGTCTCTCT	900
TCGTTAACAA	AGCTTCGTC	AAGAAGTAAC	CAGATCAGTA	AACTAGAGGG	CCTGGAACGT	960
CTCACCTCGC	TAACAAAATC	TTCTCTCTCC	GATAACCAAA	TCAGTAAGCT	AGAGGGTCTG	1020
GAACTCTCA	CCTCGTTAGC	GGAGCTTTAT	CTTTTGATA	ACCAAATCCG	TAAGCTGGAG	1080
GGCCTGGAAC	GTCTCACCTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	AATCAGTAAA	1140
CTAGAGGGCC	TGTATAGTCT	ACCTCGCTA	ACAAAATTTT	CTCTCTCCGA	TAACCAAATC	1200
AGTAACTAG	AGGGCTGGA	ACGTCTCAG	TCCTTAGCGG	AGCTTTATCT	TTTGATAAC	1260
CAAATCCGTA	AGCTGGAGGG	TCTTGATGGT	CTTGCTTCCT	TAACAAGGCT	TAGTCTAAGG	1320
CGCAACCAAA	TCAGTAAGCT	GGAAGGACTA	GACAGACTAA	AGGTTTGTAG	AAAATTTGAT	1380
GTTTCGGGCA	ATGATATTCA	CTTATTGAT	GATATTAAGC	TATTGGCTCC	GATCTGGAG	1440
CAAATTTTAG	AAAACTGAG	AATCCATGAC	AATCCATTTG	TTGCATCATC	AGGCTTGATA	1500
CTCTCTCCTT	ATGATAATCA	TTTGCCGGAG	ATTAAAGCTC	TTCTTGAAAA	AGAAAAAGAA	1560
AAACAGAAAA	AGACTTCAGT	TGAATATCAC	CCATTTTGCA	AAGTAATGCT	ATTGGGAAAT	1620
CATCTCTCGG	GTAACAACAC	ATTTCTTAGT	CAATACGATA	CAAATTATAC	GTATCAGAAA	1680
AATACACATG	TGTTGTCGAT	ACATCGAAGC	AATAACCCTA	ATGCGATCTT	TTACGACTTT	1740
GGGGGACAGG	ACTATTATCA	TGGGATTTAC	CAAGCCTTTT	TTACCACCCA	ATCGTTATAC	1800
CTTCTCTTTT	GGGATGCTAA	GAAGGATCGA	AACTTTGTGA	GCGTAGATGA	TAAAGAATAT	1860
CAGACTCTTA	ATTTCAATCG	CCCTATTGG	TTAGGACAGA	TAGCCTATGC	CTGCAATCGT	1920
TGTATGTCCG	TTGGAGGAAA	TCCTGATGCG	AAGGACACAC	CACAGACCAC	AGACGATACA	1980
ATTATCATTC	AGACTCATGC	CGATGAAACG	GGCGCTAAGC	AGCAAACCTT	AGGCTGTGCA	2040
GCCGAGAATG	GAGTATTGGA	AGAAATCTAT	GTATCCTTAG	AGCCCAAGGC	GAATAGTGCC	2100
GTACATCGCG	TCAACTATCT	GAATGAGCGG	GTGCGAGAAG	TTGTGCAAG	CAGGAGTAAA	2160
TCGAATTCAGA	TCACAGAAAA	AGATAAGGGA	TTGTACGAAG	CTCTTCCCAC	AATCGCCGGT	2220
GATAATAAAC	ACATCCCTAT	CTCTCTCGAA	GCTCTTGCGG	CTCAATTGAA	TAAGGGAAGA	2280
GCTGAAAAATG	ATCTTTACAC	CATAGAGTAT	CTACAGACCG	AATTGAACCA	GCTTAGTCTG	2340
CGAGGGGAGG	TGCTTTACTA	TCGTGAGAA	GAGAAAGCTG	ACAATTATGT	CTGGTTAGAT	2400
CCGCGAGCTT	TTGTCCAAAT	GATTTCATGGA	GAAATCCTCC	AAAAAGACAA	CATCAATAGA	2460
GGAACAGTTC	CTAAAGACAT	TTTTGAATGC	AAACTGCATA	ATCTAAGTTC	CGGAAGTATA	2520
TTTGAAGAAG	ATGGCCAAAA	TGTAATATG	ATCTTGCAGC	TATTATTGGA	AGAGCTGATC	2580
GTATATGAAG	ATAAGGACTG	CTATGTGATA	CCGGGCTATC	TCCCTTTGCA	TTCCGATGAC	2640
GAAGCCTATA	AATGGCTTAC	TTTGGGATTC	GAGAGGCCCA	ATTTTGTCTC	CAAATTCGAA	2700
CGTTTATATC	CCTTTGGCCT	GATCAACCAG	ATTATAGCCT	ACTATGGCCG	GGAAGAAGGT	2760
GCTCTAAAGC	GGTATTGGCG	AGATCAGGTC	ATCTTCACAG	CAGGCCGTGA	GATGGATAGG	2820
CAAACGCTTG	AGCAAGAAAG	AGAGAAAGAG	GGTTGCCCCA	AGACGAATGC	CGAGGATTAT	2880
CAGATCTGGA	TCAAGCTCGA	CTTTACCGAC	TTGGCCATAT	CCGTATTTCAT	CAAAGAGCAG	2940
AGAAAGACAT	CAGCTAAGGA	TATGCAGCGG	AAAGAGGCTA	CTATCCTCAG	TGATATGTTG	3000
GATATGTATT	GGAAACAATAT	CCCTCCGAGG	GAGCAAATAG	GAGATAAGGA	TACGGAGCAA	3060
ACGAGAAGCA	CTATTCGTGA	AACAAACAGA	AAGAAGAGAC	CCATCCAGGA	TCTCTACCTC	3120
TCCTGTGCCC	AAGCGGATAA	AGATTTGACG	GAGTCTCATT	ATATCCATTT	GGGCACGCTG	3180
GACGATGAAA	GCAAGACTAC	GGCGAGGATT	GCAGCCTATC	CGTTGAAGAA	CGGCGTTATC	3240
GATAAAGAGC	GGGTGCGAGA	AGTATCGACT	CGTCCCTACA	AACATCTTTT	CGTCAATAAA	3300
AATCTGGCTA	GTGCAAAACA	GATCTTTATT	TCCTATTCCA	AAGAGGATCA	GACTGAAGCTG	3360
GAGACCTGTC	TGCAATTTT	CAAACCTTTG	GAGAAGAATG	GTGAGATCGA	GATCTACTAT	3420
GATAAGTTGA	CTAAGTTTGA	AACACCTATT	CACCTGAAA	TAAGAAAGCG	TATTGTGCGAA	3480
GCCGACTGTA	TAATCGCTTT	GATCAGCCAA	CGCTATCTGG	CCACGGATTA	CATCCTGGAT	3540
CATGAGTTGC	CTGATTTTCC	GAGGATATAAC	AAGACCATAG	TGCCGATATT	GATCAAGCCT	3600
TGTACATTGC	AAGACGATGA	GTTCTTCCG	GAGAAATATT	TTGCTCAGAA	AGCTCAAATA	3660
ATCAATCTTG	GAAAAGAGGG	AAAAACCAT	AAAGCTTATG	ATAGTATTAC	GGCATCAGCC	3720
CATCGTGATG	AAAATTGGGT	GGCAGTAGTC	AGAGAGTTCA	AAGAGAAGAT	ATTAAGAATA	3780
ACAAAACAGG	AGGTAATATC	AGATGAA				3807

(2) INFORMATION FOR SEQ ID NO:112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

AAGTTTATGA	TGAAAAAAGC	ATTGTTTTC	GTACTACTGG	TTTGCCTATT	CTCCTCGTTC	60
AGCAGTTCGG	CCCAAACAAC	GACGAACAGT	AGCCGGAGTT	ATTTTACAGG	ACGAATCGAG	120
AAGGTGAGTT	TGAACCTAGG	GGTCCCCCCC	GTAAGCACAG	AGGTTTGGGG	AATGACCCAT	180
GATGCGAACG	GTCTCCCTTT	CGAAATACCT	ATCTCTTTCA	GTGCTTTCAA	CAGCCAGGGA	240
GATATAGCTA	CCACTTATTA	CATAGCGAAT	AGCGAGGCAA	CTTTGAATGA	ATGGTGGCAG	300
TATGCACACC	CGGGCGGCAT	CGTGAGGGTA	GAAGGTCGTT	TTTGGAAAAT	GACTTACAAC	360
ATACCAACCT	ACAATGCAGT	CTGCACCCGG	ATTACATTCG	AAAATCAAGA	AATAGAAGGA	420
ACGATCGTCT	TGATACCCAA	GCCCAAAGTC	TCGCTGCCTC	ATGTGTCGGA	ATCGGTGCCT	480
TGCATCCGAA	CCGAAGCCGG	GAGGGAATTT	ATCCTTTGCG	AAGAAGACGA	CACCTTTGTG	540
TCTCACGATG	GTAACGAAGT	AACGATAGGC	GGTAAACCTT	TCTTGCTCAA	TACCAACGTA	600
AAGATTGTGG	GGGACGTATC	TCAAAAGTAT	GCCGTGGGGG	TAGGAGAAAT	TCGATTCTGT	660
CAGATTGTGT	CCCAAACAGT	ATCACAACAA	AAA			693

(2) INFORMATION FOR SEQ ID NO:113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

TCGCTAATCA	ACAATTCAAG	AGACTGGAGG	GCTCCTGTCC	GATTGAGTCT	CAAAAAAAG	60
ACAAAAACTA	TGAAGACAAA	AGTTTTACGC	AAATTTCGTG	TGGCGGCTTT	CGCCGTCGCA	120
ACCCTCTGTC	CTCTCGCCCA	AGCGCAGACG	ATGGGAGGAG	ATGATGTCAA	GGTGGTCCAG	180
TACAATCAGG	AAAAACTGGT	ACAAACGAGG	ATGAGTGTGG	CGGACAACGG	ATGGATCTAT	240
GTAATGACCC	ACAGTGGATA	CGACACCGGC	AATAGCAATG	TGAAGATCTT	CCGCTCCAAA	300
GACCAAGGTG	CCACATACCA	AAAGTTGAGG	GATTGGGATC	CATCGGATGA	TTATCAGTTT	360
CAAGACTTCG	ATATCGTGGT	AACGGGTAAG	AATGAATCCG	ACATCAAGAT	TTGGTCGGTA	420
GAGCTCATGA	ATAAGCCCCG	AGGATATAAG	AGTAGAGTTG	CGGTCTTCAG	TCGCGATGCC	480
AACGCGCAGA	ATGCGAAACT	CGTGATAAAG	GAAGACTTCT	CCAATGTGCA	GTTGTACGAT	540
GTGGATATAG	CCTCCAACCTA	TCGTTCGCCT	TCTTCTCTTA	ACAATGGTGG	CAACCCCTTT	600
GCTTTGGCTT	TCGCTTACAC	CGGCTTCAAC	AATACGCACA	AAATAAGTTT	TGTGGACTAT	660
GTGTTCTCTC	TGAATGGAGG	GCAAAATTTC	AATAAAAACT	TACTCTTCAG	TCAAGATGGA	720
GAGAAGAAAA	TTGACAAGGT	GGATCTCTCA	TTGGGTAGCA	CCTCTGAATC	CATGGGTCAC	780
AATGCCTGGC	CGCTAATGGG	TGTGGTATTC	GAAATGAATA	AACAAGGGGG	AAAAAGCGAT	840
ATCGGTTTCT	TGTCGAACCT	TGTCGACAAT	GATCCCCAAT	TTCAGTGGTC	AGGCCCTATA	900
AAAGTGAGTG	AAAGCGACAT	GTCGTTTCAG	CCCAAAATCC	AAATGTTGCT	GGACGAGGAT	960
AACAATACGA	TCAATGGGGA	GAGTTGCCAC	AACTTCATGA	TTACGTACAG	CGATTATGAT	1020
TCTGAATATT	CGGATTGGGA	CATTCCGGTAT	GTATATCCCA	AGAAATCGTT	CAAGTATGAA	1080
AAAGGAAAAA	CTCCGACTAT	GGATGATCTG	GTGGAAGCTT	TCCTTACAGC	TTCTGTACCAG	1140
AGTGAGACCA	ACTCGGGGCT	GGGTATGAC	AAGAACGCCA	ATCACTACCT	GATTACATAT	1200
GCCAAAAAAG	AAGAGAACGG	TACGAACACG	CTGAAATACC	GCTGGGCCAA	TTATGACAAG	1260

ATTCATAACA	AAGATTGTG	GAGCGACACA	TTTACGTATA	CATCATCTGC	CAATGCTCTC	1320
TACACACCTC	AAGTAGACAT	CAATCCGACC	AAGGGTCTCG	TGTGCTGGTC	ATGGGTGGAA	1380
TATCTGCGCG	GCAAACGGAT	CGTTTGGTCT	GATACGCAGT	GGACCCATGC	CAACGGTGTA	1440
GAAGACATCG	TAATGCAAGA	AGGCAGCATG	AAGCTCTACC	CGAATCCGGC	TCAAGAATAT	1500
GCTGTGATTA	GCCTGCCGAC	GGCAGCAAAC	TGCAAGGCTG	TTGTTTACGA	TATGCAGGGC	1560
AGAGTAGTCG	CTGAGGCTTC	TTTCTCCGGC	AACGAATACA	GGCTGAACGT	GCAGCACTTG	1620
GCTAAGGGTA	CGTACATACT	CAAGGTCGTA	TCCGATACGG	AGCGTTTCGT	AGAGAAGCTC	1680
ATCGTGGAA						1689

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

ATCGTTTACC	TTTGTCACTG	TATGAACCAC	AGACGATCAA	AAACCATGCT	GACGATCCGA	60
AACTTCCTCC	TCTTTTGTG	TCTGTGCTG	ATAGCGTTTG	CTGCCGATGC	ACAAAGCTCT	120
GTCTCTTCGG	GTAGACGACT	GACAGAATAT	GTCAATCCCT	TTATCGGAAC	GGCCAATTAC	180
GGTACCACGA	ATCCGGGAGC	AGTATTGCCC	AATGGGTTGA	TGAGCGTTAC	CCCTTTCAAT	240
GTCAGCGGAT	CGACAGAGAA	TCGCTTCGAC	AAAGATTTCG	GTTGGTGGAG	TGCGCCTTAT	300
TCGGCCGACA	ATAGTTACTG	CATCGGTTTC	AGCCATGTGA	ATCTGAGTGG	AGTAGGCTGT	360
CCCGAACTGA	GTGGAATACT	GCTGATGGCC	ACTTCCGGCA	CATTTCGATC	TGATTACTGC	420
TGCTATGGCT	CTTCGCTCAG	TCGAGAATAT	GCGCGCCCGG	GAGAATACAA	GGCTGTATTG	480
GACAAATACG	GTATAGATGC	AGCCGTGACC	GTAACCGAGC	GGACTGCTTT	GACCGAATTT	540
GCTTTTCCCG	AAGGAGAAGG	CCATATCCTG	CTGAACCTGG	GACAGGCCCT	AAGCAATGAA	600
TCGGGAGCCT	CTGTTTCGATT	CTTAAACGAC	TCCACAGTCG	TCGGCAGCAG	GCTGATGGGG	660
ACGTTCTGCT	ACAATCCGCA	AGCAGTTTTT	CGTCAGTATT	TCGTACTTCA	GGTGAGTCGG	720
CGACCGATCT	CTGCCGGCTA	TTGGAAGAAG	CAGCCTCCTA	TGACAGTGGA	AGCCCAATGG	780
GATTCGACTG	CAGGGAATA	TAAGCAGTAC	GACGGCTACA	AGCGTGAGAT	GAGCGTGAT	840
GACATCGGTG	TCCGATTCTC	GTTCAACTGC	GATCAGGGGG	AAAAGATCTA	TGTACGATCG	900
GCCGTTTCAT	TCGTCAGCGA	AGCCAAATGCG	CTCTATAATC	TGGAAGCGGA	GCAAGAAGAG	960
GTGTTCAAAA	GTGTCGGAGG	GAATCCGGCC	AAGGCTTTCT	CCGCTATACG	CTCTCGCGCT	1020
ATAGAGCGTT	GGGAGGAAGC	CCTCGGTACG	GTGGAAGTGG	AAGGAGGCAC	ACCGGATGAA	1080
AAGACGATAT	TCTATACCGC	ACTCTATCAC	CTGCTGATAC	ATCCGAATAT	CCTACAAGAT	1140
GCCAATGGAG	AATATCCTAT	GATGGGCAGT	GGCAAAACGG	GTAATACGGC	TCACGACCGC	1200
TACACCGTGT	TCTCTCTTTG	GGACACGTAC	CGCAATGTAC	ACCCGCTGCT	CTGCCTCCTC	1260
TATCCGGAGA	AGCAGTTGGA	TATGGTACGG	ACACTGATCG	ACATGTACCG	AGAGAGCGGG	1320
TGGCTGCCGA	GATGGGAGCT	GTACGGACAG	GAGACCTTGA	CGATGGAGGG	CGACCCCTCG	1380
CTTATCGTCA	TCAATGACAC	TTGGCAAAGG	GGCCTTCGTG	CTTTCGATAC	GGCAACGGCC	1440
TATGAAGCCA	TGAAAAAATA	TGCTTCTTCG	GCAGGAGCGA	CCCATCCGAT	CCGTCTCTGAC	1500
AACGACGACT	ATCTCACCTT	CGGCTTCGTA	CCGCTTCGCG	AACAGTACGA	CAATTCCGTA	1560
TCGCATGCGC	TGGAATACTA	TCTGGCCGAC	TGGAATCTGT	CCCGGTTTGC	CCACGCACTT	1620
GGGCATAAAG	AAGACGCAGC	TCTATTCCGA	AAACGCTCGT	TGGGCTACAG	ACACTATTAT	1680
AATAAGGAGT	ATGGTATGCT	GTGTCCATTG	CTGCCGATG	GATCATTCCT	CACTCCTTTC	1740
GATCCCAAAC	AGGGTGAAAA	CTTCGAGCCT	AAATCCCGTT	TCCACGAGGG	CAGTGCTTAT	1800
AACTATGCCT	TTTTCGTTCC	CCACGATATA	CAAGGGCTTG	CCCGGCTGAT	GGGAGGAGCA	1860
AAGGTTTTTT	CGGAAAGGTT	GCAGAAAGTC	TTCGATGAAG	GATATTATGA	TCCGACCAAC	1920
GAGCCGGACA	TCGCCTATCC	TTACCTCTTC	TCCTATTTC	CCAAGGAAGC	ATGGCGAAGC	1980
CAGAAATTGA	CCCGGGAGTT	GATAGACAAA	CATTTTGTGA	ATGCTCCTAA	CGGCTTGCCC	2040
GGTAATGACG	ATGCCGGTAC	GATGAGTGCT	TGGCTTGTCT	ATTCCATGCT	GGGATTCTAC	2100
CCTGACTGTC	CGGGCAGCCC	CACCTATACA	CTGACCTCGC	CGGTATTCCC	CCGAGTTAGG	2160
ATTCGGCTCA	ATCCGCAGTA	TTATCCTCAG	GGGGAGTTGA	TCATTACGAC	CAATACAGAG	2220
AATCAACCGA	CAGATTCCAT	TTACATCCAT	ACGGTTTCTC	TTGGCAATAA	AACACTCCCG	2280
CATGGAACAA	GGCATATCAG	CCATGCCGAT	TTGGTGCGCT	GCGGTCACCT	CCGTTACGAA	2340
CTAAGCAATC	GTCCTCGA					2358

(2) INFORMATION FOR SEQ ID NO:115

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2442
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

```

CCCCGTTTTC ATCCCGGAGG GACACACGCT CAGCTTTGCA GAAATGGGAG AAGAAACCAA      60
AAATCAAATC AGTCATCTGT CTTTGGCGGT GGCACAGCTC CGCGATTTT TATTATGTGC      120
AAAATAAGAT TCAGCCTCTT GCAGGCTCTT GTCGTCTGCT TATTGTTTAC CTCTTTTCT      180
CTCCAAGCTC AAGAGGAAGG TATTTGGAAT ACCCTCTTGG CTATCCACAA GACGGAAAAA      240
GCCGTAGAAA CGCCCAAGAA AGTCTTTGCC GTAGCCAACG GAGTACTTTA CTCGGTGGGC      300
AAAGAAGCTC CCATGAGGC AAAGATCTTC GACCGTATCA GCGGACTCAG CGATACATCG      360
GTAAGCAGCA TAGCCTACTC CGAGCAACTA AAATCCTTGG TCATATACTA TGCATCAGGC      420
AATATCGACA TCTTGAGCGA AGCAGGCCGT GTGACCAACG TACCTGCATT GAAAGACAAT      480
ATCGATCTGA TAGACAAAAC GCTCAATCGC CTTTGTATCG TAGGCAACAG GGCTTATTG      540
GCAGGAGGAT TCGGCCTCTC CGTTCTGGAT GTCGCCGAAG CTCGCATACC GGCTACCTAC      600
GCCAAGGGAA CTAAGGTGAC CGATGTGGCT AAGTTGGACA ATGATCGCTT GCTGATGCTG      660
AAAGAAGGGC AGCTCTTCAT CGGAAAAGAG ACCGATAACC TGCAAGATCC GGCCGCATGG      720
ACAGCCTTGT CTTTGAATTT GCCGATGGGC TCGGTCACCG GTCTGGGCAT TGTGGGGGAA      780
GAACATCGTT TCTGTCTGCG CGATGGCCGT GTATATGTGC CTGCAAACCA ATCGTTTGAG      840
CCGGAGCTAT TGCTCTCTTC CTCCGCCGAT TCACGACTGT ATGTGACGGA TCGTGGTCTG      900
TTCATCTGTG CCGAGAAATCG AATTTATTTC ATAGAAAAAG GTCGCAAAAC GACACAATT      960
CCTATAGCCG ACGTCCTTGG TGTCGGTGCC ATGAACGAAA GCAATACGGC ATACATAGCA     1020
TTGGGAGAAG AAGGTTTGGC TCACTTCTT CTGCAGAGG GAAGTACGGC CGAAGCCATG     1080
CCTGTAGCAT TCGACGGACC GGGGGACAAT GATTCTACG AGATGCGGTT TAGTCACGGA     1140
CGTCTGTATG CAGCCAGCGG ACTCTGGGGA ACAAACCTGA TGGGACATGC CGGTATGGTG     1200
AAGCTATACG ACGGCAACCG ATGGACTAAC TTCGACAAGA AGACCGTACA GGAACAGTTG     1260
GGCGGCGGAT TCAGTTTCAA TGATGCTATC GATATAGCTG TTTCCAACGG AGACCCCGAT     1320
CACTTTTGTG TCGGTACATG GGGAAACGGT CTGTTTCAAT TCAAGGATGG CAAAGCGATA     1380
GCTCGCTATT CGGGAAACGA AACTGCTATC GCAGAATGTA ATCCCGGAGA TGCCCGTGTG     1440
AAAGCGATTG CTTTGCACAA TAAGGGCAAC CTCTGGGGGA CGCTCGGTGC CGTAGGCAAG     1500
AACATCTTCA TGTACGATCC GCAGAGTAGC ACATGGCATT CTTTCAGCTA TCCGGATGTA     1560
GCCAATCTGG CCTCCTTCGG CAATATGATT ATCCTACCCA ACGGAGACAA ATGGGTAAAT     1620
ATCCTTACC GTAGTGGCGG ATCCACGCGC AAAGGTGTCT TGATCTTCAA CGATCGGGGT     1680
ACACCGGAAA CGACTTCGGA CGACAGCCAT CTTTACGTCG AGCAGTTTGT CAATCGCCTC     1740
GGGGCAGCCA TAGGACTCTA GACTATCTAT GCAATGGCCG TCGATCATAA CGGCTCTGTC     1800
TGGATGGGAT CGGATATAGG CATTTTCGGC GTCTACAATG CAGCCGGAGT ATTGTCCTCG     1860
ACTTCTACCC CTATCGTGTG TCGGCCGGTC GGAGGAGAAG AACCCAATT GTACTATGTG     1920
CTGGACAAGG TGACGGTGAC AGCATCGTC GTGGACAAAC TCAATCACAA ATGGGTTGCC     1980
ACCCAAGGGA CAGGACTCTA TCTCCTTCG GAAGATTGCA GTAAGATCCT CGCGCAATT      2040
ACCGTAGAAA ACAGCCCTTT GCTTTCTAAC AACATACTAT CCCTGGCCTT AAATGACGAT     2100
AACGGACTGC TGTACATCGG TACGGCGGAC GGACTGATGA CGTTCCAAAC GGGTACGGGG     2160
AGTGGATCAG CTTCCGAAC TGGACGGGTC TATGTATACC CCAATCCGCT AAGGCCGGAA     2220
TATCCCGATG GCGTCACCAT TGCCGGACTG CAAGCCGGCT GTAGTGTCAA AATCACCAGT     2280
ACCACCGGCA GACTGCTATA CCAGACTGAG AGCGTAACCA CCGAAGTCAA ATGGAATGCT     2340
CGAGGTGCCG ATGGCAATAG GGTAGCTTCG GGCGTATATG CCGTTGCAGT GTACGATCCG     2400
GTATCGAAAA AGTCCAACT AATTCGCTTC GCAGTGATTC GC                        2442

```

(2) INFORMATION FOR SEQ ID NO:116

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

```
GCTATTTCTC AGATGAAACG AATACTTCCA ATAGTCGCAT TCCTTTCTCT CTTCTTGCC      60
CTTGCTTTGC CTGCGAAAGC GCAACGAGCT ATGGGGAAGA CGGCCGACCG TTCGCTAATG      120
GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGATCG CTTACGGAC      180
GAACAGCTCC GTGCCAATGG CTTCTCCGAT CCGTCCAAGG TAGGTGTGTT CGGTATAGGT      240
GGAGGGGTGC TTCCCGAAGA TCTGAGCCGG ATCACGACAG ACGATTGGCC TCCGGTACCG      300
GTACTCCGTC AGGGCAATGC GCTGTATTTT TATGCCGTGG GCCCGGTGAC ATGGTTCTAC      360
AATCCGGCCA AAACCACCAT GGAGCATACG GTGAATACAT ACAGTACGCA TGGCTACTAC      420
TTCCTGTCCG ATGCTGCCCG AGCACCTTTG CAGATGTCCC AATATACGGG TGGAGGTGCG      480
TCGGCCGAGG CTTTGATCGA CTACTACGAT GAGCTGATGC TCCATGAACA GGAATTGTAT      540
TCGCCCAAAG AATCGGACG AGATCTGTAT GGCGAGTCTT TCAGTGCAGT CAATACGCGT      600
ACGGTCAAGT TCCCTTTGAG GGGCAACACC CGCTCGTCTG GCGAACTCGG TACCGTATTC      660
TCATACATAG CCAAGGCCAG ATCGGCCGGT GGCGGCCGTG AGATGTCGCT CTCGGCGAAT      720
GGCATTTCTG TCTTCAGCGA TCCTTTTTC ATGACATCGA ATGAAGTCTC CAATTCCTAT      780
TTGGCCGGCA AGAAGCGTCG TCTCTATCAC AGTACGCCGA TGAACAGCTT GGTCAATGAG      840
TTGCGCTTGG ACGCGAAGTA TAGCATGACA GGAGATGCGG TCAATCTGGA TTTCATAGAG      900
GTGGCTACAC AGAACGACCT CCGGTACGAT GGCGCACCCA TGCATATCAG GCGGTTTTCC      960
AATTGCCCCG TTTTGGGGGG CGAGTCTGCG CGGTTCTGTT TCAGTGAGGT GCCGGAGTCT     1020
CTGGTGGTTT TGCAAGCCAA TTCTTCCCTG ACAGCATCGC TTGTTCCTCG TAAGACTGTC     1080
GGGGATAAGA CCATTGAGTT CGTGGCTCCG CCGAAGGGTC AGGATCGTAG GACTATCAAT     1140
ACGTTTTATG CCGTGGACTT GTCACAGGCT TCTGCTCCGG AGATCCTCGG AGCGGTACCC     1200
AATCAAAACC TGCATGGAGA GGAAATCCCT GATCTGATCA TTGTCTCTAC TCAGGCGCTC     1260
CTCCTTGAGG CTGATCGACT GGCCACCTAT CGTAGAGAGA AAAACGGGCT GAAGGTTTTG     1320
GTCGTGTTGC AGGAACAGGT GTTCAACGAG TTTTCGGGTG GAACTCCCGA TGCTACAGCA     1380
TACCGCCTCT TTGCCAAAT GTTCTACGAC AGATGGAAGG CAAATGCACC TGTGGGAGAG     1440
ACCTTCCCGA TGCAATGCT TCTCTTCGTT GATGGGGCTC ATGACAACAG GAAGGTCTCC     1500
GTAGCTTGGC AGAAACCGTA TCTCCAACAA ACGGAGTTCT TGCTGACATT CCAAGCCGTC     1560
AATTCGACGA ACGTAAACAG TTATGTGACG GATGATTACT TCGGCTTGCT GGATGATCAG     1620
CCGGCCTCGG TCAATATCGG TTGGCGCAAT TATAATATGG CTGTAGGGCG ATTCCCCGTA     1680
CGTACTCCGG TCGAAGCTCG CATCGCAGTG GACAAGACCA TCCGATATGA GGAGGATCGA     1740
GAGAGTGGTG CCTGGCGTAT TCGTGCTGTG TTTGCGGCAG ACAACGGGGA CAAGCACGCA     1800
ACCGAGACTT CCGTTTGAT CGATACCGTC AAGCGTTATG CTCCTGCCAT CATGCCGTA     1860
CGCGCCTTTC AGGACGTATA TCCGCATGTC ATCGAGAACG GGTGTCACAG CATTCGGGGT     1920
GCAAAGAAAA AGATGCTGGA AACCCTTACG TCGGGTATTA TCCTGCTTAA TTATGCTGGT     1980
CATGGCGGTC CTGCCGATG CTGCCGACGAG CATTGCTGTA CGCTCAACGA TATACACAAA     2040
TTCAATTATA AGCATATGCC CATTTGGATT ACTGCCACGT GCGACTTTGC CAACTATGAC     2100
AGTCAGACGA CCTCGGCAGG GGAGGAGGTT TTCTCCATG AGAAGAGTGG CACTCCGATC     2160
ATGTTCTCGA CTACGCTGT GTTTTACAAT ACGCAGAATG AGAAGATCAA TGGTTTTATG     2220
CTTCGGCGTA TGTTTCGAGA AGCTAAGGAT GGGCGTTATC GTACGATGGG CGAGATTATC     2280
CGATCGGCCA AACAGGGGAT GCTCAGTACT GTTTTCCCG ATTCTGATCA CCAGTTGAGT     2340
TTCTTTCTGA TGGGTGATCC GTCCGTGCGT ATGAATCTTC CTACCCACAA AGTGCAATTG     2400
ACCGCAATCA ACGGGCAGGA TCCCGAAGGG CAGTATGGAA CTATTATGCT CAAGTCTTTG     2460
GAACGGGTAG CTCTGAAGGG TAAGGTAACC GATGAAAAGG GGACATTCTG CGAGACATTC     2520
AGTGGCAAGG TTTTCCTGAC CGTCTTCGAT GGCAGAAAGA AAATGACAGC TTTGGAAGAG     2580
GAGGGAACG ATCTCTCTCT TGTATATTAT GACTATCCTA ACGTGATGTA TGCCGGTATT     2640
GCCGAGGTGA AAGACGGACT CTTCGAAACT TCGTTTATCG TACCCAAGGA TGTGAACTAT     2700
TCCGAGCAGC AAGGCCGGAT CAATCTTTAT GCTTATAACG AGAGCACAAA GGCGGAAGCC     2760
ATGGGGGTAG ACTTCTCCAT CAGAGTCCAA CCGGGTATTC CTGATGAGGT AACGGAAGAT     2820
AATACACCGC CTGAAATCAT AAGCTGCTTC CTCAATGACA GTACATTCCG ATCGGGAGAT     2880
GAGGTTAATC CTACTCTCT GTTTATGGCC GAAGTATTCG ACTTGAATGG AATCAATATC     2940
ACGGGTAGCG GAGTAGGGCA TGATATTACG CTTTGTATCG ATGGCCGTGC CGACCTGACC     3000
TACAACCTCA ATGCATATTT CACAAGTTCG GCTACGGATG CAGGTGTGGG CACTATTCTC     3060
TTCATGATAC CGGCTTTGGC CGAAGGAGAT CATACTGCCC GACTGACGGT TTGGGACATT     3120
TTCAATAATG CCGTCCATCA TGACTTTTCA TTCAGAGTGG TAGATGGCAT TGCTCCGGAT     3180
GTGGCTGATG TGATTCTATT CCCGAATCCG GTACGCGAGA GTGCTACGTT CCGAATCTTC     3240
CACAAATCGC CCGGAAGCGA TTTGAACGTG GCCGTGGAGA TCTATGACTT CACCGGTCGT     3300
CTTGTGAACA GTTTGCCAGT CAAGACCTAT TCGTCTCTCT ACGGAGAACC TATAGAGATC     3360
AAGTGGGATG TGACCTCAA ATACGGAGTG AAGATCGGAA ACGGATTCTA CCTCTATCGT     3420
TGTGTGTTGA ACTCTCCCG AGGACAGACG GCCTCCATGG CCAAGAAAAAT GATCGTGGTA     3480
GGACAA
```

(2) INFORMATION FOR SEQ ID NO:117

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

```
TTTACACCG GAATTGACTT GCATATAGAA AGCCAAATGA AGAAACTTTT CCCATTATTA      60
TTACTCATAT TGTCGATTTT GGTCCGATGT GGAAAAAAG AAAAACACTC TGTAACGTAA      120
ATCGCCCGAG AGAAAAAGCG TATTACTGCA TTGCTGTACG AAAAAGAACT CCCCACTGAT      180
TCTGTTAAAC AGCTTTACGA GAACAGCGTA CAGAACAAGA ACCTTGTGGG ACAAATGTTA      240
TTCGCGATCG AGGTCGGCAA ACGGATGCGT AATATGTCCC AATACACAGA TCGATGCTA      300
TATCACCAAA AAGGGTTGAA CGCTGCATTG AATCTAAGGG ACACCATCGT AGCCGCACAA      360
GCATGGAATC ATCTCGGAAC GGATAGCCGT CGTATCGGTG CTTTGGCAGA AGCTTCGGAT      420
TATCATTACA AGGCTCTTTC CTTGATAGAA TCTTTTAGCG GAAACCAGAA TAGGCTGCG      480
ATCAAAGCCA GATCGGCCGC CCTGAACGGC ATCGGCAACA TCAATCTTGA GTTAGGATAC      540
CATGATGAGG CCGAAAAGAA TTTCTTGAAA GCACTGCAAG GTGAGAAAGA ACTCGACAGT      600
CCTCTCGGGC AAGCTATCAA CTATGCGAAC CTGGACGTA TCTATCGACA ACGCAAAGAA      660
TACGACAAGG CTCGTACCTA CTTCTCTTGT TCTCTGGAGC AGAACAATAT GGCAGAGAA      720
CTGATGGGTA TCGGACTCTG TAGCATCAAT CTGGAGAGAG TAGACGAAGA AAAAGGGGAT      780
TATCAAAGG CTTTGCAAGA GTATGCCACG GCATACAAAC TGATGGAACA GTTGTCGGAT      840
CGATGGCACT GGCTGAATTC CTGTATCCCG ATGGCACGTA TCAATCTCAA ACAAGGTAA      900
GAAAGGCTCT ACCAGCATTT CATTTCTTTG GCCGAAGGGA CTGCGAAAGA AATTAATTCT      960
ACTTCACATC TGATAGAAAT ATACAATCTT CAATACGAGA ATCTCGAGCG TAAAAAGAA      1020
TACAAACAAG CCCTCGAAGC ATTCTGTCTG AGCAAGACGT TGAGCGACAG CATGTCCATT      1080
GCCACAAAGG TCAGCAGCAT ACAAGAAACG CGATTCAACT ACGAACGAAA CAAGTCCCAA      1140
AAAGAGCTTG AAGAAATACA GCAAGTAAGC AAGGCAAAAC AAGAGAAATC GAAGTTTATC      1200
CTCTTGAGCA CTCTTTTTCG CTTTTTCATC TCGATTCTTT TGATTCTCTG TCTGACATAT      1260
GCATACCGTC AGGGCAAGAA GCATAACAAG CTGATCAAAG AGACGGATAA ACTTCGCTCC      1320
GGCTTTTTC ACGGTATTAC ACACGAATTC CGTACGCCTA TCACCGTCAT ACAAGGTTTG      1380
AATGAGAAAA TGAGTTCAAG TCCTGATCTC CAAGCATCGG ACAGAACCGA GCTGCACAAG      1440
ATAATAGACA GACAGAGTAG CCATATGCTG AATTGTGGTA ACCAGCTGTT GGATATTTGC      1500
AAGATCAGAA GCGGAGTATC CACGCCGAA TGCGCAATG GCGACATCGT CTCCTTCGTA      1560
CAGATTCTCA TCGATTCTGT TGACCATAC GCACAGGCTC AAGACATAAC CTTGGAGCTA      1620
CAACCCGAGA GCAAACCTAT TGTCGTGGAC TTCGTCCCCT CTTACTTGCA AAAAATCATA      1680
TCCAATCTTT TGTCCAATGC CATCAAGTAT TCTTTAGCCG GAGGGAGAGT GGTTCATATCT      1740
CTGGCAAAAA CCAAGAATGA AAAAAATCTG ATCATACGCG TTGCAGACAA TGGCATAGGA      1800
ATAGATAAAA CTGATCAGGC TCATATCTTC GACATCTTCT ATCGAGGACA GTCCGCTACC      1860
GAAAAGCATG GATCAGGCGT CGGACTCTCG TTTACCAATA TACTGGTCTG AAACCTTCGA      1920
GGTACGATCA AAGTGGAAG CAGCCGGGG AAAGGAAGTG CCTTCACCAT CAGTATTCTC      1980
ACACAAAACC AGTCCTCTTC GGCAGAGATT CTTCTTGCG TACCCTCTC CGATGACATT      2040
GTCATGCTCG TCCACATCGC GCCCGATGAC TCACCGACAT CTCCGATGGT AGCAGCTCTG      2100
AATCATCGCT TCGAGGACGA ACGTCCGACC ATACTGCTCG TCGAGGACAA TAAGGATATC      2160
AACTGCTCG TCAAACCTCT CTTTTCGAT CGCTACAATG TGCTATCCGC CGCAAACGGA      2220
AAAGAGGGTA TAGCCCTCGC TACCGAGCAT ATTCCGACA TTATCATTAC GGATATTATG      2280
ATGCCGATAA TGGATTGGAT AGAAATGACA ATCCGGATGA AGCAATCGCC TCTGCTCTGT      2340
CACATTCCCA TTGTCTCTTT GACGGCCAAG AGTACCGAAC AGGACAGATT GGAAGGAATC      2400
AAAAGCGGTG TAGTCTCTTA TCTATGCAAG CCATTCTCTC CGGAGGAGCT TTTGATGCGG      2460
ATCGAGCAGC TTCTGAAAGA CCGTGAGTTG CTCAAGAAGT TCTATATGCA AAAACTCATG      2520
CTGGATCGGA AGCCGGAGGA GGAGCCTCAA CCGATAGATG ACAGCAGTAT GCAGTTTCTC      2580
CTTGCTGCCA AAGATGCAGT GTCCGGTGGA ATCAAACAAA ATCCGATTG TTCCGCTCAA      2640
GACTTGGCCG AAAAAATGTG CATGAGTCCA TCCAACTCA ACAGAAAGCT CACGAGTGTC      2700
GTAGGTTGCT CCACCATCGG CTACATACAG CAGATCAAGA TAAAATTGGC CTGCAAGCTC      2760
CTTGCCGATG AGAGCAAAAA CATCTCCGAC ATTAGCATTG AGGCAGGCTT TTCGATCCG      2820
GCTTACTTCT CTCGCACCTT CAAACGCTAC ATGAACTGCT CTCCTCCCA ATATCGGCAA      2880
AAACTCCTTG CCATGCCGGG GAGCGACAAG GAGACAGTT      2919
```

(2) INFORMATION FOR SEQ ID NO:118

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

```
CATCATAAAA CATATCAAAC AATGAAAAAG CTTTACAGG CTAAAGCCTT GATTCTGGCA      60
TTGGGACTCT TCCAACAGCC CGCAATCGCC CAAACGCAAA TGCAAGCAGA CCGAACAAAC      120
GGTCAATTTC CAACAGAAGA GATGCAACGA GCATTCCAGG AAACGAATCC CCCTGCAGGT      180
CCTGTGCGTG CTATCGCTGA GTACGAACGC TCTGCAGCCG TTTTGGTACG CTACCCGTTT      240
GGTATCCCGA TGGAAATTGAT CAAAGAGCTG GCCAAGAACG ACAAGGTGAT TACCATTGTG      300
GCGAGTGAAA GCCAAAAAAA CACCGTTATA ACCAGTACA CCCAAAGCGG TGTGAATCTC      360
TCTAATTGCG ATTTTCATCAT TCGGAAACT GACTCTTACT GGACACGCGA CTATACCGGT      420
TGGTTTCGCA TGTACGATAC GAACAAAGTA GGTCTCGTGG ACTTTATTTA TAACCGCCCT      480
CGTCCTAACG ATGATGAATT CCCCAAATAC GAAGCACAAT ATCTGGGCAT CGAGATGTTC      540
GGGATGAAGC TCAAGCAGAC CGGTGGCAAC TACATGACGG ACGGATATGG ATCCGCTGTG      600
CAGTCACATA TCGCATATAC GGAGAACTCC TCTCTGTCTC AAGCTCAAGT AAATCAAAG      660
ATGAAAGACT ATCTCGGCAT CACACATCAT GATGTGGTAC AAGATCCGAA CGGCGAATAT      720
ATCAACCATG TGGACTGTTG GGGCAAGTAT TTGGCACC GAACAAATCCT CATCAGGAAA      780
GTGCTGACAT ATCACCTTCA GCACCAAGCC TTGGAAGATA TGGCAGCCTA CTTTCGAGCA      840
CAGACCTGCG CATGGGGAAC GAAGTACGAG GTATATCGCG CTTTGGCCAC CAATGAACAA      900
CCGTACACGA ACTCTCTGAT TCTGAACAAC AGGGTATTTG TTCCTGTCAA TGGCCCCGCC      960
TCCGTGGACA ACGATGCTCT GAACGTCTAT AAGACGGCAA TGCCCGGTTA CGAAATTATA     1020
GGTGTCAAAG GGGCTTCAGG AACACCTTGG TTAGGAACAG ATGCCCTGCA TTGTCGTACT     1080
CACGAGGTAG CGGATAAGGG CTATCTCTAT ATCAAGCACT ACCCGATACT GGGCGAACAG     1140
GCAGGCCCTG ATTATAAGAT CGAAGCAGAT GTCGTCTCAT GCGCCAATGC TACTATCTCG     1200
CCGTATCAAT GTTACTATCG TATCAATGGT TCCGGTAGCT TTAAGGCTGC TGATATGACG     1260
ATGGAATCAA CAGGTCACAT TACTTATAGC TTTACAGGTC TTAACAAGAA TGATAAGGTA     1320
GAATACTATA TCTCTGCCGC TGACAATAGT GGTTCGCAAG AGACTTATCC CTTTATCGGC     1380
GAACCTGATC CTTTCAAGTT TACGTGTATG AACGAAACCA ATACATGTAC TGTGACCGGA     1440
GCTGCCAAG CTCTTCGTGC ATGGTTCAAC GCCGGTCGTT CAGAAGTGGC TGTTTCGGTA     1500
AGTTTGAATA TTGCCGGCAC ATATCGGATA AAGCTTTATA ACACCGCAGG AGAAGAAGTC     1560
GCTGCAATGA CCAAGGAATT AGTAGCAGGG ACGAGTGTCT TCAGTATGGA TGTGTATCTT     1620
CAGGCTCCGG GCACATATGT TCTGGTTGTT GAAGGAAATG GAATCCGTGA GACAATGAAA     1680
ATTCTCAA                                         1689
```

(2) INFORMATION FOR SEQ ID NO:119

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

```
ACCACAAATA GAAAACCAAA TACTAATATG AAACTTTCAT CTAAGAAAAT CTTAGCAATC      60
ATTGCATTGC TGACGATGGG ACATGCTGTG CAGGCACAGT TTGTTCCGGC TCCCACCACA      120
GGGATTCGCA TGTCTGTCTC TACAACCAAG GCCGTAGGCG AAAAAATCGA ATTGTTGGTT      180
CATTCCATAG AGAAGAAAGG CATCTGGATC GATCTCAATG GGGATGCCAC TTACCAACAA      240
GGAGAGGAAA TAACCGTATT CGATGAGGCA TACCACGAAT ACACGATCGG GACGCAAACC      300
CTCACTATCT ATGGTAATAC GACCCGATTG GGCTGTCTGAT CTACCGGTGC AACGGCTGTC      360
GATGTAACGA AAAACCTTAA TCTGACCTAT CTCGCATGCC CGAAAAATAA TCTGAAATCA      420
TTGGACTTGA CGCAAAACCC AAAGCTGCTG CGAGTTTGGT GCGACTCTAA CGAAATAGAA      480
AGTTTGGAAC TGAGTGGCAA TCCGGCTTTG ATCATCTCTG GCTGTGACAG GAATAAGCTG      540
```

ACTGAGCTGA	AGACCGATAA	CAACCCCAAG	TTGGCCTCTC	TTTGGTGTTC	TGATAATAAC	600
CTGACGGAGT	TGGAACCTAG	TGCCAATCCT	CGTCTCAATG	ATCTTTGGTG	CTTCGGTAAT	660
CGGATCAGCA	AATCTGATCT	GAGTGCCAAT	CCTCTATTGG	TAACACTTTG	GTGCAGTGAC	720
AATGAGCTTT	CGACCTTGGA	TCTTTCCAAG	AATTCGGACG	TTGCTTACCT	TTGGTGTTC	780
TCGAACAAAC	TTACATCCTT	GAATCTGTCT	GGGGTGAAGG	GACTGAGTGT	TTTGGTTTGT	840
CATTCCAATC	AGATCGCAGG	TGAAGAAATG	ACGAAAGTGG	TGAATGCTTT	GCCCACACTA	900
TCTCCCGCG	CAGGCGCTCA	GAGCAAGTTC	GTCGTTGTAG	ACCTCAAGGA	CACTGATGAG	960
AAGAATATCT	GTACCGTAAA	GGATGTGGAA	AAAGCTAAAA	GTAAGAAGTG	GCGAGTATTT	1020
GACTTCAACG	GTGATTCTGA	CAATATGCTT	CCATACGAAG	GAAGTCCGAC	ATCGAACTTG	1080
GCAGTAGATG	CTCCCACTGT	CAGGATATAT	CCCAATCCGG	TAGGAAGATA	TGCGCTCGTC	1140
GAGATCCCCG	AGTCTCTTTT	AGGGCAGGAA	GCTGCTTTAT	ACGATATGAA	TGGGGTAAAA	1200
GTCTATAGTT	TCGCGGTAGA	GTCTCTTCGT	CAGAACATTG	ACCTGACACA	TCTTCCCGAC	1260
GGCACTTATT	TCTTCCGTCT	CGATAACTAT	ACCACTAAGC	TCATCAAACA	G	1311

(2) INFORMATION FOR SEQ ID NO:120

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 954 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...954
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

AATCATTTGA	AGACAAATAT	CAAGATGAGA	AAAACAATAA	TTTCTGCTT	GTTGCTCGCC	60
CTATTTGGCT	GTTCTTGGGC	ACAAGAAAGA	GTCGATGAAA	AAGTATTCTC	CGCAGGAACA	120
AGTATTTTGA	GGGGCATCCT	TGAAAAGGTG	AAAGCACCGC	TTATGTATGG	AGATCGTGAG	180
GTATGGGGTA	TGGCTCGTGC	GAGCGAGGAT	TTCTTTTCTA	TACTTCCCGT	TACGGATGAC	240
CTCACTCCCG	TGCTTTTCTA	TAACCGTCTT	ACAAACGAAC	CCTGCTTTGT	GTGAGACCAA	300
GGAATAACTG	AGTATTTCAA	ATTCTGCTCA	GAAGGTGATT	ACATTGAAGT	CGAAGGAAGC	360
TCTGTATTCA	TGGCGAATCT	TTTGTACTAT	CGTTTTTTCC	CGACAAGAAT	TACCTCCTAT	420
AATGCTCCCA	TTGAAGGTGT	TGTGAGCAAG	ACGGGAAATC	CTGCTTTTAC	AATCCCGATG	480
CTCCCGGGGG	TTTCTGATTG	CATAGAAATC	TCAAACAACC	GCAAAGTCTT	TCTGACCAAT	540
CAATTAGGGG	TTGTAAACAT	CCTGACGGG	ATGGAACCTC	CGATTATTGC	CGGAGTCTCT	600
GCTTCCTATG	GATCTTCCGT	CCGGGTGTAT	GGTCATGTCT	CACAGCGGTG	GGACATCATA	660
GGCCATTGCT	ATTTGGATAT	CTACCCAACC	AATTGCTATC	CGCTCAGCAC	GAAACCCGTT	720
GCAGGAGACG	ATGAGGTTTT	TGTCAAACAA	CAAGGCAGGC	AAATAGAGAT	CGATAGCAAC	780
AGCCCCATAG	TCCAAGTGGT	CGTATACGAT	CTTGAGGGGA	AAAGTGTTTT	TCGCAAAAGA	840
ATGACCGAAA	ACGCTTATAC	CCTATCCTTT	AGAGCACCCA	TGCTCGGCTT	TATGACCATC	900
ATGATCGAAA	CACAAAATTC	GATTATCAAT	AAAAAACTTA	ATGTTACACA	GCTA	954

(2) INFORMATION FOR SEQ ID NO:121

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

AGACGGGGCAG	TTAAATCCG	ATCACCTCCC	CATATCCACT	CATTATTTGT	ACGTAAATGT	60
CTTTTTTCAG	ACTTTAAATA	CTTATATTTA	TCCCAGAAAA	TTACCCAAGA	GAGATTGGGT	120
CGATTGTGCGA	TCCGTCTTAA	GTATACAAAT	CCAATAATCA	TTATTGAAAT	GAACAAAAACA	180
ACCATTATTT	CTTTGATTGT	CTTCGGTGCT	TTCTTTGCAG	CCGTGGGCCA	AACCAAGGAC	240
AATTTCTTCT	ACAAACCTTT	TTCGAAAGAA	GATATTGCCG	GAGGAGTTTA	CTCTCTCCCG	300
ACTCAAAATC	GTGCGCAGAA	GGACAATGCC	GAGTGGCTTC	TTACAGCGAC	CGTCTCCACA	360
AACCAAGTCTG	CAGATACTCA	CTTTATCTTC	GATGAGAACA	ACCGCTATAT	CGCTCGTGAC	420
ATAAAAGCCA	ATGGGGTAAG	AAAATCCACG	GACTCCATTT	ACTACGATGC	CAACGGGCGA	480
ATATCGCATG	TGGATCTTTA	TATCTCGTTC	AGTGGCGGAG	AGCCTGCACT	CGACACCCGA	540
TTCAAGTACA	CTATGTATGA	CGAGGGAAAG	ATGACCGTGA	GGGAAGTATT	CATGCTGGTA	600
ATGGATCCGA	ATACACCTAT	CTCACGCTTG	GAATATCATT	ATGATGCACA	GGGCAGACTG	660
ACCCACTGGA	TTTCTTTTGC	TTTCGGGGCA	GAATCCCAA	AGAATACGTA	TCATAATAAT	720
AAAAAAGGTC	TGTTGGTCAG	CGAAGTGCTG	AGCAATGCAA	TGGGGACAAC	CTATTCAGAC	780
ACCGGCAAAA	CGGAATACAG	CTATGACGAT	GCAGATAATA	TGGTGAAGGC	CGAGTACTTC	840
GTCTGCCAGC	AAGGAAAGGC	ATGGCAAGTA	CTCAAAGAG	AGGAATACAC	CTATGAGGAC	900
AATATCTGCA	TACAATATTT	GGCTATTAAC	GGTACCGACA	CAAAGGTGTA	CAAGCGAGAC	960
ATCGAGAGCG	ATAAGTCCAT	CTCCGCAAAT	GTCAATTGACA	TTCCGTCAAT	GCCGGAACAG	1020
ACCTGGCCTA	ATATGTACGG	ATTCAACGCA	AAGCGACTGA	AAGAGACTTA	TTCTCTCTAC	1080
GAAGGAGATG	TGGCTACTCC	TATATTCGAC	TATATCTATA	CGTACAAGGC	TCTTACCTCA	1140
ATGGCAACAC	CTTCGACAGA	AGCTCAGGTA	GCAGTCTATC	TCAATCCGTC	AACGGACCGG	1200
TTAGTGATTC	TGGCCAAACG	CATCACACAT	CTGAGCATGT	ACGACTTGCA	GGGTAAGCTT	1260
ATCCGTGATT	GTGCCTTGAG	CGGCGATAAG	GTGGAAATGG	GTGTCGGATC	TTTGACCAA	1320
GGGACATACC	TGCTTAAAGT	GAATACGGAT	CAGGGAGCCT	TTGTGAGAAA	AGTCGTGATT	1380
CGA						1383

(2) INFORMATION FOR SEQ ID NO:122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

ATGGCAAAAAG	TTATAAAAAC	AAAAAAAGGC	CTTGCACTTA	ATCTGAAAGG	AAAACCGCTG	60
CCCAGATGTC	TGGCCGAACC	GGCCCAAAGT	CCTACTTACG	CGGTCGTGCC	CGACGATTTT	120
GAAGGTGTTA	TCCCCAAGGT	GACGGCTCGT	CCGGGGGATA	AGGTGCGTGC	CGGCTCAGCA	180
CTGATGCACC	ACAAGGCATA	TCCGGAGATG	AAGTTTACAA	GTCCGGTTAG	CGGCGAAGTG	240
ATCGCGGTGA	ATCGCGGTGC	CAAGCGCAAG	GTGTTGAGCA	TCGAGGTGAA	ACCGGACGGA	300
CTGAACGAAT	ACGAGTCATT	CCCTGTCGGG	GATCCGTCTG	CCCTCTCTGC	CGAACAGATC	360
AAGGAGCTTT	TACTGTCTGAG	CGGTATGTGG	GGTTTTATTA	AGCAACGTCC	TTACGACATA	420
TTGGCTACAC	CGGATATAGC	TCCACGCGAC	ATTTATATTA	CTGCCAACTT	TACTGCACCA	480
TTGGTCCGG	ACTTCGATTT	CATCGTTTCA	GGAGAAGAAC	GCGCCCTGCA	GACTGCCATC	540
GATGCCTTGG	CCAACTCAC	GACAGGAAAG	GTGTATGTGG	GCCTGAAGCC	GGGTTCATCT	600
CTGGGCTTGC	ACAATGCAGA	AATCGTAGAA	GTACACGGAC	CTCATCCGGC	AGGTAACGTG	660
GGCGTGCTGA	TCAATCATAC	GAAGCCAATC	AATCGGGGCG	AAACGGGTGTG	GACGCTCAAG	720
GCTACCGACC	TGATCGTGAT	CGGACGTTTC	CTGCTTACGG	GCAAAGCCGA	TTTTACCAGA	780
ATGATTGCCA	TGACCGGCTC	AGACGCTGCA	GCTCACGGAT	ACGTCCGTAT	TATGCCGGGT	840
TGCAATGTCT	TTGCTTCTCT	CCCCGGCCGA	CTGACAATAA	AGGAATCTCA	CGAGCGTGTG	900
ATCGATGGCA	ATGTGCTGAC	CGGTAAGAAG	CTCTGCGAGA	AGGAGCCTTT	CCTGTCAGCC	960
CGGTGTGACC	AGATCACGGT	GATCCCCGAA	GGCAGCATG	TGGACGAACT	CTTCGGGTGG	1020
GCTGCACCCC	GTCTCGATCA	GTACAGCATG	AGCAGAGCTT	ATTCTCTTGT	GTTGCAGGGG	1080
AAAAACAAAG	AGTACGTAAT	CGATGCCCGG	ATCAAGGGTG	GCGAACGTGC	TATGATCATG	1140
AGCAACGAGT	ATGACCGCGT	TTTCCCGATG	GACATCTATC	CGGAGTATTT	GCTCAAGGCT	1200
ATTATAGCAT	TCGACATCGA	CAAGATGGAG	GACTTAGGCA	TATATGAAGT	GGCTCCGGAG	1260
GACTTTGCCA	CTTGCGAATT	TGTGGATACA	TCCAAGATCG	AGTGCAGCG	TATCGTTTCGC	1320
GAGGGCTTGG	ATATGCTCTA	TAAGGAAATG	AAT			1353

(2) INFORMATION FOR SEQ ID NO:123

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...585
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

ATGGATAAAG	TGAGCTATGC	TCTGGGATTG	AGCATCGGTA	ATAATTTCAA	GTCTTCGGGC	60
ATCGACAGCG	TCGTTATGGA	TGATTTTCATG	CAAGGTCTGT	CTGATGTACT	GGAAGAAAAA	120
GCCCTCAGC	TCTCGTATGA	CGAGGCCAAG	CGCGAAATAG	AGGCGTATTT	CATGGATTGT	180
CAGCAGAAGG	CTGTCAAAC	GAACAAGAG	GCCGGAGAAG	AATTCCTCAA	GATAAATGCA	240
CACAAGGAAG	GTGTGACGAC	CTTACCGAGC	GGCTTGCAAT	ACGAAGTCAT	TAAGATGGGA	300
GAGGGCCCGA	AACCCACCC	TTCGGACACG	GTAACCTGTC	ATTATCACGG	TACGCTCATC	360
AACGGTATCG	TTTTCGATAG	CTCTATGGAC	AGGGGAGAAC	CGGCCAGTTT	CCCTCTAAGA	420
GGAGTTATAG	CCGGCTGGAC	GGAGATTCTT	CAATTAATGC	CTGTAGGATC	CAAGTGGAAA	480
GTAACATATAC	CGAGCGATCT	GGCGTATGGA	GATCGTGGTG	CCGGCGAACA	TATCAAACCG	540
GGTAGTACGC	TCATTTTAT	AATCGAATTA	TTGAGTATCA	ACAAA		585

(2) INFORMATION FOR SEQ ID NO:124

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 819 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...819
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

ATGAAAAAAG	CATTACTTAT	TGGTGCTGCT	CTTTTGGGAG	CAGTCAGTTT	TGCAAGTGCT	60
CAGTCTTTGA	GCACAATCAA	AGTACAGAAC	AATTCAGTAC	AGCAACCTCG	TGAGGAAGCC	120
ACTATTCAGG	TTTGTGGAGA	ATTGGCAGAG	CAAGTTGACT	GCATTGGGAC	AGGTAATTCT	180
GCAATCATAG	CCGCTGCAGC	GAAATTTGAA	AGCGATGATC	TCGAAAGCTA	TGTTGGCTGG	240
GAGATCATGA	GTGTTGATTT	CTTCCCTGGA	TATAAAGCGT	GCAAGTACAC	ATCTGCAGTC	300
TGGGCTGATG	ATATGACCAT	TTTGGGCCAA	TCAGAAGATA	GTGATCCCGA	AATGCAGACT	360
ATCAACAATC	TTGCTCTCAA	GACTAGTGTC	AAGATTGAAG	CCGGCAAGAA	TTACATAGTT	420
GGTTATATTG	CTAATACCGC	AGGTGGACAT	CCTATCGGAT	GTGATCAGGG	CCCTGCCGTT	480
GATGGTTATG	GAGATTTGGT	TTCTATATCA	GAAGATGGTG	GTGCTACTTT	CCCTCCGTTT	540
GAATCTCTTC	ATCAAGCAGT	TCCTACCTTA	AATTACAACA	TCTATGTCGT	TGTTCAATTG	600
AAGAAGGGTG	AAGGTGTTGA	GGCTGTTCTT	ACCAACGACA	AGGCTAATGC	TTATGTTTCA	660
AATGGCGTTA	TCTATGTAGC	CGGAGCTAAT	GGTCGTCAGG	TATCTCTGTT	CGACATGAAC	720
GGTAAGGTTG	TTTATACCGG	CGTTAGCGAA	ACGATTGCAG	CTCCTCAGAA	GGGCATGTAT	780
ATCCTCCGTG	TAGGTGCTAA	GAGCATCAAG	CTGGCTATC			819

(2) INFORMATION FOR SEQ ID NO:125

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1662 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

```
ATGCCAAGAA TTATGAAATT AAAAATTGCA CTCAGACTGC TGCTGGCGAC TTTTGCCATA      60
GTTTTATTTA GCCCTCTGGC CAAGGCCCCAG ATGGATATTG GTGGAGACGA TGTATTGATC      120
GAGACGATGT CCACCCTATC AGGATATTCA GAGGATTTTT ATTACAAGAT GGCTGTGGCA      180
GACAATGGAT GGATCTATGT GATGTTGGAT TTCTCTCGTA TTTATTTTGA TGATGTCAGG      240
CTGTATCGTT CCAAAGACGG TGGTGCTACT TACCAAAAGT TAGGGTCTTT GGGGTCTTTG      300
GTGCCCTATG ACTTCGATGT CTCGCATTGC GATTTTATTG TAACGGGAAA GGATGAAGAT      360
GATATCAATG TTTGGACAGT CATGACAGCA TTCGAATATG TAGGTGGTAC TATTGGCAAT      420
GGCGTTTTCG TGATGCATCG CATGATGCA GATATCAATA ATACAGAGTG TGTGTACAAG      480
AAGGATTTCC CTAATAATAG ACTGATGGGT GTAGCCATCG CCTCCAATA CCGTGCGCCC      540
TCTCCTTACG GTTTGGGGGG CGATCCTTTT GCTCTCGCTG TCGCCGTTAG TGGCTCCGGA      600
AGCGATCACA GCTTCTTGGA CTATATTTTT TCGTTAGATG GTGGAGTACA CTTTGAGCAA      660
AAGCGTATTT ACACAAGACC CCAAAAACCTG ACTATCAATA GAGTAGACCT TTCATTAGGC      720
AGTACATCTC CTTCTCTGG ATTTAATACT TGGCCACTAA TGGGAGTCGT ATTCGAAATG      780
AATAAGAACC TTGATGGCTT CGACATTGGT TTCATTTCCA ACTTTGTGGA CTATGATCCC      840
CGCTATGCGT GGTCTGAACC GATAATAATA GAAGAAGACT GTGGATGGAC TGATTTTAAT      900
CCTTTGGGAG CACTAAGTAT AGAGATCCAA ATGATGTTGG ATGACAATTC GGATAATACC      960
GTGGGTGGAG AACGCTCCCA TAACTTCCTG ATCACTTACC CGGGCCATTA CGTATATCCG     1020
AAGCAATCTT TCAATTATTC TCCCGGACAT ACACCGACAA AGAAAGATCT GGTCTTTAAA     1080
CACTGTATAG GTATTCGGGC TTTGGCATA GATAAGGAAG GCGATCGTTA TCTGACTACT     1140
TTTCAAGATC ACAATCTAAT TGATACAGA TGGATCAAAT ACGATGACAT TAACTCTTTT     1200
TATGGTTGGA GTTGGCCATA TGTATATGCA AAAGAAGCTA AAGATAAAAA GAGGCGCCGT     1260
CCGCAAGTAG CACTCAATCC TACCAATGGA AAGGCTTGTT GGGTATGGCA TACTCGCAAG     1320
AGCCCATATG ATGAAACCAA ACCACATCCT ACTCCTGTAA TTATTAACA TTTCCTATGG     1380
TCCGATACGG AGTGGGTACA TGCTCTGGAC GTGGGGGACG TATTGCAGAA GGAGGGTAGC     1440
ATGAAGCTCT ACCCCAATCC TGCCAAAGAA TATGTTCTGA TCAACCTACC CAAAGAAGGG     1500
GGGCACGAGG CAGTCGTATA CGACATGCAG GGCCGAATCG TGGAGAAAGT TTCATTTTCA     1560
GGGAAAGAAT ATAAGCTGAA TGTGCAGTAT CTGTCCAAAG GTACGTACAT GCTGAAAGTT     1620
GTAGCGGATA CGGAGTATTT CGTGGAAAAA ATCATTGTAG AG                               1662
```

(2) INFORMATION FOR SEQ ID NO:126

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1650 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

```
ATGAAATTAA AAATTGCACT CAGACTGCTG CTGGCGACTT TTGCCATAGT TTTATTAGC      60
CCTCTGGCCA AGGCCCAGAT GGATATTGGT GGAGACGATG TATTGATCGA GACGATGTCC      120
ACCTATCAG GATATTCAGA GGATTTTAT TACAAGATGG CTGTGGCAGA CAATGGATGG      180
ATCTATGTGA TGTGGGATTT CTCTCGTATT TATTTTGATG ATGTCAGGCT GTATCGTTCC      240
AAAGACGGTG GTGCTACTTA CAAAAGTTA GGGTCTTTGG GGTCTTTGGT GCCTTATGAC      300
```


TTGCGATGTCT	CGCATTGCGA	TTTTATTGTA	ACGGGAAAGG	ATGAAGATGA	TATCAATGTT	360
TGGACAGTCA	TGACAGCATT	CGAATATGTA	GGTGGTACTA	TTGGCAATGG	CGTTTTGCTG	420
ATGCATCGCG	ATGATGCGAC	TATCAATAAT	ACAGAGTGTG	TGTACAAGAA	GGATTTCCTT	480
AATAATAGAC	TGATGGGTGT	AGCCATCGCC	TCCAACCTACC	GTGCGCCCTC	TCCTTACGGT	540
TTGGGGGGCG	ATCCTTTTGC	TCTCGCTGTC	GCCGTTAGTG	GCTCCGGAAG	CGATCACAGC	600
TTCTTTGGACT	ATATTTTTTC	GTTAGATGGT	GGAGTACACT	TTGAGCAAAA	GCGTATTTAC	660
ACAAGACCCC	AAAAACTGAC	TATCAATAGA	GTAGACCTTT	CATTAGGCAG	TACATCTCCT	720
TCTCTTGAT	TTAATACTTG	GCCACTAATG	GGAGTCGTAT	TCGAAATGAA	TAAGAACCTT	780
GATGGCTTCG	ACATTGGTTT	CATTTCCAAC	TTTGTGGACT	ATGATCCCCG	CTATGCGTGG	840
TCTGAACCGA	TAATAATAGA	AGAAGACTGT	GGATGGACTG	ATTTTAATCC	TTTGGGAGCA	900
CTAAGTATAG	AGATCCAAAT	GATGTTGGAT	GACAATTCCG	ATAATACCGT	GGGTGGAGAA	960
CGCTCCCAT	ACTTCTGAT	CACTTACCCG	GGCCATTACG	TATATCCGAA	GCAATCTTTC	1020
AATTATTCTC	CCGGACATAC	ACCGACAAAG	AAAGATCTGG	TCTTTAAACA	CTGTATAGGT	1080
ATTCCGGCTT	TGGCATACTA	TAAGGAAGGC	GATCGTTATC	TGACTACTTT	TCAAGATCAC	1140
AATCTAATGA	GATACAGATG	GATCAAAATC	GATGACATTA	ACTCTTTTTA	TGGTTGGAGT	1200
TGGCCATATG	TATATGCAAA	AGAAGCTAAA	GATAAAAAGA	GGCGCCGTCC	GCAAGTAGCA	1260
CTCAATCCTA	CCAATGGAAA	GGCTTGTTGG	GTATGGCATA	CTCGCAAGAG	CCCATATGAT	1320
GAAACCAAAC	CACATCCTAC	TCCTGTAATT	ATTAAACATT	TCCTATGGTC	CGATACGGAG	1380
TGGGTACATG	CTCTGGACGT	GGGGGACGTA	TTGCAGAAGG	AGGGTAGCAT	GAAGCTCTAC	1440
CCCAATCCTG	CCAAAGAATA	TGTTCTGATC	AACCTACCCA	AAGAAGGGGG	GCACGAGGCA	1500
GTCTGATACG	ACATGCAGGG	CCGAATCGTG	GAGAAAGTTT	CATTTTCAGG	GAAAGAATAT	1560
AAGCTGAATG	TGCAGTATCT	GTCCAAAGGT	ACGTACATGC	TGAAAGTTGT	AGCGGATACG	1620
GAGTATTTTC	TGGAAAAAAT	CATTGTAGAG				1650

(2) INFORMATION FOR SEQ ID NO:127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

ATGAAACGAT	TACTCCCCCTT	TCTCCTTTTA	GCAGGACTCG	TAGCCGTAGG	AAACGTGTCT	60
GTCCAGTCAC	CCCGAATCCC	TCAAGTGGAT	GTACACACTC	GCATCGCAAG	AAATGCCCGT	120
TATCGACTGG	ACAAGATCAG	TGTCCCGGAT	TCTCGTCAGA	TATTTCGATTA	CTTCTATAAA	180
GAAGAAACGA	TACCCACTAA	AATACAAACG	ACCACAGGAG	GTGCAATTAC	AAGCATCGAT	240
TCGCTTTTCT	ATGAAGACGA	CAGGTTGGTT	CAGGTGCGCT	ATTTTGACAA	TAACCTTGAA	300
TTAAACAACG	CGGAGAAGTA	TGTATACGAC	GGTCTAAGC	TGGTCCTTCG	AGAAATTCGC	360
AAGTCGCCGA	CAGACGAAAC	GCCAAATAAG	AAAGTTAGCT	ATCACTATCT	CTGTGGCAGC	420
GATATGCCTT	TTGAGATTAC	GACAGAGATG	AGCGATGGCT	ATTTTGAAAG	CCATACGCTT	480
AACTATCTGA	ATGGAAGAGT	TGCCCGAATA	GATATCATGA	CTCAACAGAA	CCCATCGGCC	540
GAATTGATCG	AAACGGGTAG	AATGGTATAT	GAGTTTGATG	CCAATAATGA	TGCTGTACTG	600
CTTCGTGACA	GTGTATTTC	TCCTCTTCAA	AACAAGTGGG	TAGAAATGTT	TACTCACCGT	660
TATACATACG	ACAATAAGCA	TAATTGTATT	CGTTGGGAAC	AAGACGAATT	CGGCACCTTC	720
ACCCTTGCCA	ACAACCTCGA	ATACGACACC	ACTATCCCTC	TGTCGTCTGT	ATTGTTCCCC	780
ACGATGAGG	AGTTCTTCCG	TCCTCTTCTT	CCCAATTTTA	TGAAGCATAT	GCGTACGAAG	840
CAAACGTATT	TCAATAACTC	CGGAGAAGGC	TTGTCAGAGG	TATGCGATTA	CAACTACTTC	900
TATACCGATA	TGCAGGGTAA	TGCACTGACC	GATGTTGCCG	TGAACGAATC	GATCAAGATT	960
TATCCTCGTC	CTGCCACGGA	TTTTCTGCGT	ATAGAAGGTT	CGCAACTGCT	TCGCCTTTTC	1020
CTATTCGACA	TGAACGGGAA	GCTCATCAGA	GCTACCGAAT	TGACAGGCGA	TTTGGCCATT	1080
ATCGGAGTTG	CATCTCTTCC	GAGAGGCACT	TACATCGCAG	AAATAACTGC	TGCAACACAG	1140
AAAACCATAC	GTGCAAAAGT	ATCGCTCAGA				1170

(2) INFORMATION FOR SEQ ID NO:128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

```
ATGAGACAGC ATTTATCTCT ATTTCTTTT ATCTTGTTTC TGCTTCTTGC CTTCTCTTAT      60
GTCGGTTGCA GAACAGTCCG ACAAACACCT AAGCAGTCGG AACGGTACGT CGTAGTCCTG      120
TCTTTGGACG GCTTCCGACC GGAATATACC GATCGGGCAC GTACACCGGC GTTGGATCGG      180
ATGGCACAGG AGGGATTGAG CGGGTCGCTC CAACCATGCT TCCCCTCGCT TACATTTCCC      240
AATCATTAAC GCATGGGTAC GGGGCTTTAC CCCGATCATC ACGGTATCGT AGCCAATGAG      300
TTGTGTGGATT CGCTACTGGG CATCTTTTCT ATATCCGACC GAAAAGCCGT GGAGACCCCC      360
GGATTTTGGG GCGGCGAGCC GGTTTGGAAT ACGGCCGCAC GCCAAGGCAT CCGTACCGGT      420
GTCTACTTTT GGGTAGGATC CGAAACGGCT GTGAACGGAA ATCGGCCCGTG GCGGTGGAAA      480
AAATTCCTCT CCACCGTTCC GTTTCGTGAC CGTGCCGACT CCGTCATCGC GTGGCTCGGA      540
CTGCCCGAAA AGGAGCGACC GCGCTTGCTC ATGTGGTACA TCGAGGAGCC GGATATGATC      600
GGACACAGCC AAACGCCCGA AAGCCCCTG ACACTGGCAA TGGTAGAGCG GTTGGACAGT      660
GTGGTCGGCT ATTTCCGCAA GGGGTTGGAC TCTCTGCCCA TAGCCGCACA GACCGACTTC      720
ATCATAGTAG CCGATCACGG TATGGCCACG TACGAAAATG AGAAATGTGT CAATCTGTCTG      780
CATTATCTGC CTGCGGACAG TTCTCTTAC ATGGCCACCG GGGCCTTCAC CCACTTGTAC      840
CCGAAGCCCT CCTATACCGA GCGAGCCTAT GAGATCTGCG GGGCCATTCC ACATATATCG      900
GTTTACCACA AGGGGGAGGT GCCCAAGCGT TTGCGCTGTG GCACCAATCC TCGTTTGGGC      960
GAACTGGTCG TGATTCCGGA CATAGGCTCC ACCGTCTTTT TCGCAATAAA TGAAGACGTT     1020
CGTCCGGGAG CGGCACATGG CTATGACAAC CAAGCACCGG AAATGCGGGC TTTACTCCGG     1080
GCTGTCGGAC CCGATTTCCT TCCGGGCAGT AGGGTGGAAA ACCTGCCGAA TATCACCATC     1140
TATCCGCTCA TATGCAGCT GTTGGGTATA GAGCCTGCAC CCAACGATGC GGACGAAACG     1200
TTGCTGAACG GCCTGATCCG AGACAAACGA CCA                                     1233
```

(2) INFORMATION FOR SEQ ID NO:129

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

```
ATGAAAGTAG GTTGTTCAT CCCCTGTTAT GTCAATGCAG TGTATCCGGA AGTGGGTATC      60
GCCACGTACA AACTGCTGAA GAGTTTGGAC ATAGATGTCG ACTACCCGAT GGATCAGACA      120
TGTTGCGGCC AGCCTATGGC CAATGCCGGA TTCGAACAGA AAGCTCAAAA GCTGGCTTTG      180
CGATTCTAAG AGCTGTTTGA GTCGTATGAT GTAGTCGTAG GGCCATCGGC CAGTTGCGTT      240
GCTTTCGTGA AAGAAAACTA TGATCATATC CTCAGACCGA CAGGACATGT CTGCAAGTCG      300
GCAGCCAAGG TTCGGGATAT ATGCGAGTTC TTGCACGATG ACCTGAAGAT CACCAGCCTC      360
CCCTCCCGAT TCGCCCATAA GGTGAGCTG CACAACAGTT GCCACGGTGT GCGCGAACTG      420
CATCTGTCCA CCCCAGTGA AGTGCACCGA CCGTACCACA ACAAGGTGCG CCGGCTATTG      480
GAGATGGTGC AGGCATAGA GGTATTCGAG CCGAAGCGAA TAGACGAATG CTGCGGTTTC      540
GGCGGTATGT ACTCGGTGGA GGAGCCGAG GTATCCACCT GTATGGGGCA TGACAAGGTG      600
CTGGATCACA TATCCACAGG TGCGGAGTAC ATCACAGGGC CGGACAGCTC GTGCCTCATG      660
CATATGCAGG GAGTGATAGA CAGAGAGAAA TTGCCGATCA AGACAATTCA TGCAGTAGAA      720
ATTTAGCAG CAAACTTA                                     738
```

(2) INFORMATION FOR SEQ ID NO:130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

ATGGATATTG TAAGTATGGC CGATAAAGCT CTTGTAGTGG AGATGAGAGA TGTGACGCTC	60
TGTCAGGAGG AAAACGTCAT TTTTCAAAAT TTGAATCTGA CCCTTTCCGC CGGAGACTTC	120
GTCTATCTGA TAGGCTCAGT GGGATCGGGG AAGAGCACTT TGCTGAAGGC TTTGTATGCT	180
GAGGTGCCTA TCTCTGCCCG TTATGCCCGC GTGATAGATT ATGATCTGGC AAAGTTGAAA	240
CGGAAGCAGT TGCCTATCT GCGCAGGAAT TTGGGCATTG TGTTCAGGA TTTCCAGTTG	300
CTGAACGGAC GTACTGTTGC GGAGAATTG GATTTTCGTT TGCAGACTAC GGACTGGAAA	360
AACCGAGCCG ATCGCGAGCA GCGTATCGAG GAGGTTTTGA CCCGTGTGGG AATGTCTCGG	420
AAGGCTTATA AGAGACCGCA CGAACTGTCC GGAGGGGAGC AACAAACGTGT GGGTATAGCC	480
AGAGCTTTGC TGGCGAAGCC TCGTTGATC CTGGCCGACG AACCCACAGG CAACCTCGAT	540
TCGGTGACCG GATTGCAGAT CGCTTCTCTG CTCTACGAAA TCAGTAAGCA GGGCACTGCA	600
GTACTTATGA GCACGCACAA CAGCAGCCTG CTGTCGCATC TGCCGGCACG GACATTGGCC	660
GTTCGTAAGA ATGGCGATGC CTCTCTTTG GTCGAGCTGA GTGCAGATGC TGTTCGAAGA	720
AAAAATACGG AAATAGAT	738

(2) INFORMATION FOR SEQ ID NO:131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

ATGGCCGATA AAGCTCTGT AGTGGAGATG AGAGATGTGA CGCTCTGTCA GGAGGAAAAC	60
GTCATTTTTC AAAATTGAA TCTGACCCCT TCCGCCGGAG ACTTCGTCTA TCTGATAGGC	120
TCAGTGGGAT CGGGGAAGAG CACTTTGCTG AAGGCTTTGT ATGCTGAGGT GCCTATCTCT	180
GCCGGTTATG CCCGCGTGAT AGATTATGAT CTGGCAAAGT TGAAACGGAA GCAGTTGCCC	240
TATCTGCGCA GGAATTGGG CATTGTGTTT CAGGATTTC AGTTGCTGAA CGGACGTACT	300
GTTGCGGAGA ATTTGGATTT CGTTTTGCGA GCTACGACT GGAAAAACCG AGCCGATCGC	360
GAGCAGCGTA TCGAGGAGGT TTTGACCCGT GTGGGAATGT CTCGGAAGGC TTATAAGAGA	420
CCGCACGAAC TGTCCGGAGG GGAGCAACAA CGTGTGGGTA TAGCCAGAGC TTTGCTGGCG	480
AAGCCTGCGT TGATCTTGGC CGACGAACCC ACAGGCAACC TCGATTCTGGT GACCGGATTG	540
CAGATCGCTT CTCTGCTCTA CGAAATCAGT AAGCAGGGCA CTGCAGTACT TATGAGCAGC	600
CACAACAGCA GCCTGCTGTC GCATCTGCCG GCACGGACAT TGGCCGTTTC TAAGAATGGC	660
GATGCCTCCT CTTTGGTCTG GCTGAGTGCA GATGCTGTTT CAAGAAAAAA TACGGAAATA	720
GAT	723

(2) INFORMATION FOR SEQ ID NO:132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

```
ATGAGAGATG TGACGCTCTG TCAGGAGGAA AACGTCATTT TTCAAAATTT GAATCTGACC      60
CTTTCGCCCG GAGACTTCGT CTATCTGATA GGCTCAGTGG GATCGGGGAA GAGCACTTTG     120
CTGAAGGCTT TGTATGCTGA GGTGCCTATC TCTGCCGGTT ATGCCCGCGT GATAGATTAT     180
GATCTGGCAA AGTTGAAACG GAAGCAGTTG CCCTATCTGC GCAGGAATTT GGGCATTGTG     240
TTTCAGGATT TCCAGTTGCT GAACGGACGT ACTGTTGCGG AGAATTTGGA TTTCGTTTTG     300
CGAGCTACGG ACTGGAAAAA CCGAGCCGAT CGCGAGCAGC GTATCGAGGA GGTTTTGACC     360
CGTGTGGGAA TGTCTCGGAA GGCTTATAAG AGACCGCACG AACTGTCCGG AGGGGAGCAA     420
CAACGTGTGG GTATAGCCAG AGCTTTGCTG GCGAAGCCTG CGTTGATCCT GGCCGACGAA     480
CCCACAGGCA ACCTCGATTG GGTGACCGGA TTGCAGATCG CTTCTCTGCT CTACGAAATC     540
AGTAAGCAGG GCACTGCAGT ACTTATGAGC ACGCACACAA GCAGCCTGCT GTCGCATCTG     600
CCGGCACGGA CATTGGCCGT TCGTAAGAAT GGCGATGCCT CCTCTTTGGT CGAGCTGAGT     660
GCAGATGCTG TTTCAAGAAA AAATACGGAA ATAGAT
```

(2) INFORMATION FOR SEQ ID NO:133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

```
ATGATTGAAA TCAGCAACCT CACCAAGGTT TTCAGAACAG AAGAAATAGA GACGGTAGCC      60
CTCGATGGCG TATCGCTCAA AGTGGACAAA GGCGAATTTA TCGCCATAAT GGGGCCTTCG     120
GGATGCGGTA AGTCCACTCT GCTCAATATC CTCGGCCTTC TCGACAATCC CACTTCCGGT     180
ATCTACAAGC TCGATGGGGC AGAAGTGGGC AACCTCCGGG AAAAAGACAG GACTGCCGTC     240
CGTAAGGGCA ATATCGGCTT CGTATTCCAG AGCTTCAACC TCATCGAAGA GATGACGGTA     300
AGCGAGAACG TGGAGTTGCC GCTCGTCTAT CTGGGTGTGA AGGCCTCCGA GCGGAAAGAG     360
CGAGTGGAGG AGGCACTGCG CAAGATGAGC ATCAGCCACC GGGCCGGCCA CTTCCCAAT     420
CAGCTCTCCG GAGGACAACA GCAGCGCGTG GCTATCGCCC GTGCCGTGGT GGCCAATCCG     480
AAGCTCATCC TCGCCGATGA ACCCACGGGT AACCTCGACT CCAAAAACGG AGCCGATGTC     540
ATGGAAGTGC TCAGAGGTCT CAATCGCGAA GGTGCAACCA TCGTCATGGT GACGCACTCC     600
GAGCACGATG CACGTAGTGC CGGCCGCATC ATCAATCTGT TCGACGGTAA GATTTCGC      657
```

(2) INFORMATION FOR SEQ ID NO:134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

```
ATGAAAGAAT TTTTCAAAAT GTTTTTTCGCC TCGATCCTCG GGGTTATAAC GGCAGGAATC      60
ATCTTGTTCT GTATCTTTCT ATTTATCTTT TTCGGCATCG TAGCCGGTAT TGCCTCCAAG      120
GCAACGGGAG GAACCATTCG GAAGATCGAA GCAAACCTCA TCCTACATAT ANACAATTCT      180
TCTTTCCCTG AGATCGTATC GGCCAAATCCC TGGAGCATGC TCACAGGCAA AGACGAGTCC      240
GTATCGCTCT CACAGGCAGT CGAAGCCATC GGCCAAGCCA AAAATAATCC CAACATAACC      300
GGTATCTTCC TCGATCTGGA CAACCTTTCC GTCGGTATGG CATCGGCAGA GGAATTGCGT      360
CGCGCGTTGC AGGATTTCOA GATGTCGGGC AAGTTCGTCG TATCCTATGC CGACAGATAC      420
ACCCAAAAGG GTTACTACCT CTCAGTATT GCAGACAAAC TCTACCTCAA TCCGAAAGGA      480
ATGTTGGGGC TTATCGGGAT TGCGACCCAA ACAATGTTCT ACAAAGATGC CCTCGACAAA      540
TTCGGCGTGA AGATGGAGAT CTTCAAGGTA GGCACCTACA AGGCAGCCGT AGAGCCATTC      600
ATGCTCAACA GGATGAGCGA TGCCAATCGC GAACAAATCA CCACATACAT AAACGGGCTT      660
TGGGACAAGA TCACATCCGA TATTGCAGAG TCGCGCAAGA CGGCAATGGA TTCCGTGAAA      720
ATGTTTGCCG ACAAAGGCGA AATGTTCCGT CTGCGGAGA AAGCGGTGGA GATGAAGCTC      780
GTGGATGAGC TGGCTTACCG TACCGATGTG GAGAAAGAAC TCAAAAAGAT GTCCCAACGC      840
GGAGAGAAAG ATGAACCTCG GTTCGTATCG CTTTCTCAGG TTCTGGCCAA TGGCCCCGATG      900
AACAAACGCA AAGGCAGTCG GATCGCCGTT CTCTTTGCCG AAGGTGAAAT AACGGAAGAA      960
ATAATAAAGA AGCCGTTCTG CACTGACGGT AGCTCCATCA CACAAGAACT CGCCAAAGAA     1020
ATCAAGGCAG CAGCCGATGA CGATGATATC AAAGCCGTAG TACTTCGTGT CAATTCTCCG     1080
GGAGGTAGTG CTTTCACTTC CGAACAGATA TGGAAGCAGG TAGCCGATCT CAAGGCCAAA     1140
AAGCCTATCG TGGTCTCCAT GGGCGACGTA GCAGCCTCGG GCGGATACTA CATAGCCTGC     1200
GCAGCCAACA GTATCGTGGC AGAGCATACG ACTCTGACCG GCTCCATCGG CATATTCCGGC     1260
ATGTTCCCGA ACTTCGCGGG CGTAGCCAAG AAGATAGGAG TGAATATGGA CGTCGTACAG     1320
ACATCCAAGT ATGCAGACTT GGGCAACACC TTCGCTCCGA TGACGGTCGA AGATCGTGCC     1380
TCATCCCAAC GCTACATAGA CAGGGGCTAC GACCTCTTCC TACTCGCGT ATCGGAAGGC     1440
CGCAACCGCA CCAAGGCACA GATCGACAGC ATCGCTCAAG GCCGTGTATG GCTCGGCGAC     1500
AAAGCTCTTG CACTCGGTTT GGTGGATGAG CTTGGAGGTT TGGACACAGC TATCAAACGG     1560
GCCGCGAAGC TGGCTCAGCT CGGTGGCAAC TACAGCATAG AGTATGGCAA GACCAAGCGC     1620
AACTTCTTCG AAGAGTTGCT CTCCTCATCA GCAGCGGATA TGAAGTCTGC CATCCTGAGT     1680
ACCATTCTCT CCGATCCGGA AATAGAAGTT CTGCGCGAAC TCCGCTCCAT GCCGCCCCGT     1740
CCTTCGGGCA TACAGGCACG TCTCCCTAT TACTTCATGC CGTAC      1785
```

(2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

```
ATGTTTTCG CCTCGATCCT CGGGGTATA ACGGCAGGAA TCATCTTGTT CTGTATCTTT      60
CTATTTATCT TTTTCGGCAT CGTAGCCGGT ATTGCCTCCA AGGCAACGGG AGGAACCATT      120
CCGAAGATCG AAGCAAACCT CATCTACAT ATANACAATT CTTCTTTCCC TGAGATCGTA      180
```

TCGGCCAATC	CCTGGAGCAT	GCTCACAGGC	AAAGACGAGT	CCGTATCGCT	CTCACAGGCA	240
GTGGAAGCCA	TCGGCCAAGC	CAAAAATAAT	CCCAACATAA	CCGGTATCTT	CCTCGATCTG	300
GACAACCTTT	CCGTCCGTAT	GGCATCGGCA	GAGGAATTGC	GTGCGCGCTT	GCAGGATTTC	360
AAGATGTCGG	GCAAGTTCGT	CGTATCCTAT	GCCGACAGAT	ACACCCAAAA	GGGTTACTAC	420
CTCTCCAGTA	TTGCAGACAA	ACTCTACCTC	AATCCGAAAAG	GAATGTTGGG	GCTTATCGGG	480
ATTGCGACCC	AAACAATGTT	CTACAAAGAT	GCCCTCGACA	AATTCGGCGT	GAAGATGGAG	540
ATCTTCAAGG	TAGGACCTTA	CAAGGCAGCC	GTAGAGCCAT	TCATGCTCAA	CAGGATGAGC	600
GATGCCAATC	GCGAACAAAT	CACCACATAC	ATAAACGGGC	TTTGGGACAA	GATCACATCC	660
GATATTGCAG	AGTCGCGCAA	GACGGCAATG	GATTCCGTGA	AAATGTTTGC	CGACAAAGGC	720
GAAATGTTTC	GTCTTGCCGA	GAAAGCGGTG	GAGATGAAGC	TCGTGGATGA	GCTGGCTTAC	780
CGTATCCGATG	TGGAGAAAGA	ACTCAAAAAG	ATGTCCCAAC	GCGGAGAGAA	AGATGAACTT	840
CGGTTCTGAT	CGCTTTCTCA	GGTTCTGGCC	AATGGCCCCG	TGAACAAAAC	GAAAGGCAGT	900
CGGATCGCCG	TTCTCTTTGC	CGAAGGTGAA	ATAACGGAAG	AAATAATAAA	GAAGCCGTTC	960
GACACTGACG	GTAGCTCCAT	CACACAAGAA	CTCGCCAAAG	AAATCAAGGC	AGCAGCCGAT	1020
GACGATGATA	TCAAAGCCGT	AGTACTTCGT	GTCAATTCTC	CGGGAGGTAG	TGCTTTCACT	1080
TCCGAACAGA	TATGGAAGCA	GGTAGCCGAT	CTCAAGGCCA	AAAAGCCTAT	CGTGGTCTCC	1140
ATGGGCGACG	TAGCAGCCTC	GGGCGGATAC	TACATAGCCT	GCGCAGCCAA	CAGTATCGTG	1200
GCAGAGCATA	CGACTCTGAC	CGGCTCCATC	GGCATATTTC	GCATGTTCCC	GAAGTTCCGC	1260
GGCGTAGCCA	AGAAGATAG	TGTGAATATG	GACGTCTGAC	AGACATCCAA	GTATGCAGAC	1320
TTGGGCAACA	CCTTCGCTCC	GATGACGGTC	GAAGATCGTG	CCCTCATCCA	ACGCTACATA	1380
GAGCAGGGCT	ACGACCTCTT	CCTCACTCGC	GTATCGGAAG	GCCGCAACCG	CACCAAGGCA	1440
CAGATCGACA	GCATCGCTCA	AGGCCGTGTA	TGGCTCGGCG	ACAAAGCTCT	TGCACTCGGT	1500
TTGGTGGATG	AGCTTGGAGG	TTTGGACACA	GCTATCAAAC	GGGCCGCGAA	GCTGGCTCAG	1560
CTCGGTGGCA	ACTACAGCAT	AGAGTATGGC	AAGACCAAGC	GCAACTTCTT	CGAAGAGTTG	1620
CTCTCCTCAT	CAGCAGCGGA	TATGAAGTCT	GCCATCCTGA	GTACCATCTT	CTCCGATCCG	1680
GAAATAGAAG	TTCTGCGCGA	ACTCCGCTCC	ATGCCGCCCC	GTCCTTCGGG	CATACAGGCA	1740
CGTCTCCCTT	ATTACTTCAT	GCCGTAC				1767

(2) INFORMATION FOR SEQ ID NO:136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

ATGAGAGCAA	ACATTTGGCA	GATACTTTCC	GTTTCGGTTC	TCTTTTCTT	CGGGACAGCG	60
ATCGGACAGG	CTCAGAGTCG	AAACCGTACA	TACGAGGCTT	ATGTGAAACA	GTACGCCGAC	120
GAAGCTATCC	GACAGATGAG	CGCTACAAT	ATACCGGCAA	GCATCACCAT	AGCACAGGCT	180
TTGGTGGAGA	CAGGAGCCGG	AGCCAGTACA	CTGGCCAGCG	TACACAACAA	TCACTTCGGG	240
ATCAAATGCC	ACAAATCGTG	GACGGGCAAG	CGCACCTATC	GTACCGACGA	TGCGCCGAAC	300
GAATGCTTCC	GCAGCTATTC	GGCCGCTCGC	GAATCGTATG	AAGATCATTC	CCGATTCTGT	360
CTCCAAGCAC	GCTATCGTCC	CCTGTTCAAA	CTCGACAGAG	AAGACTATCG	GGGCTGGGCT	420
ACGGGGTTGC	AACGCTGTGG	CTATGCCACC	AATCGGGGCT	ATGCCAATCT	GCTGATCAAG	480
ATGGTGGAGC	TGTATGAGCT	ATATGCTTTG	GATCGCGAGA	AGTACCCCTC	ATGGTTCCAC	540
AAGTCTTACC	CCGGGTCCAA	CAAAAAATCC	CATCAAACGA	CCAAGCAGAA	GCAGAGCGGA	600
CTCAAGCAGC	AAGCTTACTT	CAGCTACGGA	CTGCTCTACA	TCATAGCCAA	GCAAGGCGAT	660
ACCTTCGATT	CTTTGGCCGA	AGAGTTCGAC	ATGAGAGCCT	CCAAACTGGC	CAAATACAAC	720
GATGCTCCCG	TGGATTTCCC	GATCGAAAAG	GGCGATGTGA	TCTATCTGGA	GAAAAAGCAC	780
GCATGCTCCA	TCTCAAACA	CACACAGCAC	GTAGTGCGTG	TGGGCGATTG	GATGCACAGT	840
ATCTCCCAAC	GCTATGGCAT	CCGGATGAAG	AACCTCTACA	AGCTCAACGA	CAAGGATGGC	900
GAATATATAC	CCCAAGAGGG	CGATATACTG	CGCTTGCGC			939

(2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1569
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

ATGGACGGAC	GTCTGATATTC	GGATGGCCTC	CATCAGGCTA	TCGAAGCCAA	AGAGCATGTG	60
AAAGTAGAGG	CTGCGACACA	GACATTTGCA	ACTATCACTT	TGCAGAACTA	TTTCCGCATG	120
TATCATAAGC	TGGCAGGGAT	GACCGGTACT	GCTGAAACTG	AAGCGGGAGA	GCTTTGGGAC	180
ATCTACAAAC	TGGACGTTGT	AGTTATTCCG	ACAAACAAGC	CTATCGCCCG	TAAGGATATG	240
AATGATCGTA	TCTATAAGAC	GGCACGTGAA	AAATATGCAG	CAGTTATCGA	AGAGATTGTA	300
CGTCTTGTG	AAGAGGGCAG	ACCTGTACTT	GTCCGGTACTA	CTTCGGTGGA	AATATCCGAA	360
TTGTTGAGCC	GTATGTTACG	CTTGCCTGGC	ATCCAACACA	ATGTACTCAA	TGCCAAATTG	420
CATCAGAAGG	AGGCCGAGAT	TGTAGCTCAG	GCCGGTCAGA	AAGGAACTGT	TACCATCGCA	480
ACGAACATGG	CCGGTCGTGG	TACCGACATC	AAGCTCTCTG	CCGAGGTTAA	GAAAGCCGGG	540
GGTTTGGGCTA	TCATTGGTAC	GGAAAGGCAC	GAATCCAGAC	GAGTGGACAG	ACAGCTTCGT	600
GGTCGTTCCG	GCCGTCAGGG	TGATCCCGGT	TCGTCCATAT	TCTATGTTTC	CCTTGAAGAT	660
CATCTGATGC	GCCCTCTTGC	CACAGAAAAG	ATTGCATCAT	TGATGGATCG	TTTAGGTTTC	720
AAGGAAGGAG	AAGTGCTCGA	AAACAACATG	CTGAGTAAGT	CCGTGGAGCG	TGCTCAAAAG	780
AAGGTGGAAG	AGAACAACCT	CGGTATCCGT	AAACATCTGC	TTGAGTACGA	TGATGTAATG	840
AATTCGCAGC	GTGAAGTCAT	TTATACCCGT	CGCGTCATG	CTTGATGGG	AGAGCGTATC	900
GGTATGGATG	TACTCAATAC	CATATACGAC	GTATGTAAGG	CTCTGATTGA	CAATTATGCA	960
GAAGCCAATG	ATTTCAAGG	CTTCAAGGAA	GATCTGATGC	GTGCACTCGC	GATAGAATCT	1020
CCTATCACGC	AAGAAATATT	CAGAGGTAAG	AAAGCAGAAG	AGCTGACCGA	TATGCTTTTC	1080
GATGAAGCTT	ACAAGTCTTT	CCAACGTAAG	ATGGATCTGA	TCGCAGAAGT	GGCCCACCCT	1140
GTGGTTTCATC	AGGTATTCTGA	GACCCAAGCC	GCCGTGTACG	AGCGCATTTCT	AATCCCCATT	1200
ACGGATGGTA	AACGTGTCTA	TAACATAGGA	TGCAATTTGC	GTGAAGCGGA	TGAAACTCAA	1260
GGGAAAAGCA	TCATCAAAGA	ATTTGAGAAA	GCTATCGTAC	TGCATACTAT	CGATGAGTCT	1320
TGGAAAGAAC	ATCTGCGTGA	GATGGACGAG	CTTCGTAATT	CCGTTTCAGAA	TGCCAGCTAC	1380
GAAAACAAAG	ATCCACTACT	TATCTATAAA	CTCGAATCTT	ACGAACTGTT	CCGCAAGATG	1440
GTAGAAGCCA	TGAACCGTAA	GACCGTAGCG	ATCCTAATGC	GTGCTCGGAT	ACCGGTACCG	1500
GAGGCTCCTT	CCCAAGAAGA	GCTGGAACAC	AGCGGGCAAA	TAGAAATCCG	ACATGCAACC	1560
CAACAACGT						1569

(2) INFORMATION FOR SEQ ID NO:138

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1125
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

ATGAATTTCT	TAAAAAAGA	ACCGTTTAAA	ATATTCTCTA	TGATTATCT	GCTGTTAGAT	60
ACAATAACAA	ACCGTGCCGG	TACAGAACGC	GCCGTGATCA	ACTTGGCTAA	CAACCTGCAT	120
GCCAATGGTC	ATCGCGTATC	ATTAGTCAGC	GTTTGTACAA	AAGAAGGAGA	GCCTTCCTTC	180
CAAGTAGAAA	AAGGAATAGA	AGTACACCAT	CTCGGAATTA	GGCTTTATGG	CAATGCATTA	240
GCCCGCAAAA	CAGTATATTT	CAAGGCTTAT	CGAAGGATAA	AAGCCCTATA	CAAGAAGCGT	300
GAACCGGTTT	TATTGATAGG	GACTAATATT	TTTATCAATA	CAATTTTGTC	TCAGATCAGT	360
AACAGAGGCA	GAATATTTAC	GATCGGATGC	GAACATATCT	CTTATGATAT	TGCCCGCCCT	420
ATTACAAAAC	GCATAAGGG	GTTTCTGTAT	TCAGGGCTTG	ATGCCGTTGT	AGCACTGACA	480
AAAAGAGATC	AGCAATCGTT	CGAGGCAATC	TTACGTGGAC	GCTCTAAAGC	ATATGTCATA	540

CCCAATCAAG	TTTCATTAC	TACAGTCCAA	AGAGATGCTA	CTACTCACAA	ACAAATGTTG	600
GCGATTGGCA	GGCTTACCTA	CCAGAAGGGT	TTTGAATTCA	TGATAGAAGA	TGCATCACGA	660
GTGCTGCGAG	AAAGGCCCTGA	TTGGAAGCTT	ATCATAGTCG	GAGATGGCGA	AAATGAATCG	720
ATGCTACGTA	AAGAAATTGC	ATCTCGCAAT	ATGGAGTCGC	AAATAGAAAT	ACATCCATCT	780
ACACCGGAAA	TTCGCAAATA	CTACGAATCA	TCTGCTATTT	ATCTAATGAC	GTCCCGTTTC	840
GAAGGACTAC	CAATGGTACT	TCTCGAAGCA	GAAGCATATG	CACTACCTAT	AATCTCATAC	900
GATTGTCCGA	CCGGCCCGAG	GGAACTGATC	GAAAACGGTC	GCAATGGTTT	CCTTGTGCCA	960
ATGGAAGCAC	ATGAAGACTT	CGCGGATAAG	TTACGCTTAT	TGATGGATGA	TGAAACTCTT	1020
CGTAAGAAAA	TGGGACAAGA	ATCAGAGTTG	ATGGTCAAAT	CCTACTCTCC	GGCAAATATC	1080
TATGAATGTT	GGAAGAAACT	ATTCGTCGAA	ATCGGCTACA	TGAAT		1125

(2) INFORMATION FOR SEQ ID NO:139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

ATGATTTATC	TGCTGTTAGA	TACAATAACA	AACCGTGCCG	GTACAGAACG	CGCCGTGATC	60
AACTTGCTA	ACAACCTGCA	TGCCAATGGT	CATCGCGTAT	CATTAGTCAG	CGTTTGATCA	120
AAAGAAGGAG	AGCCTTCCTT	CCAAGTAGAA	AAAGGAATAG	AAGTACACCA	TCTCGGAATT	180
AGGCTTTATG	GCAATGCATT	AGCCCGCAAA	ACAGTATATT	TCAAGGCTTA	TCGAAGGATA	240
AAAGCCCTAT	ACAAGAAGCG	TGAACCGGTT	TTATTGATAG	GGACTAATAT	TTTTATCAAT	300
ACAATTTTGT	CTCAGATCAG	TAACAGAGGC	AGAATATTTA	CGATCGGATG	CGAACATATC	360
TCTTATGATA	TTGCCCGCCC	TATTACAAAA	CGCATAAGGG	GGTTTCTGTA	TTCAGGGCTT	420
GATGCCGTTG	TAGCACTGAC	AAAAAGAGAT	CAGCAATCGT	TCGAGGCAAT	CTTACGTGGA	480
CGCTCTAAAG	CATATGTCAT	ACCCAATCAA	GTTTCATTTA	CTACAGTCCA	AAGAGATGCT	540
ACTACTCACA	AACAAATGTT	GGCGATTGGC	AGGCTTACCT	ACCAGAAGGG	TTTGAATTC	600
ATGATAGAAG	ATGCATCAGC	AGTGCTGCGA	GAAAGGCCTG	ATTGGAAGCT	TATCATAGTC	660
GGAGATGGCG	AAAATGAATC	GATGCTACGT	AAAGAAATTG	CATCTCGCAA	TATGGAGTCG	720
CAAATAGAAA	TACATCCATC	TACACCGGAA	ATTTCGCAAAT	ACTACGAATC	ATCTGCTATT	780
TATCTAATGA	CGTCCCCTTT	CGAAGGACTA	CCAATGGTAC	TTCTCGAAGC	AGAAGCATAT	840
GCACTACCTA	TAATCTCATA	CGATTGTCCG	ACCGGCCCGA	GGGAAC TGAT	CGAAAACGGT	900
CGCAATGGTT	TCCTTG TGCC	AATGGAAGCA	CATGAAGACT	TCGCGGATAA	GTTACGCTTA	960
TTGATGGATG	ATGAACTCT	TCGTAAGAAA	ATGGGACAAG	AATCAGAGTT	GATGGTCAAA	1020
TCCTACTCTC	CGGCAATAT	CTATGAATGT	TGGAAGAAAC	TATTCGTCGA	AATCGGCTAC	1080
ATGAAT						1086

(2) INFORMATION FOR SEQ ID NO:140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

ATGGGAAAAA	TCATTGGAAT	TGACTTAGGC	ACAACGAACT	CTTGTGTCTC	TGTATTGGAA	60
GGTAACGAAC	CTATCGTTAT	TACAAACAGT	GAGGGCAAGC	GCACAACGCC	CTCGGTAGTG	120
GCTTTTGTGG	ATGGTGGCGA	GCGTAAGGTG	GGCGATCCGG	CCAAGCGTCA	GGCCATCACC	180
AATCCGACCA	AGACGATATA	CTCTATCAAA	CGCTTCATGG	GCGAAACTTA	CGATCAGGTT	240
TCCAGAGAAG	TGGAGAGAGT	GCCATTCAAG	GTAGTACGTG	GGGACAATAA	TACTCCGCGC	300
GTAGATATAG	ACGGTCGTCT	CTATACGCCG	CAGGAAATTT	CGGCCATGAT	CCTTCAGAAG	360
ATGAAGAAGA	CGGCCGAAGA	CTACCTCGGT	CAGGAAGTAA	CGGAGGCCGT	GATCACTGTG	420
CCCGCATACT	TCAACGACGC	TCAACGTCAG	GCAACGAAAG	AAGCAGGAGA	GATCGCCGGC	480
CTGAAAGTTC	GCCGTATTGT	GAACGAGCCT	ACGGCAGCTT	CTCTGGCCTA	CGTCTGGAC	540
AAGTCCAATA	AGGATATGAA	GATCGCTGTC	TTCGACTTGG	GTGGCGGTAC	CTTCGATATC	600
TCATCTTTGG	AATTGGGCGA	CGCGTTTTC	GAAGTGAAT	CGACCAACGG	TGATACGCAC	660
CTCGGAGGAG	ACGACTTCGA	CCACGTGATC	ATTGACTGGC	TGGCAGAAGA	GTTCAGTCT	720
CAGGAAGGTG	TGGATCTTCG	CCAGGATCCT	ATGGCTATGC	AGCGTCTGAA	AGAAGCTGCC	780
GAAAAAGCCA	AGATAGAGCT	CTCCAGCACT	TCATCTACGG	AGATCAACCT	CCCTTATATC	840
ATGCCGCTGA	ACGGCATCCC	CAAGCACTTG	GTGATGACGC	TTACAAGGGC	TAAGTTCGAG	900
CAGTTGGCCG	ATCGTCTGAT	TCAGGCATGT	GTGGCACCTT	GCGAAACGGC	CTTGAAAGAT	960
GCCGGTATGT	CACGTGGCGA	TATCGATGAA	GTGATTCTCG	TAGGTGGTTC	CACACGTATT	1020
CCTGCTATTG	AGGAGATTGT	GGAGAAGATC	TTCGGTAAGG	CTCCGTCCAA	GGGTGTGAAT	1080
CCCGACGAAG	TGGTAGCTGT	GGGTGCCGCT	ATTCAAGGCG	GTGTTCTGAC	CGGTGAGGTA	1140
AAGGATGTCT	TGCTGTTGGA	CGTTACCCCC	TTGTCGCTCG	GTATCGAGAC	TATGGGAGGC	1200
GTGATGACTC	GTGATGACTC	TGCCAATACC	ACTATCCCGA	CGAAGAAGAG	CGAAATCTTT	1260
ACCACAGCAG	TGGACAATCA	ACCTTCGGTA	GAGATTCATG	TACTTCAGGG	TGAGCGTTCT	1320
TTGGCTAAGG	ACAATAAGAG	CATCGGCCGT	TTCAACTTGG	ACGGTATTGC	TCCGGCGCCC	1380
CGTCAGACAC	CGCAGATCGA	AGTAACGTTT	GACATCGATG	CCAACGGTAT	CCTGAATGTA	1440
ACGGCTCATG	ACAAAGCTAC	CGGCAAGAAG	CAGAATATCC	GCATCGAAGC	CTCCAGCGGT	1500
TTGTCCGATG	ATGAGATCAA	GCGCATGAAG	GAAGAGGCGC	AGGCCAATGC	CGAAGCAGAT	1560
AAGAAAGAGA	AAGAACGTAT	CGACAAGATC	AATCAGGCGG	ACAGCATGAT	CTTCCAGACG	1620
GAAAAGCAGT	TGAAGGAGTT	GGGAGACAAA	TTCCCGGCCG	ACAAGAAGGC	TCCGATCGAT	1680
ACCGCTCTCG	ACAAACTGAA	AGAAGCACAC	AAAGCACAGG	ATGTAGCTGC	TATCGATACA	1740
GCCATGGCCG	AACTGCAAAAC	CGCTCTTTCC	GCAGCGGGCG	AAGAGCTTTA	CAAGAATGCC	1800
GGAGCAGCCC	AAGGTGGCGC	ACAACCCGGT	CCGGACTTCG	GCGGTGCTCA	AGGTCCCTCT	1860
GCCGGTGATC	AGCCCTCTGA	CGACAAGAAC	GTCACAGACG	TAGACTTCGA	GGAAGTGAAG	1920

(2) INFORMATION FOR SEQ ID NO:141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

ATGCGCTACG	ACTTAGCTAT	CATCGGTGGA	GGGCCGGCCG	GTTATACGGC	TGCCGAACGT	60
GCTGCCAAAG	GTGGCCTGAA	AACCCTCCTA	ATTGAGAAGA	ATGCTCTCGG	TGGTGTATGC	120
CTCAACGAAG	GATGTATACC	GACCAAGACG	CTACTCTACT	CGGCCAAAGT	GCTACATCAA	180
ATTGCTACGG	CATCTAAATA	TGCAGTAAGT	GGAACGGCCG	ATGGACTTGA	CCTCGGCAAG	240
GTGATTGCCA	GAAAAGGTAA	AATCATTCGC	AAGCTGACTG	CAGGCATCCG	TTCACGCCTG	300
ACAGAGCCCG	GAGTAGAGAT	GGTGACGGCA	GAAGCTACCG	TAACGGGATG	CGATGCAGAC	360
GGCATCATCG	GCATTACTGC	GGGCGAAGCA	CAGTACAAAG	CTGCCAACCT	GCTACTATGT	420
ACCGGTTCCG	AGACGTTTAT	TCCACCCATC	CCCGGAGTGG	AGCAGACAGA	GTATTGGACA	480
AACCGTGAAG	CTCTACAGAA	CAAAGAGATT	CCGACCTCTC	TCGTATCAT	CGGTGGTGGA	540
GTGATCGGAA	TGGAGTTTCG	TCTTTTCTTC	AACGGTATCG	GTACGCAAGT	GCACGTGGTG	600
GAGATGCTGC	CGGAAATACT	CAACGGTATC	GATCCCGAAC	ATGCAGCTAT	GCTACGCGCT	660
CAGTATGAAA	AAGAAGGAAT	CAAATTCTAC	CTCGGGCACA	AAGTAACATC	GGTTCGCAAC	720
GGAGCTGTTA	CGGTAGAATA	CGAAGGAGAA	AGCAAAGAGA	TGCAAGGAGA	ACGTATCCTG	780
ATGAGTGTGG	GACGTCGCCC	CGTGCTGCAA	GGATTTCGAGT	CGCTCGGATT	GGTGCTTGCC	840
GGCAAAGGTG	TAAAGACTAA	TGAGAGGATG	CAAACCTCCC	TGCCCAATGT	CTATGCTGCA	900
GGTGATATTA	CAGGCTTCTC	TCTTTTGGCA	CATACGGCTG	TACGGGAAGC	AGAGGTAGAC	960
GTAGATCAGA	TTTTTGGCAA	AACAGACGAA	ACGATGAGCT	ACCGTGCCGT	ACCAGGTGTG	1020
GTGTACACCA	ATCCCGAGGT	CGCCGGTGTG	GGAGAGACGG	AAGAATCGCT	TGCAAAGCA	1080

GGACGTGCCT	AACTGTTTCG	TCGCCTTCT	ATGGCCTTCT	CCGGTCGATT	TGTAGCAGAA	1140
AACGAACAAG	GCAATGGAGA	GTGCAAACTA	CTACTTGATG	AAGAGAACCG	CTTGATCGGA	1200
GCACACCTCA	TTGGCAATCC	GGCCGGCGAA	CTCATCGTAA	CCGCTGCCAT	GGCCATCGAG	1260
ACCGGCATGA	CGGATCGACA	AATCGAACGA	ATCATATTCC	CTCATCCGAC	TGTAGGCGAA	1320
ATCCTAAAAG	AAACTCTCGC	CGGAGGT				1347

(2) INFORMATION FOR SEQ ID NO:142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

ATGGAATTGA	AAAGATTTT	ATCACTTGGT	CTTCTGCTTG	TGGGATTCAT	TCCGATGAAG	60
CTTTCTGCCC	AACAGGCTCA	GCCACTCCCT	ACAGATCCGG	CTGTTCTGTT	CGGTAAGTTG	120
GACAACGGAT	TGACTTATTT	CATCCGTCAC	AACGAGAAC	CGAAAGATCG	TGCGGATTTC	180
TTTATCGCAC	AAAAGGTAGG	TTCTATTCTT	GAAGAAGATA	GCCAGTCCGG	TTTGGCTCAC	240
TTCTTGGAAC	ACATGGCTTT	CAACGGTACG	AAGAACTTCC	CCGTAAGAA	CTTGATCAAC	300
TATCTCGAAA	CGATCGGTGT	ACGTTTCGGT	CAGAACCCTGA	ACGCTTCTAC	CGGATTCGAC	360
AAGACGGAAT	ATACGATAAT	GGATGTGCGG	ACTACACGTC	AGGGAATCAT	CGACTCCTGC	420
TTGCTTATCC	TGCATGATTG	GAGTAACAAT	ATTACCCTCG	ACGGGCATGA	GATCGACGAG	480
GAGCGCGGTG	TGATCCAGGA	AGAGTGGCGT	GCTCGTCGCG	ATGCCAACCT	TCGTATGTTT	540
GAGGCTATAC	TTGCCAAGGC	TATGCCGGGT	AATAAATATG	CAGAACGCAT	GCCCATCGGT	600
CTGATGGACG	TCGTGCTCAA	CTTCAAGCAT	GATGAGCTGC	GCAACTATTA	TAAGAAATGG	660
TATCGTCCCG	ACCTGCAAGG	TCTGGTGATC	GTGGGAGATA	TCGATGTGGA	CTATGTGGAG	720
AACAAGATCA	AGAAACTCTT	CAAGGACGTT	CCTGCTCCCG	TGAATCCAGC	AGAGCGTATC	780
TATACGCCGG	TAGAGGACAA	CGATGAGCCT	ATCGTAGCCA	TTGCTACCGA	TGCTGAGGCT	840
ACTACCACGC	AGTCTCCAT	CAGTTTCAAG	AGCGACCCCA	CTCCTCAAGA	AGTGCAGGGA	900
TCGATATTCC	GACTTGTGGA	AGACTATATG	AAACAGGTGA	TCACTACAGC	CGTGAATGAG	960
CGTCTGTCGG	AGGAAAGAGA	GACGCTTAC	GCTCCTTTCC	TCAGTGCAGG	AGCTTCTTTC	1020
TCTAATTCCA	TGTACATCAC	CCAGACTAAG	GACGCATTCA	ATTTTGTGTC	CACGGTTTCGT	1080
GAGGGTGAAG	CGGAGAAAGC	GATGAACGCA	TTGGTGGCAG	AGATAGAAAG	CCTCCGTACG	1140
TTCCGTATCA	CCAAAGGCGA	ATACGATCGT	GCACGCACGA	ATGTGCTCAA	GCGATACGAG	1200
AATCAATACA	ACGAAAGAGA	CAAGCGTAAG	AACAATGCTT	ATGCCAATGA	ATACTCCACC	1260
TACTTCACCG	ATGGCGGCTA	TATCCCGGGT	ATTGAGGTGG	AATATCAGAC	GGTGAATGCT	1320
TTTGCTCCTC	AGGTTCCTCT	GGAAGCATT	AATCAGGCTA	TTGCCCAAAT	GATCGATCCG	1380
GTGAAGAAAT	CTGTCGTTAC	CCTCACCGGT	CCTTCAAAGG	CTGAAGCCAA	GATTCCGAGC	1440
GAAGCAGTAT	TTCTCGCTGC	TTTCAAAGCT	GCTCGTCAGC	AGAAAGTAGA	AGCCAAAGAA	1500
GACGAAGTCT	CCGACCAAAA	ATTGATGGAG	AAAGCTCCTA	AGGCCGGAAG	GATCGTTTCC	1560
GAGAAGAAAG	ATCAGAAGTT	CGGTACCACG	GAACTTACCC	TTAGCAATGG	CATCAAAGTA	1620
TACCTCAAGA	AGACCGATTT	CAAATCAAAC	GAAATCCTGA	TGAGTGCTCT	CAGCCCAGGT	1680
GGTATCCTCT	CCGAAAGCA	TGCTCCCAAC	CAATCTGTGA	TGAATTCGTT	CATGAACGTG	1740
GGTGGCTTGG	GCAACTTCGA	TGCTATCCAG	CTGGATAAGG	TGCTGACAGG	TCGCTCTGCT	1800
TCCGTATCTC	CCTCTTTGTC	TCTGCTCAGT	GAAGGTCTTT	CGGGCAAAAC	GACTGTAGAA	1860
GATATGGAAA	CTTTCTTCCA	GTTGATCTAT	CTCCAAATGA	CTGCTAACCG	CAAGGATCCC	1920
GAAGCGATTCA	AGGCCACACA	GTTAAAGTTG	TACAATAACT	TGAAAAATCA	GGAAGCCAAC	1980
CCGATGGCTG	CGCTTATGGA	CTCTATCCGT	CATACCATGT	ACGGCGATAA	TCCGATGATG	2040
AAACCCATGA	AAGTGTCTGA	CGTGGAGAAA	GTAAATTACG	ATCAGGTAAT	GGCTTTCTAC	2100
AATGAGCGAT	TCGCTGATGC	CGGCGACTTT	ATGTTCTTCT	TTATCGGTAA	TCTGGATGAA	2160
GCCAAAGATGA	ATAAGGCTCA	GGTACCGGCT	GCCCCGTTCCG	GAAAGATCGA	TTGCAAGTTC	2220
GATAAGATGA	ATAAGGCTCA	GGTACCGGCT	GCCCCGTTCCG	GAAAGATCGA	TTGCAAGTTC	2280
GAGAAGGAAA	TGGATACTCC	TTGACTACT	ATATTCGATG	TCGTGTCCCG	AAATGTGGAA	2340
TATACGCTCA	AGAACAGTCT	CCTGCTGGAA	GTCTTCTCAG	CCGTAATGGA	TCAGGTGTAC	2400
ACGGCTACCG	TTGCGAGAA	GGAAGGCGGT	GCATACAGTG	TGGCTGCATT	CGGCGGTCTC	2460
GAGCAATATC	CTCAGCCCAA	GGCTCTGATG	CAGATCTATT	TCCCCACGGA	TCCTGCTCGT	2520
GCCGAGGAAA	TGAATGCTAT	CGTTTGTGCT	GAGTTGGAGA	AGCTTGCCAA	GGAGGGCCCC	2580
AATGTGGAAT	ACTTTAAGAA	GACTATCGAA	AACCTGAATA	AGCAGCACAA	AGAAAGTCTG	2640
CGTGAGAATC	GTTTCTGGGT	CGAAGCCATG	AAGGCGTCTT	TCTTCGAAGG	AAATGACTTC	2700
ATCACAGACT	ACGAATCCGT	ACTGAACGGT	CTTACTCCTG	CTGAATTGCA	AAAGTTTGCG	2760
GCAGACCTCT	TGAAGCAGCA	GAATCGGGTT	GTTGTCATGA	TGGCTCCTGT	TGCAAAGGCT	2820

(2) INFORMATION FOR SEQ ID NO:143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

```

ATGAGTAAGA AAGGAACAAT CGGGGTAACG AGCGACAATA TATTCCTCCG CATCAAAAAA    60
TTCCTGTACA GCGACCATGA GATATTCTCG CGTGAGATCG TCTCCAATGC CGTGATGCT    120
ACGCAGAAAGC TGAAAACGCT TACATCCGTC GGCGAATTCA AAGGCGAGAC GGGTGACCTC    180
CGCGTAACGG TCAGCGTGGA TGAAGTGGCA CGCACGATCA CGGTCAGCGA CCGCGGCGTA    240
GGGATGACCG AAGAGGAGGT GGAGAAGTAC ATCAATCAGA TTGCTTTCTC CAGTGCGGAA    300
GAGTTTCTTG AAAAGTACAA AGACGACAAG GCCGCCATTA TCGGCCACTT CGGACTCGGA    360
TTTTACTCGG CTTTCATGGT GTCCGAGCGA GTGGACGTGA TCACGCGCTC TTCCGAGAA    420
GATGCTACGG CGGTGAAATG GAGCTGCGAC GGATCGCCCC AATACACGCT CGAACCTGCG    480
GACAAGGCTG ACCGTGGCAC CGACATCGTG ATGCACATCG ATGAGGAGAA TAGCGAGTTC    540
CTCAAAAAAG AAAAGATAGA GGGGCTCCTC GGCAAATACT GTAAGTTCCT TACCGTGCCG    600
ATCATTTCG GCAAGAAGCA GGAATGGAAA GACGGCAAGA TGCAAGATAC GGACGAGGAC    660
AATCAGATCA ACGACACACA TCCTGCCTGG ACCAAAAAGC CTGCCGACCT CAAGGACGAA    720
GACTATAAGG AATTTTACCG TTCGCTCTAT CCCATGTCCG AAGAGCCTCT CTCTGGATC    780
CACCTCAATG TGGACTATCC GTTCAATCTG ACAGGTATCC TCTATTTCCC GAAGATCAAA    840
AACAACTTGG ATCTGCAGCG CAACAAGATT CAGCTCTACT GCAATCAGGT TTACGTCACC    900
GATGAAGTAC AGGGTATCGT GCCGGACTTC CTCACCTCC TGACGCGGGT CATCGATTTC    960
CCGGATATTC CCCTCAACGT ATCGCGCTCC TATCTGCAGA GCGATGCCAA TGTGAAGAAG   1020
ATCTCGTCTC ATATCACCAA GAAGGTGGCA GACCGTCTGG AAGAAATTTT CAAAAACGAC   1080
CGCCCCACAT TCGAGGAGAA ATGGGATAGT CTGAAGCTCT TCGTCGAATA CGGTATGCTG   1140
ACGGATGAGA AGTTCATGTA GCGTGACGCC AAATTCTTCC TTTTACCGA TATGGACGGA   1200
CACAAGTACA CGTTCGAGC ATACCGAAGC CTGTCGAAG GTGTACAGAC GGATAAGGAC   1260
GGACAGGTAG TGTATCTCTA TGCTACGAGC AAGCATGGAC AGTACAGCCA CGTGAAACGT   1320
GCATCCGACA AAGGCTACAG CGTGATGCTG TTGGATGGTC AGTTGGATCC GCATATCGTG   1380
AGCCTGTCTG AGCAAAAGTT GGAGAAGACA CACTTTGTCC GTGTGATAG CGATACGATC   1440
AACAATCTGA TCCGCAAGGA GGAAAGAGCC GAAGTGAAC TGTCCGATC GGAGCGCGCC   1500
ATCTCTGTGA AGCTGTTCTG AGCACGCTG CCACGGGACG AGAAGAAGCA CTTCATGTA   1560
GCTTTTGAAT CGCTCGAGC CGAAGGTGAA GCCATCCTTA TCACACAAGC CGAATTCATG   1620
CGCCGTATGC GCGATATGGC ACAGCTGCAG CCGGGAATGA GCTTCTACGG CGAACTCCCC   1680
GATTTCGTACA ATCTGGTACT TAATACCGAT CATCCGCTCA TCGACAGGGT ACTCTCCGGT   1740
GAGAAAGAAT CGGTAGAGCC TTCGCTCACA GAGCTTAGAG CGAAAATCGC CGAGCTGAAA   1800
GCGGAAGAGG CCAAGCTGCT CGATGAGGAA AAAGGGAAGA AACCGGAGGA AATCCCTGTT   1860
GCCACGAAGG AAGCCAAGGA GAACAACGCC GTCGAACAGG CCAAAACCGA AGGCAGTATC   1920
AACGATCAAC TGACCAATA TGCTCAGGAC AACGAGCTGA TAGGTCAGCT CATCGACTTG   1980
GCTCTGCTCG GAAGCGGATT GCTGACGGGA GAGGCTTTGG CCGAATTCAT TCGTCGCAGC   2040
CAGCGTCTTC TC                                     2052

```

(2) INFORMATION FOR SEQ ID NO:144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

```
ATGGAAAAAC TGATCGATAT TTTGGTCGTA GACGATGATG TGGCAGTCTG TGCCGCACTG      60
CGTCTGGTGC TCAAGCGAGC GGGCTATAAT CCCGTTATAG CCAACAGTCC CGACGAAGCT      120
TTGTCCATAA TGCGGAATCC TGATGGCGGC TGTAAGCCGG CTGTGATTCT GATGGATATG      180
AATTTCTCCC TTTCGACCTC CGGCAGGGAA GGATTGGAAC TACTGGAGAA GATGCAGATA      240
TTCAC TTCCT GCCCTGTCAT ACTGATGACG GCTTGGGCTT CGATTCCACT GGCAGTGGAG      300
GGAATGAGGC TTGGAGCTTT CGACTTCATA GGCAAGCCAT GGGACAACGA TCGGCTCCTT      360
CGTACCATAG ATACGGCCTT GCATCTGGCT GCTCCCTCAG CTGTGGCGAA TCCATCGGAA      420
CAGTCTGACA GAGATACAGC CGGTCAGCCG AAAGCTACAG TCCAAGAGAA TGACCCCTGT      480
GCCCATATCA TAGGCCGGAG CGATGCCATC TGTAAGATCA AGGAACGGAT ACGCCGCATA      540
GCTCCCACCC ATGCCCTGTG CTGTATCAGC GGCGAGAGCG GTACGGGCAA AGAGTTGATA      600
GCCGAAGCTC TGCACCGTGG GAGCAAACGA GCCTCAGCCC CATTTCGTCAA GGTCAATTTG      660
GGTGGGATTC CCGAAAGTTT GTTCGAAAGT GAGCTGTTCG GACATAAGAA AGGAGCTTTT      720
ACCAATGCTT TTTCCGACAG GAAAGGACGG TTCGAGCTGG CTGATGGCGG CACGATCTTT      780
CTGGACGAAA TAGGCGAAGT ACCGGTCGGC AACCAAGTAA AACTGCTGCG AGTGCTACAG      840
GAACAGACAT TCGAGCCGTT GGGCGAGAGC GTCTCCCACC GAGTGGACAT CCGTGTGGTA      900
TCGGCTACGA ATGCTTCCTT GGAGCGAATG GTAGCCGAAG GACGTTTCAG AGAGGACCTC      960
TACTATCGAA TCAACCTGAT ACATCTGCAT CTGCCTCCGC TGCCTGAGCG TCAGGAGGAT     1020
ATACAGCTGC TGGTGGGAAG CTCAGTGAA GCCTTTGCCC AATCGAACGG ATTGCCCCAT     1080
GCCGTTTGGA GTGCGGAAGC TATGCGACGT ATCTGTGCCA TGCCCCCTACC GGGCAATGTA     1140
CGCGAACTGA AAAACGTAAGT GGAGCGTACG CTATTGCTCT CGGGATCGAG AGAAATCAGT     1200
GCCCGGGATG TGGCTGACTT CGGTTTCGAG GTGACGGCAG CAGACCACTC CGACGAACGG     1260
GCTTTGACCG ACATGGAGGA AGCTGCTATC CGAGAGACGC TGACTAAATA CAACGGCAAC     1320
GTTAGTCGTG CTGCACGAGC CTTGGGATTG AGCCGGGCAG CTCTTTACCG GCGAATGGAG     1380
AAATACGGAC TG                                     1392
```

(2) INFORMATION FOR SEQ ID NO:145

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

```
ATGCTTAAGA TAAAGAACCT CCACGCCACA GTACAGGGCA AAGAGATATT GAAAGGAATC      60
AATCTGGAGA TCAATGCCGG AGAGATTTCAT GCTATCATGG GGCCGAACGG ATCGGGGAAA     120
AGTACGCTCT CTTCCGTTTT GGTGGGACAT CCTCCTTTG AAGTCACGGA AGGAGAGGTG     180
ACATTCAATG GAATCGACCT GCTCGAACTC GAACCGGAAG AACGTGCACA CCTCGGACTC     240
TTTCTCAGTT TCCAATATCC GGTTCGAGATC CCGGGCGTCA GCATGGTGAA TTTCATGAGG     300
GCAGCTGTCA ATGAACATAG GAAAGCGATC GGAGCAGAAC CCGTATCGGC AAGCGACTTC     360
CTCAAGATGA TGCGAGAGAA GCGTGCCATT GTGGAGCTGG ACAACAAATT GGCCAGCCGT     420
TCTGTGAACG AAGGCTTCTC CGGTGGAGAA AAAAAGAGGA ACGAAATCTT CCAAATGGCT     480
ATGCTCGAAC CCAAGCTGGC TATTTGGAC GAAACCGATA CGGGGCTCGA TATCGACGCT     540
CTCCGCATCG TAGCAGGCGG GGTAACCGA CTCCGCTCTC CGGAGAATGC TGCTATTGTG     600
ATCACACACT ATCAGCGTTT GCTCGAGTAC ATCAAGCCGG ACTTCGTACA CGTCCTTTAC     660
AAGGGGCGCA TCGTCAAGTC GGGAGGAGCC GAGCTGGCTC TCACGCTCGA AGAAAAAGGC     720
TACGACTGGA TCAAGGAAGA GATAGGAGAA                                     750
```

(2) INFORMATION FOR SEQ ID NO:146

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

```
ATGGCTAAGG AGAAAACGAT CTACGTCTGC CGTTCGTGCG GAACCAAATA CGCCAAATGG      60
CAAGGCAACT GCAATGCCTG TGGAGAGTGG AACTGCATTG ATGAGGAGAA GGTGCCGGCA      120
CCGGCATCGG GCAAGCATGC AGCCAAGAGT TTTATGCCTC GGGAGCAGGA CAACCGGCCA      180
AGACTCTTAC AGGATGTGGA GTCCGGCGAT GAAGAGCGTA TTCGCCTCGG CGATGAAGAG      240
TTTCGACCGC TACTGGGTGG AGGAATTGTC AAAGGAGCAT TTGTCTCTGCT TGGCGGCGAG      300
CCGGGAATCG GTAAGTCCAC GCTTATCCTC CAGACGGTGC TGCCTCTGCC GCAGTTGCGC      360
ACGCTCTATG TGTGGGCGA AGAAAGTGCC CGACAACTGA AGATGCGCGC CGAACGACTG      420
GGGCAAGCCA TGAATGGGTG CTACGTATAC TGCGAAACGA ATATAGAGAG GATACTCTCC      480
CGTGCAGAAG AACTCACACC CGATCTCCTC GTGATAGACT CTATACAGAC GGTCTATACC      540
GAGGAAATGG AAAGCTCGGC CGGCAGCGTG GGGCAGATCC GCGAATGTGC CGCCTTACTG      600
CTCAAATACT GCAAGACTAC GGGTATCCCC GTCATCGTCA TCGGACACAT CACCAAAGAA      660
GGTAGCATAG CCGGACCGAA GGTGCTGGAG CATATAGTGG ATACGGTGCT TCTCTTCGAC      720
GGGGATAAGC ATCATCTCTA CCGGATACTC CGAGGACAGA AGAACCGCTA TGGCAGTACT      780
TCCGAGCTGG GGATATACGA GATGCGGCAG GACGGTCTGC GTGGCGTGGA GAATCCGAGC      840
GAACATCTCA TCACACGCAA TAGGGAAGAC CTCAGTGCCA TAGCCATAGC CGTAGCGATG      900
GAGGGCATTC GCCCGATACT CATCGAAGCG CAGGCTTTGG TCAGCTCGGC CATTTATGCC      960
AATCCGCGAG GTTCGGCCAC GGGCTTTCGAT ATTGGCGCGA TGAACATGCT CTTAGCCGTA     1020
CTGGAGAAAC GTGCCGGCTT CAAGCTCATA CAGAAGGATG TGTTTCTGAA CATTGCCGGA     1080
GGTATCAAAA TAGCCGATCC GGCTACGGAT CTGGCCGTTA TCTCGGCAGT GCTGGCGTCG     1140
AGTCTGGACA TCGTTATCCC GCCGGCCGTA TGCATGACGG GCGAGGTCGG ACTCTCCGGA     1200
GAGATACGTC CCGTGAGCCG CATCGAGCAG CGCATAACGG AAGCGCGTCG CATAGGGTTC     1260
AAAGAGATAT TGGTACCGGC CGATAATTTC CGGCAGGAGG ATGCCGGCCG CTTCCGTATT     1320
CGGCTCGTGC CGGTGAGAAA GGTGGAGGAA GCCTTCCGCC ATCTGTTCTC GAAAGGAAGA     1380
GAA
```

(2) INFORMATION FOR SEQ ID NO:147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

```
ATGAATAGCA GACATCTGAC AATCACAATC ATTGCCGGCC TCTCCCTCTT TGTACTGACA      60
TTGGGCGGCT GCTCCGTAGC CCAACAAGAT ACGCAGTGGA CTCTCGGCGG AAAGCTCTTT     120
ACTTCGGCGT GGATACAACG TTCGGCCGAA TATCAAGCGC TTTGCATTCA GGCATACAAC     180
ATCGCTACGG AAAGAGTGGA CGCTCTACCG GCAGAACGTA AACAAGGAGA TAGGCCTTAT     240
GCCATCGTAA CGGACATAGA CGAAACCATT TTGGACAATA CGCCTAATC CTGTATCAG      300
GCTCTCAGGG GCAAGGATTA TGATGAAGAG ACTTGGGGGA AATGGTGTGC ACAGGCCGAT     360
GCCGACACAC TGGCAGGAGC TTTGTCTTTC TTCCTCCATG CAGCGAACAA GGGGATCGAG     420
GTCTTTTACG TCACCAACCG CAGAGACAA CTGCGCGAAG CAACTCTTCA GAACCTTCAG     480
CGTTACGGAT TCCCCTTTGC CGATGAAGAA CATTTGCTTA CGACCCATGG GCCATCCGAC     540
```

AAAGAACCCC	GTCCGCTCAA	AATACAAGAA	CAGTATGAAA	TAGTATTGCT	CATAGGAGAC	600
AACTTGGGCG	ACTTCCACCA	CTTCTTCAAT	ACGAAAGAAG	AGTCCGGACG	CAAACAGGCT	660
CTGGGCCTGA	CAGCCGGGGA	GTTTGGCCGG	CACCTTCATCA	TGCTGCCCAA	TCCCAACTAC	720
GGATCTTGGG	AACCGGCATG	GTACGGCGGG	AAGTATCCGC	CACTGCCCCG	AAGAGACAAA	780
GCACTTAAAC	AACTGCACTC	ACAGAACAGC	AGA			813

(2) INFORMATION FOR SEQ ID NO:148

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1251
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

ATGAGCACCA	ATATAGATGT	ACAACAGATC	AAACAGCGTT	TCGGCATCAT	CGGTAGCAGT	60
CCGCTGATGG	AACATGCCAT	ACGAGTGGCA	GCACAGGTGG	CTCCTACCGA	CATGTCCGTC	120
CTCGTGACGG	GGGAGAGCGG	TTCGGGGAAA	GAGTTCTTCC	CACAGATAAT	CCACTACTAC	180
AGCGCCCCGA	AACATCATAG	CTACATTGCA	GTCAATTGCG	GAGCCATCCC	CGAAGGAACC	240
ATCGATTCCG	AGCTGTTCCG	ACACCGCAAA	GGTTCCTTTA	CCGGAGCCGT	ATCGGATCGC	300
AAGGGGTACT	TCGAAGAAGC	ATCCGGCGGC	ACGATCTTTC	TGGACGAAGT	GGGCGAACTG	360
CCTTTGCCCA	CGCAGGCGAG	GCTGCTGAGG	GTGCTGGAGA	CGGGCGAGTT	CATCCCCGTA	420
GGAGCCAGCC	AGTCGCAGAA	GACGGATGTC	CGTATCGTAG	CGGCGACGAA	TGTGAACCTC	480
AAGGAGGCGG	TAGCGAACGG	GAAGTTCCGG	GAAGACCTCT	TCTTCCGGCT	CAATACGGTA	540
CCGATCGAGG	TGCCTGCGCT	GCGTATGCGA	CCGGACGACG	TGCCCTTGCT	TTTTCGCCGA	600
TTCCGCCCGC	ACAGCGCCGA	GAAGTATCGG	ATGCCTCCGC	TGCGCCTATC	GGACGAAGCC	660
CGTACCATAT	TAATGCGTTA	CCGCTGGCCC	GGCAATGTGC	GAGAGCTGCG	CAATATAACC	720
GACAGGCTGA	GCATCCTGGA	GGAGAGCGGG	ACGGTATCGG	CAGAGACCAT	CACCTCGTAC	780
CTGGACGCTG	AGGGGATGCA	AGACCTCCAC	CCCGTCGTGA	TCCGACGGAA	CGAAACGACC	840
GAAGCGGACA	AACAAATCCC	CCATTACGAG	CGCGAAATCA	TCTACCAGGT	GCTATACGAT	900
ATGAAGAAAG	AGATAGCCGA	TTTGAAGGGG	ATGATGAACC	GCCTGGCGCA	CCACGAACAG	960
CCCTCATGGC	CTGTAGGGTC	GGACGTCTGG	GGCAACGACG	ACAAGCGCAC	CGCAGATCCG	1020
AAGTGGGGCG	TACGACGCGA	CAAGGCCCCC	ATCGCGAACG	CGGCAGAACC	CGTGGAGCCG	1080
ATACAGGAAG	CCAGCGAATA	CACCGAGGAT	CCGGTTTCGC	TGGAGGAGGT	AGAGAAGAAA	1140
ATGATTTCCC	TTGCATTGGA	ACGCCACGGC	GGAAGGCGCA	AGCAGACAGC	CGAGGAACTG	1200
AAGATTTCCG	AGCGGACACT	ATACCGTAAA	ATCAAGGAGT	ATGGACTGGA	A	1251

(2) INFORMATION FOR SEQ ID NO:149

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1806 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCCTAC	TCTTCGGCGG	TACTACGGAA	GGCCGTGCCG	CAGCTCGCGT	GCTGGATGAA	60
------------	------------	------------	------------	------------	------------	----

GCGGGAAGTC	CGTTTTTCTA	CTCCACCAAA	GGCAATCTGC	AAGAGATCCA	GAGTAGCCAC	120
GGCCATCGTC	TGACAGGAGC	CATGACGGTT	GCCGACATGG	TTTCGTTTTG	TCGGAAAGAA	180
GAGATCCGAC	TGATCGTGGA	GCCCGCTCAT	CCTTTGCGCG	AAGAATTGCA	CGCTTCAGTG	240
GCAGAAGCCT	CTGAACAAAC	AGGTATCCCC	GTAAGTAAGAT	ACGAGAGACA	ATACCCTCCA	300
CGCGAAGAAG	GTATCGTCTG	GTGTGCAAAC	TACGATACGG	CTGCCGAGCG	GATGCTTGGC	360
GATGGCGTGC	AGCGTCTGCT	GATGCTCACA	GGAGTGAATA	CGATCCCCAA	GCTGGCTGCT	420
TTCTGGAAAG	AGCGCACCAC	CTTTTGCCCG	ATATTGAAGC	GAGACGAATC	GGTTGCTTTG	480
GCAGAGAAGA	ACGGCTTTCC	TGCGGAGCGC	ATCGTTTTCT	TCGAACCGCA	TGCGGACGAG	540
GAGCTGATGC	AAGCCGTTTC	CCCCGATGCC	ATTATCACAA	AAGAAAGCGG	AGAGACGGGT	600
TACTTCCGAG	AAAAGATAGA	AGCTGCCCGA	CGGATGGGCA	TCCGTATATA	TGCCGTCGTA	660
CGTCCCCCTT	TGCCTCCTTC	ATTCAATTCC	GTAGGCGGGC	CTGTCGGTTT	GAGACGGGCG	720
GTAGAACGCC	TCGTGCCGGG	ATTCTTTTCA	CTCCGAAGCG	GATTCACTAC	CGGCACCACA	780
GCTACCGCTG	CAGTAGTAGC	AGCCATGTAC	CGATTGATGG	GGCTTGGCTC	TCTCGCCGAA	840
GCTCCCGTAG	AATTGCCTTC	GGGCGAAATA	GTCAGTCTGC	CCATAGCGGA	AATTCGAGAG	900
GAAGAAGATG	CTGTGCTATC	CGCAGTCTTG	AAAGATGCAG	GTGATGATCC	GGATGTGACC	960
AATGGCATGG	CGGTATGCGC	TACGATCAGG	CTCAATCCCG	AACATGAGGA	AGTCCGCTTC	1020
CTGCAGGGTG	AAGGGGTGGG	GGTAGTGACG	CTCCCGGGCC	TCGGTCTGGA	GGTCGGAGGT	1080
CCGGCTATCA	ACCTCGTACC	TCGACGAATG	ATGACAGCAG	AGGTACGCCG	ACTCTATGCG	1140
CAGGAGGGTG	TGGATATTAC	GATTAGCGTA	CCCGAAGGCC	GAGAGGCTGC	TACCAGACA	1200
TTCAATCCCC	GACTCGGCAT	ACGGGACGGC	ATCTCTATTA	TCGGAACATC	GGGAGTCGTG	1260
AAACCTTTTT	CGGCCGAAGC	GTTCGTTGGT	GCCATCCGTA	AGCAAGTGGG	TATTGCCACC	1320
GCCTTGGGAG	CCAATCATAT	CGTCTCAAT	TCGGGAGCCA	AGAGTGAGCG	TTATGTAAAA	1380
GGAGCCTATC	CGGCACTCAT	TCCACAGGCC	TTTGTGCAGT	ATGGCAATTT	CGTCGGCGAA	1440
TCACTCAGTT	GTGTAGCTTC	CTTCCCTTCT	GTCCGTTTCG	TAACGGTAGG	AATCATGCTC	1500
GGCAAAGCAG	TGAAACTCGC	CGAAGGCTAT	CTGGATACGC	ACAGTAAAAA	GGTAGTGATG	1560
AATCGGGATT	TCCTGCACGA	ACTGGCTCGT	CAGGCAGGTT	GTTCGGAAGA	CATCCATGCC	1620
ATAATAGACA	GCCTGAATTT	GGCTCGTGAG	CTATGGACTA	TGCCGAGTGC	GGAGGACAGC	1680
GATCGACTGC	TACGAAAGAT	TGCCGAACGA	TCTTGGGAAA	CTTGCCGCCC	ATCGGTACCA	1740
TCGGCCGAAT	TAGAACTCCT	GCTGATCGAT	GAGTCCGGAG	CGATTCGTTT	TCGTATCGGT	1800
GGAGAA						1806

(2) INFORMATION FOR SEQ ID NO:150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTTGAGGA	CTTTCGAAT	CGGTGGTATT	CACCCCCCG	AAAACAAGTT	GTCCGCAGGC	60
AAGCCCGTAG	AGGTGTTGCC	TATCCCCTCA	CAGGTAGTCA	TCCCTCTTGG	TCAGCACATC	120
GGTGACCCGG	CAACTGCCAC	GGTCAAGAAA	GGGGATGAAG	TTAAGGTCCG	GACTATCATT	180
GCTCAGGCCG	GAGGATTCTG	ATCAGCTAAT	ATCCACTCAT	CTGTGTCGGG	TAAGGTGCTG	240
AAGATCGATA	ACGTATACGA	CTCAAGCGGC	TATCCCAAGC	CCGCAGTCTT	CATTAGCGTA	300
GAAGGTGACG	AATGGGAAGA	GGGCATCGAT	CGCTCACCAG	CCATCGTCAA	AGAATGCAAT	360
CTGGATGCAA	AAGAAATCGT	AGCCAAAATT	TCTGCAGCCG	GTATTGTGGG	TCTTGGCGGT	420
GCTACCTTCC	CTACCCATGT	GAAGCTGTCC	CCTCCTCCGG	GCAACAAAGC	TGAGATCCTG	480
ATCATCAACG	CCGTAGAGTG	CGAGCCTTAT	CTGACGAGCG	ACCATGTCCCT	TATGCTGGAG	540
CACGGCGAAG	AGATCATGAT	CGGCGTGAGT	ATCCTGATGA	AAGCCATTCA	GGTAAACAAG	600
GCCGTCATCG	GAGTTGAGAA	TAATAAGAAA	GATGCTATTG	CTCACCTCAC	CAAACTGGCC	660
ACTGCATATC	CGGGCATAGA	GGTAATGCCG	TTGAAGGTGC	AATATCCTCA	AGGCGGTGAG	720
AAGCAGCTGA	TCGATGCAGT	GATCCGCAAG	CAGGTAAAAA	GCGGTGCCTT	GCCTATCAGC	780
ACAGGTGCCG	TAGTACAAAA	CGTGGGTACG	GTATTGCGCC	TGTACGAAGC	AGTACAGAAG	840
AACAAGCCTC	TGGTCGAGCG	CATCGTGACG	GTTACAGGAA	AAAAACTGTC	TCGTCCGTCT	900
AACCTCCTCG	TTCGTATAGG	TACTCCTATT	GCGGCTTTGA	TCGAAGCAGC	AGGTGGCTTG	960
CCGGAGAAATA	CGGGCAAGAT	CATCGGCGGA	GGTCCGATGA	TGGGACGCGC	TCTGTGTGTA	1020
CCGGATGTGC	CTGTGACCAA	AGGCAGCTCC	GGAGTATTGA	TTCTCGATAG	AGAAGAGGCA	1080
GTTTCGCAAGC	CTATGCGCGA	CTGTATCCGA	TGCGCCAAGT	GCGTCGGAGT	GTGTCCGATG	1140
GGACTCAATC	CGGCTTTCCT	TATGCGCGAC	ACCTTATATA	AGAGCTGGGA	AACAGCGGAA	1200
AAAGGCAACG	TGGTTGACTG	TATCGAATGC	GGTTCTGTGA	GCTTCACTTG	TCCGGCCAAC	1260
CGTCTCTGTC	TGGATTATAT	CCGCCAAGCC	AAGAAGACTG	TGATGGGTAT	CCAAAGAGCA	1320

(2) INFORMATION FOR SEQ ID NO:151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

```
ATGAAAAGAA TACAATAAC TCTTATCGCT CTCTTCGCCG CTGTTGCCGG TTTGGTCGCT      60
CAAAATGCTT ACGAGGGAGT AATTTTCATAT AAAATTTTCGT TGGACAAAAC CGGAAACAAG      120
GTTGTACTGA ATGGTGCAGC AGATTATGAGT AATTAAAGC TCAAGAGCAC TCAGATGATC      180
ATTGTTACGC CTATTCTTCG TACAGAAGAT GGTACCAGCC GGGTGGAATT TCCTTCGGTA      240
GTCATTACAG GCCGCAATAG AACAAAAGCT CTCAAGCGTG AAATCGCATT TAGTTCGGCT      300
TTGCCCCAAG CAAACATGC AGTCAATAC ATTCGCCGTC ATAATGGGAA GAGCGAGCAG      360
TTTGCTTTTA CAGGAGAACA TGCTTATGCA TCATGGATGA TGGATGCCAA GTTGTGGTT      420
CGTGAGGAGG TACGAGGTTG TGCTAAATGC CCTGTAGGTC TCTCGAGTAA TATTGTTCCCT      480
TTTGATCCAC TCTTCAATCC GGCAGAGGCT CCTTATTTGT TGGCACACAT TACTCCGGCA      540
GAAGAAGTGG AAAACAGCG AGAGTCCAGC TTCGATGCTT ATATCAACTT CAAAGTCAAT      600
AAGGCAGATG TCCTTCCTGA GTATCGCAAC AATAAGGCCG AGTTAGAGAA AATCAAAGAA      660
TTTGTACGCA CCGTTAAGGC TAATCCAAAC TATTCGGTCA ATAAAATGAT CATCGAAGGG      720
TTTGCTTCTC CCGAGGCTTC AATAGCCCAC AATAAGGCTT TGTCGGAGCG CCGTGCTAAA      780
AGACTCGCGG AAGAATTGGT GCGTAAGTAT GGCAAAACAT TGCCGAATAT AACCCTGAA      840
TTCGGCGGTG AAGATTGGAA GGGGCTGAAA CTGGCTATCG AAAAGAGTGA TATAGCCGAT      900
CGTGACCGCG TATTGGAGAT AATCAACTCC GATAAATATG CCGATGATGA TGCACGTGAA      960
CAGGCTCTGA AGCAACTTTC GTCTTATCGT TATATCTTGG ATCAGATCTA TCCGAATTG      1020
CGTCGCAATA CGATAACCAT GGGGTATATC GTTCGTGATT ATACCCTCGA AGAAGCTCGT      1080
GAAATCATT AAGACTGCTCC GAAAGAACTT AGTGAGGCCG AAATGTACCG TGTGGCAATG      1140
TCTTATCCTG AGGGGCACCA AGAGCGTTTG TTGCTCTGA ATACGACCTT TAAGTATTTC      1200
CCTGAAAGTG TAACGGGCCG AATCAATTG GCTGTAGCCG CTTTAAATGG TGGAGACGTT      1260
CAACAGGCAA TTGCTCTGTT GAGTCCGATT CAGACAGAAA AGGGTGTAAG CAATATCCTT      1320
GGAGCTGCTT ATGCTCGTAC GGGAGATTTT GCTCGTGCCG AAACCTTCTT CCGTAAGGCC      1380
GTTGCAGAAG GAGATGCAAA TGCGCAGCGC AACCTCGATA TGCTGCTTGG CAAAAAG      1437
```

(2) INFORMATION FOR SEQ ID NO:152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

```
ATGGCAGAAA AAAGAGACTA TTACGAAGTC CTCGGTGTAT CGAAGAATGC CACCGACGAT      60
GAACTGAAAA AAGCATATCG CAAGAAGGCT ATCCAATACC ATCTGATAA GAACCCCGGT      120
```


GACAAGGAGG	CCGAAGAGCA	CTTCAAAGAG	GTAGCTGAAG	CCTACGACGT	ATTGAGCGAT	180
CCGCAGAAGC	GCACTCAATA	TGACCAGTTC	GGCCATGCCG	GATTGGGCGG	AGCTGCCGGT	240
GGAGGTTTTCA	GCGGAGGCCG	TATGTCCATG	GAGGATATTT	TCAGTCGCTT	CGGTGATCTA	300
TTCGGTGGGT	TCGCGGTTT	CGGCGGATTC	TCCGATATGG	GCGGTGGCAG	TCGCAGACGT	360
GTTTCGCAGAG	GGTCTGACCT	GCGAGTACGA	GTGAAGCTTT	CTTTGGCCGA	TATAAGTAAA	420
GGTGTGGAGA	AGAAAGTGAA	GGTAAAAAAG	CAGGTAGTGT	GCAGCAAATG	TCGTGGCGAT	480
GGCACGGAAG	AAGCCAATGG	CAAGACTACC	TGCCAGACCT	GCCATGGAAC	CGGCGTGGTT	540
ACACGTGTGA	GCAACACTTT	CCTTGGGGCC	ATGCAGACCC	AGAGCACTTG	TCCCACTTGC	600
CACGGAGAGG	GTGAGATCAT	CACGAAGCCA	TGCTCCAAGT	GTAAGGGCGA	AGGTGTGGAG	660
ATCGGCGAAG	AGGTGATCTC	ATTCACATC	CCTGCCGGTG	TAGCCGAAGG	AATGCAAATG	720
TCCGTGAACG	GCAAGGGAAA	TGCCGCGCCC	CGAGGAGGCG	TGAATGGCGA	CTTGATAGTC	780
GTGATCGCCG	AGGAACCGGA	TCCGAATCTG	ATCCGCAATG	GCAACGATCT	GATATACAAT	840
CTGTTTATAT	CCGTTCCGTT	GGCTATAAAA	GGAGGTAGTG	TGGAAGTGCC	GACGATAGAC	900
GGACGAGCCA	AGATCCGCAT	CGAGGCGGGG	ACACAACCCG	GCAAGATGCT	GCGTTTGC	960
AATAAGGGGT	TGCCCAGCGT	AAACGGCTAT	GGCATGGGAG	ACCAACTGGT	GAATGTCAAT	1020
GTCTATATCC	CCGAATCGAT	CGATGCCAAA	GATGAGCAGG	CTATCGCAGC	GATGGAAAAC	1080
TCGGACAGCT	TCAAACCTAC	CGATGCTGCT	CGTAAGGATA	TAGACAAGAA	ATACAGAGAG	1140
ATGCTGGAT						1149

(2) INFORMATION FOR SEQ ID NO:153

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

ATGAAAAAAC	TGATTTTAGC	GACTTTGGGA	CTTATGGCCA	TTGCCATGCT	CTCATGTTCA	60
AGCAACAACA	AGGATTTGGA	GAACAAAGGG	GAGGCTACTC	TTTGGTAAC	GTTTGGTAGC	120
TCCTATAAAG	CTCCACGCGA	AACCTATGCG	AAGATTGAGA	AGACTTTTGC	CGCAGCTTAT	180
CCCGATCAAA	GGATAAGCTG	GACATACACG	TCTTCTATTA	TCCGAAAGAA	ACTGGCTCAG	240
CAGGGTATTT	ATATCGATGC	TCCGGATGAG	GCTTTGGAGA	AATTGGCTCG	TCTGGGTTAT	300
AAGAAGATCA	ATGTACAGAG	TCTTCATGTG	ATTCCC GGCC	GAGAATATGA	TGAGATGATC	360
GACTTTGTCA	ATAAGTTTAA	GGCAGCACAT	AGTGATATTA	CTGTGAAGGT	AGGGGCTCCG	420
CTTTTCGATA	CCGATGAAGA	TATGCGCGAG	GTGGCAGAGA	TCTTGCACAA	GCGTTTTTCAG	480
CAAACGATAG	AGAAAGGTGA	AGCTATTGTA	TTCATGGGAC	ACGGCACCGA	GCATGCTGCC	540
AATGACAGGT	ATGCCCGTAT	CAATAAGATC	ATGAAGAACT	ATAGCAAGTT	CATGATCGTC	600
GGAACCGTCG	AGTCCGATCC	CTCTATCAAT	GATGTTATTG	CCGAAC TGAA	AGAAACCGGT	660
GCCACGGCCG	TAACAATGAT	GCCGCTGATG	AGTGTGGCAG	GCGACCATGC	TACGAATGAT	720
ATGGCCGGAG	TAGAGGACGA	ACGTTGGAAG	ACGTTGCTGA	CCAATGCCGG	CTACACAGTT	780
TCTATAGACA	AGCTGGACAA	TGGCAATTC	TCAGCTCTTG	GAGATATAGA	AGAGATCCGG	840
AATATCTGGC	TCAAGCATAT	GAAAGCCACC	TCTGCTCGC			879

(2) INFORMATION FOR SEQ ID NO:154

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

ATGACATCCG	TCAGCCACTT	ACGTACAATT	TCTGTCGCAG	GTATCCTGGC	TGCGCTGGGA	60
GGGGCTGTAC	TCATTCTCTT	CGGGGTAAAT	CTCTTCCTCG	GCTCGGTGGC	TATTCGGATG	120
AGCGAGATCT	TCCGACATCT	TTTTTCAGAT	CGTCCCAGAG	GAGGAGAAGC	ACTCGTGAC	180
TACAATATCC	TATGGAAATC	CCGCCTGCCC	GAAGCCCTCA	CGGCTGCTTT	TGCCGGCGCA	240
GGTTTATCCG	TTAGTGGCTT	GCAGATGCAG	ACCGTCTTTC	GCAATCCTTT	GGCCGGTCCG	300
TCCGTTCTCG	GCATCAGCTC	CGGTGCCAGT	TTGGGTGTTG	CTTTGGTCGT	TCTGCTGAGC	360
GGCTCGCTGG	GAGGAGTGGC	ATTGAGTAGC	CTGGGTATA	TGGGCGAGGT	GGCCATGAAT	420
ATAGCCGCTG	CCGTAGGCTC	GCTGGCAGTA	ATGGGGCTGA	TCGTTTTTGT	CAGCACCAAG	480
GTGCGCAGCC	ACGTTACGCT	GCTCATTATC	GGCGTTATGA	TCGGATATGT	AGCCACTGCC	540
GTCAATCGGG	TATTCAAGTT	TTTCAGTATC	GAAGAAGATA	TTCGGGCATA	CGTAATTGG	600
GGGTTGGGCA	GCTTTTCCCG	TGCCACGGAT	TCGCAACTGA	GTTTCTTTGC	CATTCTGATG	660
TTGATCTTTA	TTCCGGCCGG	TATGCTCCTT	GTCAAGCAGT	TGAATCTCTT	ATTGCTGGGA	720
GAAAGCTACG	CACGTAATCT	GGGACTGAAT	ACTCGTCGGG	CACGGCTGCT	CGTGATCTCT	780
TCCGCCGGTT	TGCTCATCGC	TCCGTCACG	GCCTATTGCG	GTCCCATCGG	CTTTTGGGG	840
ATGGCTGTGC	CACACTTGGC	ACGGGTATC	TTTCACACAT	CGGATCATCG	GATCCTGATG	900
CCTGCTACCT	GTTTGATTGG	AAGTGCTCTG	GCTCTTTTCT	GCAATATCAT	TGCTCGTATG	960
CCGGGGTTTG	AGGGGGCTTT	GCCCGTCAAT	TCCGTAACGG	CTTTGGTGGG	AGCACCTATT	1020
ATCGTCACCG	TTTGTTCCTG	GCGCAGACGC	TTCAAGGAAG	AAACCGAC		1068

(2) INFORMATION FOR SEQ ID NO:155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...2271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ATGCGGACAA	AAACTATCTT	TTTTGCGATT	ATCTCTTTTA	TTGCTCTATT	GTGCTCTTCT	60
CTGTGCGGCT	AGAGCAAAGC	CGTTTTAACC	GGTAGTGTGT	CGGATGCCGA	AACCGGAGAG	120
CCTCTTGCCG	GTGCTCGAAT	CGAAGTCAAA	CACACCAACA	TAGTAGCCGG	TGCCGATGCC	180
GGCGGACATT	TCGAGATCAA	GAACCTGCCG	GCAGGGCAGC	ATACTATTAT	ATGTTTCGTTG	240
GGGGGGTATG	GACAGAAAGA	GGAGGTGGTT	GCCATCGAAG	CCGGACAGAC	CAAAACGATC	300
TCTTTTGCAT	TGCGACTGCG	AACGAACAAC	TTGGAGGAAG	TCGTCGTTAC	CGGTACCGGT	360
ACACGTTACC	GCTTGGTCSA	TGCTCCTGTG	GCAACGGAAG	TCCTTACCGC	TAAGGACATA	420
GCCTCTTTCT	CGGCTCCTAC	TTCCGAGGCC	TTATTGCAGG	GGCTGAGTCC	GTCTTTTGAC	480
TTCCGCCCCA	ATCTGATGGG	CTCTTTTCATG	CAGCTGAACG	GCCTTAGCAG	TAAGTATATC	540
CTCATCCTTA	TCGATGGTAA	GCGTGTGTAC	GGCGATGTAG	GCGGTCAGGC	CGATTTGAGT	600
CGTATTTTCT	CTGATCAGAT	CGAACGGATC	GAAGTGGTGA	AAGGTGCTTC	GAGTTCGCTC	660
TACGGATCCG	ATGCCATCGC	CGGGGTAATC	AATGTGATCA	CAAAAAGAA	TACGAATCGA	720
CTGAGTGCAT	ATACGTCACA	TCGCATATCG	AAGTACAACG	ATCGGCAAAC	CAATACTTCG	780
CTCGATATAA	ACATCGGTAA	GTTCAAGTAGC	AATACCAACT	ATTTCTTCTA	CCATACGGAT	840
GGCTGGCAGA	ATATGCTCGT	CGAAATAAAA	AAGAAAAAAG	GATCCGGCGA	ACCGGTCTTG	900
GAGGAAACGT	ATAAGAAAAC	TTTTCGTGCA	CAGGAAAATC	AGGGTGTAAG	CCAATCGCTT	960
TCCTATTATG	CAACTAACAA	TCTTAGCTTC	AGCGGAAATG	TGCAGTACAA	TAAACGTCAG	1020
ATCTTCACTC	CGACTTTTTT	CGAAAAGAAG	GCCTATGACA	TGGATTATCG	TGCTTTGACG	1080
GCTTCACTCG	GTACGAACTA	TCTTTTCCCC	AATGGTCTGC	ATACGCTTTC	TTTCGATGCC	1140
GTCTACGATC	GCTTCCGTTT	CGGATATTTG	TATCATGACA	AGGACAGCAG	TGAGAGCCTG	1200
ATCAACAACC	AAGGTCAGAG	CGAGCAACCC	ACATTCTTTC	CGGGTCAGCT	ACGCAATAAA	1260
AACGATCAGA	TCCGATACAC	GGCAGAGGCT	CGCGGTGTAT	TTACTACTGCC	TTATGCGCAG	1320
AAACTGACCG	GCGGTTTGGA	GTATTTCCGT	GAGGAATTGA	TCTCTCCCTA	TAATTTGATT	1380
ACCGACAAGG	CAGATGCTTC	CACGCTCTCT	GCTTATGTAC	AAGATGAATG	GAAACCGCTC	1440
GATTGGTTCA	ATATGACAGC	CGGTTTCCGT	CTGGTACACC	ATCAGGAGTT	CGGTACACGA	1500
ATGACGCCTA	AGGTATCCAT	ACTCGCCAAG	TATGGGCCGC	TGAACTTCCG	CGCTACGTAT	1560
GCTAACGGCT	ATAAGACTCC	CACGCTGAAA	GAGCTTTTTG	CACGGAACGA	ACTCACCCT	1620
ATGGGTTCCG	ACAATCTCTA	TCTCGGCAAT	GCGGATCTTA	AGCCACAGAT	GTCCGATTAT	1680

TATGCTTTGG	GCTTGGAGTA	CAATCAAGGC	CCTATCTCGT	TCAGTGCAAC	GGTTTATGAC	1740
AATGAAC TTC	GCAATCTGAT	CTCCTTTATG	GATATACCGA	CCTCACCCGA	GCACGAAGCT	1800
CAGGGAATCA	AGAAAACCAA	GCAGTATGCC	AACATAGGAA	AAGCTCGCAG	CCGCGGCCTT	1860
GATGTCCTAT	GTGATGCCTC	TATCGGTTGG	GGTATCAAGT	TAGGAGCCGG	ATACAGCCTC	1920
GTGGAAGCTA	AGAATCTCCA	GACGGATGAG	TGGCTGGAAG	GAGCTGCACG	TCATCGTGCC	1980
AATGTGCACG	CCGATTGGGT	TCACTACTGG	GGTCAGTATA	GACTTGGCCT	GAGCCTTTTC	2040
GGCCGTATTC	AGAGCGAGCG	TTACTACAAA	GACGGCAATG	CTCCGGACTA	TACCTTGTGG	2100
CGACTCGCCA	CATCGCATCG	TTTCGTCAT	TTCCGCCACA	TCATCCTGGA	TGGAACGCTC	2160
GGTATAGACA	ACCTGTTTGA	CTACGTGGAT	GATCGTCCTA	TGGGTGTCAA	TTATGCTACC	2220
GTAACGCCGG	GACGTACTTT	CTTTGCTCAA	ATAGCGATTC	GATTCAACAA	C	2271

(2) INFORMATION FOR SEQ ID NO:156

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 993 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...993
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGACGGACA	ACAAACAACG	TAATATCGTA	TTCCCGGCGT	TTCTCCTCTT	GCTGGGAGTC	60
ATCGCAGTGG	TGACGATCGT	TGGTTTTTTC	ATGCTCAGAC	CGGCCGAGGA	GATTATCCAA	120
GGACAGATAG	AAGTGACCGA	ATACCGAGTG	TCCAGCAAAG	TGCCCGGGCG	CATCAAGGAA	180
CTTAGGGTAT	CCGAGGGACA	GCAGGTGCAG	GCCGGCGATA	CCCTCGCTGT	CATCGAAGCC	240
CCCGACGTAG	CGGCTAAGAT	GGAGCAGGCA	AAGGCTGCCG	AAGCAGCTGC	ACAGGCTCAG	300
AACGCCAAGG	CTCTCAAAGG	AGCACGCAGC	GAACAGATAC	AGGCAGCCTA	TGAGATGTGG	360
CAGAAAGCTC	AGGCCGGCGT	AGCCATAGCG	ACCAAGACAC	ACCAGCGCGT	GCAGAACCTC	420
TATGACCAGG	GAGTGGTACC	GGCTCAGAAG	TTGGACGAAG	CCACTGCCCA	GCGCGATGCG	480
GCCATCGCTA	CGCAAAAAGC	GGCCGAAGCC	CAGTACAATA	TGGCTCGCAA	CGGTGCCGAA	540
CGCGAAGACA	AGCTGGCAGC	TTCTGCCCTC	GTCGATAGAG	CGAGAGGAGC	CGTCGCCGAG	600
GTGGAGTCGT	ACATCAACGA	AACCTACCTC	ATCGCCCCAC	GGGCAGGCGA	AGTGTCGGAG	660
ATATTCCCCA	AAGCCGGCGA	ACTCGTAGGT	ACCGGCGCAC	CTATCATGAA	TATCGCCGAG	720
ATGGGCGATA	TGTGGGCCAG	CTTTGCCGTT	CGTGAGGATT	TCCTCAGCAG	CATGACCATG	780
GGAGCCGTTC	TGGAGACTGT	GGTGCCGGCT	CTGAATGAAG	AAAAAGTACG	CTTCAAGATC	840
ACATTTCATCA	AGAACATGGG	TACCTATGCT	GCCTGGAAAAG	CGACCAAGAC	AACAGGGCAG	900
TACGACCTGA	AGACCTTCGA	GGTAAAGGCC	ACCCTTGCGG	ATAAAGACAA	GGCACAAAAG	960
CTACGCCCGG	GTATGTCCGT	GATCATACGC	AAG			993

(2) INFORMATION FOR SEQ ID NO:157

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...801
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

ATGCGTATTG	TCAGTAATTT	TTTGTTCGTC	TCTTTTTCGG	TTTTGCTTTT	TGCATCATGC	60
CGTTCCAGC	GAGAAAAGGT	CGTTTACCTG	CAAGATATCC	AAACTTTTAA	TCGGGAGATT	120
ATCGCTAAAC	CATATGACGT	AAAAATTGAG	AAGGACGATG	TGCTGAACAT	CCTTGTGAGC	180
AGTAGAGACC	CGGAGCTTTC	AACGCCCTAC	AACCAAGTGT	TGACCACTCG	TGCACTGGCC	240
CGCAACGGCT	ATGGAACGAA	CTCGAACGAA	GGCTTCCTGG	TCGATTGCGA	AGGGTACATC	300
AATTATCCTA	TTTTAGGCCA	GATCTATGTA	GAGGGCCTTA	CTCGTACCGA	ACTGGAGAAG	360
GAGATACAGA	AGAGGATTAT	TTCCAGTGGA	TTTATCAAGG	ATCCTACGGT	AACGGTGCAG	420
CTTCAAAATT	TCAAGGTGTC	GGTTTTGGGA	GAGGTGAATC	ATCCGGGTTC	GATGTCGGTA	480
AAAGGAGAGC	GAATAACTCT	TTTGGAAGCG	ATCGGAATGG	CCGGAGACCT	GACAATCTAT	540
GGTCGCCGCG	ATCGGGTTTT	TGTGATTAGA	GAAACCGATG	GGCATCGCGA	GGTTTTCCAG	600
ACGGATCTCA	GAAAGGCCGA	CTTGCTCGCA	AGCCCCGTGT	ACTATCTGCA	TCAGAACGAC	660
GTCATCTATG	TGGAGCCGAA	CGACAAGAAA	ACACAGATGA	GCGAGATCAA	CCAGAATAAT	720
AACGTAAACG	TATGGCTGAG	TGTTACCTCC	ACTTTGGTAT	CCATTTCCAC	GCTGACGATT	780
ACGATAATAG	ATAAGACCAA	A				801

(2) INFORMATION FOR SEQ ID NO:158

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

ATGAAAAAGA	CCAATCTGTT	TTTATCTCTG	CTGGTGATCT	TTATCACCGG	TAGTTTTATG	60
ACTGCCTGTG	CACAGAAGTC	CAAGACGAAC	AAACTCACCG	AAGAAGATCG	GAGCCGCAAT	120
GAGTATGTAC	AGTCGATGGA	TGTGCTTAGC	AATATTATCG	GTAACGTCAG	GCTGTATTTC	180
GTCGATACCA	TAAGTATCAA	ACATATGACT	CGGCGTGGTA	TAGATGCGAT	GTTGGGCGGG	240
CCTGACCCCT	ATACCGAATA	CATTCCCTAC	GAGGAAATGG	ATGAACTGAA	ATTGATGACT	300
ACGGGAGAGT	ATGCCGGAGT	CGGAGCTATC	ATATCGCAGC	GCCCCGATAG	TGCTGTGATT	360
ATCCAGAGAC	CTATGGAAGG	TATGCCCCCA	GACGAAGCAG	GATTGATAGC	AGCGCACC GC	420
ATCCTGACTA	TCGATGGGAA	AGACTTCCGC	AAATCCACCA	CACCGAAAGT	AAGCCAAGCA	480
CTGAAAGGGA	TAGCCGGTAC	TGTTGCAAA	GTGACAGTAA	TGCGCTATGG	CGAAACCAAA	540
CCTCGTACTT	TTTCCGTGAA	ACGTCAAAAA	GTGATTATGA	ATTCCGTCAC	TTACAGCGGA	600
ATGCTCGATG	GCTCGATAGG	ATATATCCGC	TTGAACAAC	TTACGGACAA	AAGTGCAGAA	660
GAGGTGCGCA	CGGCCTTGTT	GGATCTTCGT	GACAAACAAG	GAGCGAAAGG	TCTCATTTTG	720
GATTTAAGAG	GCAATGGTGG	CGGACTGATG	CAGGCTGCTA	TCGAGATAGT	CAATCTGTTC	780
GTCCTTAAGG	GCAAAGAGGT	GGTAACGACC	AAAGGTCGCA	TTGCAGAGTC	GGCGTCCGTA	840
TTTCGCACAT	TGACTGAACC	GATCGACACG	AAACTCCCCG	TAGTAGTCCT	GATCGATGGA	900
CAATCGGCAT	CTTCTCGGGA	GATTGTAGCC	GGAGCACTGC	AGGATATGGA	CAGGGCTGTA	960
CTGATGGGAC	ATAAGAGGTA	TGGCAAAGGG	CTTGTAACAA	CGACTCGTCA	GCTACCATAC	1020
AACGGCGTGA	TCAAATTGAC	TACGGCCAAG	TACTACATCC	CAAGCGGACG	TTGTATTTCAG	1080
CGTTTGGACT	ACAGCCGCAC	CAATCGGACA	GGTATGGCAA	CGGCCATTCC	TGACAGTCTG	1140
CACAAAATCT	TTTACACTGC	TGCCGGAAGA	CGTGTAGAAG	ATGCAGGAGG	AATCCTGCCT	1200
GACATCGAGG	TCAAACAAGA	TACAGCTGCG	ACATTACTTT	ATTATATGGC	CATCAATAAT	1260
GACGTTTTTC	ATTTTCGTCAC	AGGTTATGTG	CTCAAGCATA	AAACGATTGC	CAAGCCGGAG	1320
GATTTTTCCT	TAACGAACGA	GGACTATGCA	GCTTCTGCA	AGATGATGGA	AGAAAAGAAA	1380
TTTGACTACT	ATCGCCAGAG	TGGCAAGATG	CTTGACAAAC	TGGAGGAACT	GGCTAAGATA	1440
GAAGGCTACC	TGCCGGAAGC	CAACTCGGAG	CTTAAAGCAC	TACGCGAAAA	GCTAAAAACCC	1500
AACCTGTGCG	GTGATCTGCT	ACGATTCAAA	AAGGAGATAA	CAAACTATCT	CAACAATGAG	1560
ATTGTCACTC	GCTATTATTA	TGAGCGAGGC	AGTATCCGCC	AGAGTTTGCC	GGAAGATAAG	1620
GTAGTCAAAG	AAGCTATTAA	GCTGCTGAAG	GACCATCCGG	AACAAATTTC	ACAGATCCTT	1680
GCAGCTCCGA	AAGCAGAGAA	TAAAGGG				1707

(2) INFORMATION FOR SEQ ID NO:159

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2943 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

```
ATGCAAAACA AAGGATTGTG GATTGTTATC ACATCGGCTC TGGCCATCAT CTGTGCGTTT      60
TACCTGTCAT TCTCTTTCGT TACGAACCGT TACGAAAAGA AGGCTAAGGC GATGGGCGAT      120
GTTGCCGGAA TGGCCTATCT TGATTCCATG TCGAATGAGA AGGTCTGGTT CGGCTACACG      180
CTGAAAGAAG CTCAAGCCCA GCAAATTGGT CTGGCCTTG ACTAAAGGG GGGTATGAAC      240
GTTATCTTGA AACTTAACGC AAGCGATCTG CTTCGTAACC TCTCTAACAA AAGTTTGGAT      300
CCCAACTTCA ACAAAGCTCT GGAGAATGCT GCCAAGAGCA CGGAGCAATC CGACTTCATC      360
GATATTTTCG TGAAGGAATA TCGCAAGCTC GATCCCAACG GTCGCTTGGC CGTTATCTTC      420
GGTTCGGGTG ACCTTCGCGA CCAGATTACC GCAAAGTCTA CGGATGCAGA CGTAGTGCCT      480
CTGCTCAAAG AAAAATATAA TAGTGCTGTA GAAGCTTCGT TCAATGTGCT CCGTGCTCGT      540
ATCGATGCTT TCGGTGTGGT TGCACCTAAT TTGCAGCGAT TGGAAGGGCA AGGGCGTATC      600
CTTGTCGAAC TCCCGGAGT GAAAGACCTT GAGCGTGTTT GTACCTTTT GCAACGCAGT      660
GCCAACCTAC AGTTCTGCGG TACATACAAA TTGGAAGAGG TCAGCGGAGA CTTGATCGCT      720
GCCAATGATC GTCTGAGCGA ATTGGCTATG AACAAACACG ATGCTACCCC GGAAACAGAG      780
CCTGCAACTA CTGACTCTGT AGCTGCAACA GCCGATTCTG CTGCTGTACA AGCTGTAGCT      840
GATTCTGCTA CTGTAGCACA AAAAGAGGCC AAGGATGCTA CTCGTAAAGA CGCACTCTTC      900
TCTCTGCTTA ACCTCCGTGA TCGTGGCGGT GCAGTAGTGG GTGTGGCTCG TCGTGCTAAT      960
ATGGCTCAGA TATCTGAAAT GCTCCAGCAA GCTCACGATC TGAAGGTTAC ACGTGAAGAT     1020
GTGCTTTTCC TCTGGGGTGC TAAAGCAATC GAAGACCCCG AAACCAAAAA GGAGACCGAC     1080
CTCTACGAAC TCTATGCTAT TCGTACCAAT CGTACGGGAG ATCCTGATTT GGGAGGTGAT     1140
GTAGTGACTT TCGCCAAGAG TGATATCCAA AATGACTTCG GTCGTTCCGA ACCGATCGTT     1200
TCGATGACGA TGAATGAAGA AGGTGCTCGT AAATGGGCGC GTATCACAAA GGATAACGTG     1260
GGACGGGGCA TCGCTATCGT TTTGGATGGT GTGGTTTATT CTGCTCCGAA CGTGAATGAT     1320
GAGATCACGG GCGGTCGCTC TCAGATCTCC GGGCACTTCA CCGTGGAGGA GGCCGGTGAC     1380
GATTGCCAAG TACTCAAGTC CGGTAAAATG GATGCTACGG TAAGCATCGA ACAGGAAAAC     1440
GTGATTGGTC CTACGCTGGG TGCCGAGTCC ATTAAAGCCG GATTCTTGTC GTTCCTGCTC     1500
GCTTTGGTTA TCCTGATGTG TTACATGTGT CTGGCTTACG GTTTCTTGCC GGGTCTTATC     1560
GCAAACGGCG CATTGATTGT AAACAGCTTC TTCACATTGG GCGTATTGGC TTCTTTCCAT     1620
GCCGTGCTGA CCCTCTCGGG TATCGCAGGT TTGGTGCTGA CGCTGGGTAT GGCTGTGGAT     1680
GCCAACGTAC TTATCTTCGA GCGTATCAAA GAAGAGCTTC GTGCCGGTAA GACTCCGATT     1740
CGTGCCGTTA CGGATGGTTA TGGCAACGCT TTCTCTGCCA TCTTCGACTC GAACGTTACG     1800
ACTATTATTA CCGGTATCAT CCTATTCCTC TACGGGACGG GGCCGATTCT CGGTTTTGCC     1860
ACTACGTTGA TTATCGGTCT TATCGCTTCT TTCATTACGG CTGTCTTCTT GACTCGTATC     1920
GTCTTCGAGA AACTGGCGAA AAAAGGTCGT TTGGATAAGA TTACATTCAC TACGAGCATT     1980
ACTCGCAATC TCCTTGTCAA TCCTCATAC AACATCTTGG GTAAGCGCAA GACCGGCTTT     2040
ATCATTCCGG TGATTATCAT CGTTTTGGGA CTTATAGCTT CATTTACAAT CGGTCTCAAT     2100
AGGGGTATTG AATTCTCCGG AGGACGTAAC TACGTAGTTA AATTGACCA GCCTGTATCT     2160
TCCGAAGCCG TTCGTTCCGG CTGTCTTCTT CCCCTGCAGG AAAAGGTATT GGTACCTCC     2220
ATCGGTACTG AAGGGACAGA GGTGCGTATA TCTACGAACT ATAAGATCCA GGAGGAAAGC     2280
GAAGAAACTG AAGCAGAGAT TACTGACAAA TTGTATCAGA GCCTGAAAGG TTTCTACACC     2340
CAGCAGCCTA CTGCTGATCA GTTCTTGAC AATATCATT GCTCTCAGAA AGTAAGTCCC     2400
AGTATGTCGA GTGACATCAC GAGAGGTGCT ATTTGGGCTG TGCTGTTATC GATGATCTTC     2460
ATGGCCATTT ATATTCTGAT TCGCTTCCGT GACATTTCTT TCTCTGCCGG GGTATTCGTA     2520
TCTGTGGCCG CTAATACATT CTGCATTATT GCTCTGTATG CGTTGCTGTG GAAGATTCTG     2580
CCCTTCACCA TGGAGATCGA TCAGAACTTC ATCGCTGCTA TTCTGGCTAT CATCGGTTAC     2640
TCGCTCAATG ACACCGTGGT TGTATTTGAC CGTATCCGAG AGACGATGAA ATTGTACCCC     2700
AACAGAGATC GCTATCAGGT GATCAACGAT GCCCTTAATT CAACATTGGG TCGAACATTA     2760
AATACGCTCT TGACTACGTT TATCGTTATG TTGGTAATCT TCATCTTTGG AGTGCTACG     2820
ATGCGTAGTT TCACGTTCTC GATCTGCTC TCGGTACATA CTCTACGCTC     2880
TTTGTGCTA CACCCCTTGC CTACGAGATC CAAAAGCGCA AGCTCAACAA AGCAGCTAAG     2940
AAA                                                                                   2943
```

(2) INFORMATION FOR SEQ ID NO:160

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3051 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

```
ATGAAAAGAA TGACGCTATT CTTCCTTTGC TTGCTGACGA GCATTGGGTG GGCTATGGCC      60
CAGAATAGAA CCGTGAAGGG TACAGTTATC TCCTCCGAGG ATAATGAGCC CCTGATCGGC      120
GCGAATGTCG TGGTTGTCGG AAACACCACT ATCGGTGCTG CAACCGACTT GGATGGCAAC      180
TTCACGCTTA GCGTGCCTGC CAATGCCAAA ATGTTGAGAG TGTCCTATTC CGGTATGACT      240
ACCAAAGAGG TCGCCATCGC TAATGTGATG AAGATCGTAC TGGATCCGGA CTCTAAGGTT      300
CTGGAGCAGG TAGTTGTATT GGGTTACGGT ACGGGACAGA AACTCAGCAC TGTTTCCGGT      360
TCTGTGGCCA AAGTGTCCAG CGAAAAGCTC GCGGAAAAGC CCGTTGCCAA TATCATGGAT      420
GCCTTCCAAG GTCAGGTAGC CGGTATGCAG GTTATGACTA CATCCGGTGA CCCTACTGCC      480
GTCGCTTCTG TGGAGATCCA TGGTACAGGG TCGTTGGGGG CAAGCTCTGC ACCATTGTAT      540
ATCGTGGATG GTATGCAAAC TTCTTTGGAT GTTGTGGCTA CGATGAATCC GAATGATTTT      600
GAATCTATGT CCGTTTTGAA AGATGCTTCT GCAACATCTA TTTATGGAGC TCGTGTGCA      660
AACGGAGTCG TTTTCATTCA AACGAAGAAA GGTAAAATGA GCGAGAGAGG TCGTATTACC      720
TTTAATGCCA GTTACGGGAT TTCTCAAATC CTGAATACTA AGCCCCCTGA TAATATGATG      780
ACTGGAGATG AATTGTCTGA TTTTCAGGTG AAGGCAGGTT TTTGGGGGAA CAATCAAACC      840
GTTCAGAAGG TTAAAGATAT GATCCTTGCC GGAGCTGAAG ATTGTATGGA CAATTATGAT      900
TCTTTGAAAG ATGAGTATGG TAAGACATTG TTCCAGTGG ATTTTAATCA TGATGCAGAC      960
TGGCTCAAGG CTTTGTTTAA AACAGCACCC ACCAGTCAAG GTGATATTTC TTCTCCGGA      1020
GGGTCTCAGG GAACCTCATA TTATGCTCTT ATAGGCTACT TCGATCAGGA AGGTATGGCT      1080
CGTGAACCGG CAAATTTTAA GCGCTATAGT GGCCGGCTCA ACTTCGAAAG TCGTATCAAT      1140
GAATGGCTGA AAGTTGGTGC AAATTTGTCT GGTGCGATAG CGAATAGACG ATCTGCCGAC      1200
TATTTTGGAA AGTATTATAT GGGGTCAAGT ACTTTCGGTG TGTTAACGAT GCCTCGTTAT      1260
TATAACCCCT TTGATGTGAA TGGGGATTGA GCAGATGTCT ATTACATGTA TGGAGCTACC      1320
AGACCTTCTA TGACAGAACC GTACTTCGCA AAAATGAGAC CGTTCAGTTC CGAATCACAT      1380
CAGGCCAATG TAAATGGTTT CGCCAGATT ACTCCGATCA AAGGCCTTAC TTAAAGGCA      1440
CAGGCTGGTG TTGATATTAC TAATACTCGC ACTTCTTCTA AGAGAATGCC CAATAATCCG      1500
TATGATTCTA TCCTCTTTGG GGAAGAAGA GAAAGAGCTT ATCGAGATGT TAGCAAGTCT      1560
TTTACAAATA CGGCTGAATA TAAGTTTTC AATTGATGAAA AACATGATCT TACAGCATTG      1620
ATGGGGCATG AATATATTGA ATATGAAGGG GATGTTATTG GGGCATCTTC TAAAGGATTT      1680
GAAAGTGATA AGTTGATGTT ACTGAGCCAG GGA AAAACCG GAAATAGTTT GTCTTTGCCT      1740
GAACACAGAG TTGCTGAATTA TGCTTATTG TCTTTCTTTA TCGTTTTTAA TTACGGTTTT      1800
GACAAATGGA TGTATATAGA TTTCTCTGTT CGTAATGACC AATCCTCTCG ATTCCGATCC      1860
AATAATAGAA GCGCGTGGTT CTATTCTGTC GGTGGAATGT TTGACATATA TAATAAATTC      1920
ATTCAAGAAA GTAATTGGCT CAGTGATCTT CGACTGAAAA TGAGTTATGG TACAACGGGT      1980
AACTCGGAGA TTGCTAATTA CAACCAACCA GCACCTCGTTA CTGTGAACAA TTATACTGAA      2040
GATGCTATGG GGCTTAGCAT TTCTACAGCA GGCAATCCCG ACCTCTCGTG GGAAGAGCAG      2100
TCTCAGTTCA ACTTCGGTTT GGTGTCAGGG GCTTTCAATA ATCGCTTATC TGCAGAGGTA      2160
GATTTCTATG TCCGCACTAC GAATGATATG TTGATTGATG TCCCGATGCC TTATATCAGT      2220
GGTTTCTTCT CACAGTATCA GAATGTAGGC TCATGAAAA ATACGGGTGT AGACCTTTCT      2280
CTTAAGGGGA CGATCTACCA AAATAAGGAC TGAATGTAT ATGCTTCTGC GAATTTCAAC      2340
TACAATAGAC AGGAATAAAC AAGCTTTTC TTCGGTCTCA ATAAGTACAT GTTGCCATAAT      2400
ACCGGTACTA TATGGGAAAT TGGGTACCCC AATTCGTTCT ATATGGCTGA ATATGCTGGA      2460
ATCGACAAAA AAACCGGTAA GCAGTTGTGG TATGTTCCGT GTCAAGTCGA TCGGGATGGT      2520
AATAAAGTTA CAACAAGCCA GTACTCAGCT GACTTGAGA CACGAATTGA TAAGTCTGTT      2580
ACTCCTCCTA TTACAGGTGG TTTCTCCTTA GGTGCTTCTT GGAAGGACT TTCTTTAGAT      2640
GCTGATTTTG CCTACATCGT TGGTAAATGG ATGATCAATA ATGACCGTTA CTTTACAGAG      2700
AATGCAGGTG GATTGATGCA ATTAATAAAA GATAAAATGC TATTGAATGC CTGGACAGAG      2760
GATAATAAAG AAACAGATGT TCCAAAATG GGACAGTCTC CTCAGTTTGA TACGCATTG      2820
TTGGAGAATG CTTCTTTTCT GCGTTTGAAG AATCTCAAAC TCACCTATGT ACTCCCCAAT      2880
AGTCTTTTGT CTGGGCAGAA TGTGATTGGT GGAGCTCGTG TCTATTTGAT GCGCGCAAT      2940
CTGTTAACTG TTACGAAGTA TAAAGGCTTT GACCTGAAG CAGGGGGGAA TGTGGGAAAA      3000
AATCAATATC CTAATTCTAA GCAGTACGTT GCGGGTATTC AGTTGTCTTT C      3051
```

(2) INFORMATION FOR SEQ ID NO:161

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3042 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

```
ATGACGCTAT TCTTCCCTTG CTTGCTGACG AGCATTGGGT GGGCTATGGC CCAGAATAGA      60
ACCGTGAAGG GTACAGTTAT CTCTCCGAG GATAATGAGC CCTGATCGG CGGAATGTC      120
TTGGTTGTTCG GAAACACCAC TATCGGTGCT GCAACCGACT TGGATGGCAA CTTACGCTT      180
AGCGTGCCTG CCAATGCCAA AATGTTGAGA GTGTCCTATT CCGGTATGAC TACCAAAGAG      240
GTCGCCATCG CTAATGTGAT GAAGATCGTA CTGGATCCGG ACTCTAAGGT TCTGGAGCAG      300
GTAGTTGTAT TGGGTTACGG TACGGGACAG AAATCAGCA CTGTTTCCGG TTCTGTGGCC      360
AAAGTGTCCA GCGAAAAGCT CGCGGAAAAG CCCGTTGCCA ATATCATGGA TGCCCTCCAA      420
GGTCAGGTAG CCGGTATGCA GGTATGACT ACATCCGGTG ACCCTACTGC CGTCGCTTCT      480
GTGGAGATCC ATGGTACAGG GTCGTTGGGG GCAAGCTCTG CACCATTGTA TATCGTGGAT      540
GGTATGCAAA CTCTTTTGA TGTGTGGCT ACATGAATC CGAATGATT TGAATCTATG      600
TCCGTTTTTGA AAGATGCTTC TGCAACATCT ATTTATGGAG CTCGTGCTGC AAACGGAGTC      660
GTTTTTCATT AAACGAAGAA AGGTAAAAAT AGCGAGAGAG GTCGTATTAC CTTAATAGCC      720
AGTTACGGGA TTCTCAAAT CCTGAATACT AAGCCCCTTG ATAATATGAT GACTGGAGAT      780
GAATTGCTGG ATTTTCAGGT GAAGGCAGGT TTTTGGGGA ACAATCAAC CGTTCAGAAG      840
GTTAAAGATA TGATCCTTGC CGGAGCTGAA GATTTGTATG GCAATTATGA TTCTTTGAAA      900
GATGAGTATG GTAAGACATT GTTCCAGTG GATTTTAATC ATGATGCAGA CTGGCTCAAG      960
GCTTTGTTTA AAACAGCACC CACCAGTCAA GGTGATATT CTCTCTCCGG AGGGTCTCAG     1020
GGAACCTCAT ATTATGCCTC TATAGGCTAC TTCGATCAGG AAGGTATGGC TCGTGAACCG     1080
GCAAATTTTA AGCGCTATAG TGGCCGGCTC AACTTCGAAA GTCGTATCAA TGAATGGCTG     1140
AAAGTTGGTG CAAATTTGTC TGGTGCAGTA GCGAATAGAC GATCTGCCGA CTATTTTGGA     1200
AAGTATTATA TGGGGTCAGG TACTTTCGGT GTGTTAACGA TGCTCGTTA TTATAACCTT     1260
TTTGATGTGA ATGGGGATTG AGCAGATGTC TATTACATGT ATGGAGCTAC CAGACCTTCT     1320
ATGACAGAAC CGTACTTCGC AAAAAATGAG CCGTTCAGTT CCGAATCACA TCAGGCCAAT     1380
GTAAATGGTT TCGCCCAGAT TACTCCGATC AAAGGCCTTA CTTTAAAGGC ACAGGCTGGT     1440
GTTGATATTA CTAATACTCG CACTTCTTCT AAGAGAATGC CCAATAATCC GTATGATTCT     1500
ACTCCTCTTG GGGAAAGAAG AGAAAGAGCT TATCGAGATG TTAGCAAGTC TTTTACAAAT     1560
ACGGCTGAAT ATAAGTTTTC AATTGATGAA AAACATGATC TTACAGCATT GATGGGGCAT     1620
GAATATATTG AATATGAAGG GGTGTTATT GGGGCATCTT CTAAAGGATT TGAAAGTGAT     1680
AAGTTGATGT TACTGAGCCA GGGAAAAACC GGAATAGTT TGCTTTTGCC TGAAACACAGA     1740
GTCGCTGAAT ATGCCTATTG GTCTTCTTTT AGTCGTTTTA ATTACGGTTT TGACAAATGG     1800
ATGTATATAG ATTCTCTGT TCGTAATGAC CAATCCTCTC GATTCTGGAT CAATAATAGA     1860
AGCGCGTGGT TCTATTCTGT CCGTGGAATG TTTGACATAT ATAATAAAT CATTCAAGAA     1920
AGTAATTGGC TCAGTGATCT TCGACTGAAA ATGAGTTATG GTACAACGGG TAACTCGGAG     1980
ATTGGTAATT ACAACCACCA AGCACTCGTT ACTGTGAACA ATTATACTGA AGATGCTATG     2040
GGGCTTAGCA TTTCTACAGC AGGCAATCCC GACCTCTCGT GGGAAAAGCA GTCTCAGTTC     2100
AACTTCGGTT TGGCTGCAGG GGCTTTCAAT AATCGCTTAT CTGCAGAGGT AGATTTCTAT     2160
GTCGCCACTA CGAATGATAT GTTGATTGAT GTCCCGATGC CTTATATCAG TGGTTTCTTC     2220
TCACAGTATC AGAATGTAGG CTCTATGAAA AATACGGGTG TAGACCTTTC TCTTAAAGGG     2280
ACGATCTACC AAAATAAGGA CTGGAATGTA TATGCTTCTG CGAATTTCAA CTACAATAGA     2340
CAGGAAATAA CAAAGCTTTT CTTCGGTCTC AATAAGTACA TGTGCCTAA TACCGGTACT     2400
ATATGGGAAA TTGGGTACCC CAATTCTGTC TATATGGCTG AATATGCTGG AATCGACAAA     2460
AAAACCGGTA AGCAGTTGTG GTATGTTTCT GGTCAAGTCG ATGCGGATGG TAATAAAGTT     2520
ACAACAAGCC AGTACTCAGC TGACTTGGAG ACACGAATTG ATAAGTCTGT TACTCCTCCT     2580
ATTACAGGTG GTTCTCTCTT AGGTGCTTCT TGGAAAGGAC TTTCTTTAGA TGCTGATTTT     2640
GCCTACATCG TTGGTAAATG GATGATCAAT AATGACCGTT ACTTTACAGA GAATGCAGGT     2700
GGATTGATGC AATTAAATAA AGATAAAATG CTATTGAATG CCTGGACAGA GGATAATAAA     2760
GAAACAGATG TTCCAAAATT GGGACAGTCT CCTCAGTTTG ATACGCATTG GTTGGAGAAT     2820
GCTTCTTTCC TCGGTTTGAA GAATCTCAA CTACCTATG TACTCCCCAA TAGTCTTTT     2880
GCTGGGCAGA ATGTGATTGG TGGAGCTCGT GTCTATTTGA TGGCGCGCAA TCTGTAACT     2940
GTTACGAAGT ATAAAGGCTT TGACCCTGAA GCAGGGGGGA ATGTGGGAAA AAATCAATAT     3000
CCTAATTCTA AGCAGTACGT TGCGGGTATT CAGTTGTCTT TC                      3042
```

(2) INFORMATION FOR SEQ ID NO:162

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2463 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

```
ATGAAGAAAA AGAATTTTT GCTTCTTGGC ATTTTCGTTG CTTTGCTGAC TTTCATCGGC      60
AGCATGCAGG CACAACAGGC CAAAGATTAT TTCAACTTTG ACGAACGGGG CGAGGCCTAC      120
TTCTCATTTA AAGTGCCTGA TAGGGCCGTT CTACAAGAGC TGGCTCTGAT CATGTCCATC      180
GACGAGTTTG ACCCCGTAAC CAATGAAGCC ATTGCCCTATG CCAGCGAAGA GGAGTTCGAG      240
GCATTCCTGC GCTATGGGCT CAAGCCTACA TTCTTGACTC CTCCATCCAT GCAGCGCGCT      300
GTGAGATGT TCGACTACCG CTCAGGAGAA AAATACGAAT GGAATGCTTA CCCCACCTAT      360
GAAGCCTATA TCAGCATGAT GGAAGAGTTT CAAACAAAGT ATCCATCACT TTGTACTACT      420
TCCGTCAATTG GCAAGTCCGT AAAGGATCGT AAACGTGATG TTTGCAAGCT GACGTCTCTT      480
GCCAATACAG GGAAAAAGCC TCGCGTGCTC TATACTTCTA CGATGCACGG AGACGAAACG      540
ACCGGATATG TGGTACTGCT CCGACTCATA GACCATCTGC TGTCGAACTA CGAATCCGAT      600
CCGAGGATTA AGAACATTCT GGATAAAACG GAAGTATGGA TCTGCCCTTT GACCAATCCG      660
GACGGAGCAT ACAGAGCCGG AAACCAACAC GTACAAGGAG CTACTCGCTA CAATGCCAAC      720
AATGTCGATT TGAACCGTAA CTTCAGGAT GATGTAGCCG GTGATCACCC CGATGGAAAA      780
CCTTGGCAGC CGGAGGCAAC TGCATTTCAT GATTTGGGAG GAAACACCTC TTTCGTGCTC      840
GGTGCCAAAT TACATGGAGG AACAGAGGTG GTGAACATAT CATGGGATAA TAAAAAAGAA      900
AGACATGCAG ACAGATGAGTG GTACAAACTG ATCAGTCGCA ACTACGCAGC CGCTTGTCAG      960
AGTATTTCCG CCAGCTACAT GACCTCCGAA ACCAATTCGG GAATCATCAA CGGTTTCAGAC     1020
TGATATGTAA TTCGCGGAAG TCGTCAGGAC AATGCAAATT ATTTCCATCG TCTGCGAGAA     1080
ATTACCCTTG AAATCAGCAA CACGAAGTTG GTGCCGGCCT CTCAACTTCC AAAGTATTGG     1140
AATCTGAACA AAGAATCTCT GCTTGCTCTG ATCGAAGAAT CCTTATACGG CATCCATGGT     1200
ACAGTGACTT CCGCTGCGAA CGGACAGCCT CTCAAATGCC AGATCTTGAT AGAAAACCAT     1260
GACAAGCGCA ACTCCGATGT TTAATCCGAT GCTACCACAG GCTACTACGT ACGTCTCTATC     1320
AAAGCCGGCA CTTATACGGT GAAATACAAA GCCGAGGGTT ATCCTGAGGC AACTCGTACC     1380
ATTACGATCA AGGACAAAAG AACCCTCATC ATGGACATTG CATTTGGGCA CTCGGTTTCCT     1440
CTGCCTGTAC CCGATTTTAC AGCTTCTCCT ATGACCATCT CAGTAGGCGA AAGCGTCCAA     1500
TTCCAAGATC AAACGACAAA TAACCCACAG AATTGGGAGT GGACGTTCTG AGGCGGACAG     1560
CCTGCCATGA GTACAGAGCA GAATCCGCTC GTATCCTATA GTCATCCCGG TCAGTACGAC     1620
GTTACGCTCA AAGTGTGGAA TGCAAGTGGT TCCAACACGA TTACGAAAGA AAAATTCATC     1680
ACTGTCAATG CCGTTATGCC TGTAGCTGAA TTCGTGCGTA CCCCAGCGGA AATAGAAGAG     1740
GGCCAGACGG TATCTTTTCA AAACCAATCC ACCAATGCCA CCAACTACGT ATGGATATTC     1800
GATGGCGGCA CTCCCGCTAC CAGTGAAGAC GAAAACCCGA CTGTGCTTTA CAGCAAAGCC     1860
GGCCAATACG ATGTCACGCT CAAGGCGATC AGTGCTTCCG GTGAAACGGT GAAGACGAAA     1920
GAAAAATACA TCACTGTCAA GAAAGCTCCG GTCCCTGCTC CGGTAGCCGA CTTCGAAGGA     1980
ACACCTCGAA AAGTAAAGAA AGGCGAGACA GTTACTTTCA AAGACTTGTC TACGAACAAT     2040
CCGACTTCAT GGCTTTGGGT GTTCGAAGGC GGCTCTCCTG CCACCAGCAC GGAGCAAAAC     2100
CCGGTGGTCA CCTACAATGA AACAGGCAAG TACGATGTCC AGCTGACTGC CACCAACGAG     2160
GGCGGAAGCA ATGTGAAGAA AGCAGAAGAC TACATTGAGG TTATCCTCGA TGACAGTGTC     2220
GAGGACATAG TGGCACAGAC GGGTATCGTC ATTCGTCCGC AAAACGGGAA GAAGCAGATC     2280
CTCATAGAAG CCAACGCTGC TATCAAAGCG ATCGTTCTCT ATGACATCAA TGGACGGGTC     2340
GTACTCAAAA CTACTCCGAA TCAGCTCCGC TCGACCGTAG ATCTTTCCAT CTGCCCCGAA     2400
GGAATCTACA CCATCAATAT CAAAACGGAA AAATCCGCTC GCACGGAAAA GATCCATATC     2460
GGG                                                                                   2463
```

(2) INFORMATION FOR SEQ ID NO:163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

ATGCGACTGA	TCAAGGCTTT	TCTCGTGCAA	CTCTTACTGC	TCCCCATTTT	CTTCTACAAG	60
CGGTTTATAT	CGCCGCTTAC	ACCGCCTTCA	TGCCGGTTTA	CCCCCTCATG	TTCGTCCTAT	120
GCCATCGAAG	CCTTACGTAA	ATATGGCCCG	GGCAAAGGAC	TATTGCTGAG	CATCAAGCGT	180
ATTCTCCGCT	GTCACCCGTG	GGGTGGAAGT	GGCTATGACC	CCGTTCGG		228

(2) INFORMATION FOR SEQ ID NO:164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

ATGGCATAACG	ACTTTACACA	AACATTCCGC	AACAGCCTGG	AGTACAGCTA	TCAGGAAGCA	60
ACCCGTCTCG	GCGTCGTAGC	CGTGACGCAA	GATATGCTCG	TACTCGGTAT	CATTCGCGAC	120
GGAGACAATG	GCGCGATCGA	CATCATGCGG	CACTATGGGA	TCAACTTGTA	CGAACTCAA	180
CGGTTGATCG	AGTTGGAAGC	CATCGCCGAG	AGTTTGCCCTG	CTTCGCCTGA	GGGATCGCCC	240
ATCTTCACCC	CTTCGGCTCG	GGAGGCTATC	GATGATGCCA	CAGACATCTG	TGCCGACATG	300
GAGGACGAGG	CCGTCAGCCC	GGTCCATCTG	TTGCTGAGTA	TCCTCAACTC	GACACAGGAG	360
AGCTTAGTAC	AAAAGATATT	TATGAAACAA	GGTATAAAAT	ACGACACCAT	CCTGTCCGGAT	420
TACTTCGGAC	AGCGCAACCC	CTCCGAAGGG	AAGTCTCCCT	CCGAAATGGA	GATCCTCGAC	480
GGGTACCAAG	ACAACGACTT	CGACGACGAA	GAGGACGAAT	CCTCTCCGCC	TTCCGGGAAT	540
AGCGGGACAG	GCGGAGGCTC	CGGCGACGCC	CCCGAACAGA	ATACCGGCGG	AGGCGATACT	600
ACCACCACGA	CACGGAGTGG	AGGCGACACG	CCTGCACTGG	ACACCTTCGG	CACCGACATC	660
ACTGCCATGG	CGGCAGCAGG	CAAGCTCGAC	CCGGTAGTGG	GTCCGGAGCA	GGAGATCGAA	720
AGGGTGATAC	AGATACTCAG	CGGGCGCAAA	AAGAACAATC	CGGTGCTCAT	CGGCGAACCC	780
GGTGTAGGCA	AGAGTGCCAT	CGTGGAAGGA	CTGGCCGAAC	GCATCGTGAA	CAGGAAGGTG	840
AGCCGTATTC	TTTTCGACAA	GCGGATCATC	AGCCTCGATT	TGGCTCAGAT	GGTAGCCGGC	900
ACCAAATATC	GCGGACAGTT	CGAAGAGCGG	TTGAAAGCCG	TGCTCGATGA	GCTGAAGAAG	960
AATCCGACAG	TCAATCTCTT	CATCGACGAG	ATACATACCA	TCGTGGGAGC	AGGCTCTGCA	1020
GCCGGATCGA	TGGATACGGC	CAATATGCTC	AAACCCGCTC	TTGCCCGTGG	ACAGGTACAG	1080
TGCATCGGAG	CCACTACGCT	GGATGAGTAT	CGTAAGAACA	TAGAAAAGGA	CGGAGCACTC	1140
GAACGCCGCT	TCCAGAAGGT	GCCGATAGCC	CCCTCGACTG	CAGAAGAAAC	GCTGACCATC	1200
CTGCAAAACA	TCAAAGAGAA	ATACGAGGAC	TATCACGGTG	TACGCTATAC	GGACGAAGCG	1260
ATCAAAGCGG	CAGTGGAAGT	GACCGATCGC	TATGTATCCG	ATCGTTTCTT	CCAGATAAAG	1320
GCGATAGATG	CCATGGACGA	GGCCGGCGCG	AGCGTCCATA	TCACCAATGT	GGTGGCTCCG	1380
AAAGAAATCG	AGATACTGGA	GGCCGAATTG	GCATCGGTGC	GAGAGAACAA	GCTCTCGGCC	1440
GTAAAGGCTC	AGAAGTACGA	ACTGGCTGCC	TCCTTCCGCG	ATCAGGAGCG	GCGCACTCAG	1500
CAGCAGATAG	CGGAAGAGAA	GAAAAAATGG	GAAGAGCAGA	TGTCCAAGCA	CCGCGAGACG	1560
GTGGACGAGA	ATGTAGTGGC	GCATGTAGTG	GCGTTGATGA	CAGGCGTTCC	GGCTGAGCGG	1620
CTGAGCACGG	GCGAAGGCGA	ACGTCTGCGC	ACGATGGCAG	ATGATCTCAA	GACCAAAGTA	1680
GTAGGTCAGG	ACACAGCCAT	CGAAAAGATG	GTGCATGCCA	TCCAGCGCAA	TCGTCTGGGA	1740
CTTCGCAATG	AAAAGAAACC	GATCGGTTCT	TTCTTTTTC	TCGGCCCCAC	GGGGGTAGGC	1800
AAGACCTATT	TGGCCAAGAA	GCTCGCCGAA	TACCTGTTCT	AGGATGAGAA	TGCCATGATC	1860
AGGGTGGATA	TGAGCGAGTA	TATGGAGAAG	TTCTCCGTTT	CGCGTCTCGT	GGGTGCCCTT	1920
CCGGGATATG	TGGGCTATGA	AGAAGGCGGC	CAACTGACGG	AGCGCGTAAG	ACGCAAACCC	1980
TATTCCGTGG	TTCTCTTGGA	TGAGATCGAA	AAGGCGCATG	CCGATGTCTT	CAATCTGCTC	2040
TTACAGGTGA	TGGACGAAGG	TCAGCTGACC	GACAGTCTGG	GACGGCGCGT	GAATTTCAAAG	2100
AACACCGTGA	TCATCATCAC	CTCCAACGTG	GGTACACGCC	AGCTCAAAGA	CTTCGGGCAG	2160
GGTATCGGGT	TCGGTTCCGA	AAAAGACGAG	GAGAGCATAG	CCGTTCCGTG		2220
ATCCAAAAAG	CTCTGAACAA	GACGTTTCAGC	CCCGAATTTC	TCAACCGTTT	GGACGATATC	2280
ATCCTCTTCG	ACCAACTGGG	CAAGACGGAG	ATTCGCCGGA	TGGTGGACAT	AGAGCTTAAA	2340
GCCGCTCTTG	CGCGCATCCA	TCGTGCCGGA	TACGACCTCG	TCCTTACCGA	TGAAGCCAAG	2400
GATGTGATAG	CGACGAAGGG	ATACGACCTC	CaATACGGAG	CACGACCGCT	CAAGCGCACA	2460
CTCCAGAACG	AAGTGGAGGA	TCGCCTCACG	GATCTTATCC	TCTCCGGACA	GATCGAGAAA	2520
GGGCAGACGC	TTACGCTCTC	TGCTCGCGAT	GGCGAGATCA	TCGTACAAGA	ACAAGCA	2577

(2) INFORMATION FOR SEQ ID NO:165

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1251
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

```

ATGAATTACC TGTACATACT GATTACACTT TTACTCTCCG GCTTTTTTTC CGGTGCTGAG      60
ATTGCTTTCC TTTCTTCGGA CAAACTGCGT CTTGAGTTGG ACAGGAATAG AGGCGATCTC     120
ACAGGCAGAG CGTTAACTTT GCTGTATCGA CATCCGGACC AACTGGTGAC TACTCTCCTT     180
GTGGGTAATA ATATCGTTTT GGTAGTCTAT GGTCTGCTGA TGGCGGGATT GCTGGCCGCA     240
CCTTTGGCGC AATGGATTGA TAACGATGCT ATGATCGTCG TTCTCCAATC TGTCTTATCC     300
ACTATCATCA TACTGTTTAC CGGGGAATTT CTACCCAAAG CCATTTTCAA GACCAATGCC     360
AATATGATGA TGAGGGTATT CGCCTCCCT ATCGTAGCGA TCTATTATCT GCTTTATCCT     420
CTGTCTAAAC TCTTCACCGG TTTATCTCGC TCTTTTATTC GTCTGGTGGA CAAGAATTAT     480
GTGCCTACAA CAGTAGGGTT GGGGCGCGTA GATCTCGATC ATTATTGGGC AGAAAATATG     540
TCCGGAGAAA ACGAACAGAA CGACTTGACT ACCGAAGTGA AAATCATCCA GAATGCGCTG     600
GATTTTTCCG GTATTAGGT GCGAGACTGC ATGATCCAC GCAATGAGAT GATAGCATGT     660
GAGTTGCAAA CGGATATTGA AGTACTCAA ACGACTTTTA TCGATACCGG TTTGTCCAAG     720
ATCATTATCT ACAGACAGAA CATAGATGAC GTAGTAGGAT ATATCCATTC GAGCGAAATG     780
TTTCGTGGGC AAGACTGGCA AAAACGTATC AATACTACTG TATTCGTACC CGAAAGCATG     840
TATGCCAATA AACTGATGCG ACTACTCATG CAGCGCAAGA AAAGCATTGC GATCGTCATC     900
GATGAACCTG GAGGTACGGC CGGAATGGTC ACATTAGAGG ATTTGGTAGA AGAGATTTTC     960
GGTGACATTG AGGACGAACA CGCACTCGC AAGATCATAG CCAAACAGCT CGGCCCTCAT    1020
ACCTATCTGG TCAGTGGTCG TATGGAAATA GATGATGTGA ACGAACGTTT TGGGTTGTCC    1080
TTGCCTGAGT CTGACGACTA CCTTACCGTG GCCGGATTTA TCCTGAATAG CCATCAAAAT    1140
ATCCACAGG CCAATGAGGT CGTGGAGATT GCTCCTTATA CTTTACCAT TCTCAGATCT    1200
TCTTCCACCA AGATCGAACT GGTGAAAATG TCCATCGACG ACCAATCGAA C              1251

```

(2) INFORMATION FOR SEQ ID NO:166

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

```

ATGAAACAGA ACTACTTCAA AAGAGTCTGC TCACTGCTTT GGCTGGTTTT ACCCATGCTT      60
ATTATGCCAT TGGAAGTAGC AGCTCAAGAG ATTATTCGGA ACGAAGAGGT GTTGAATCA     120
TTGACTTTTC TTGCACCGGT TGAGGAGACA GACGCAATAG AGGCAGAGGT AGAAGCTCTG     180
CAGGAGATAG TCGCTACTGA GGAGATTGCG GAGCAGGCTG TTCGTTCTTA TACCTACACG     240
GTCTATCGTG ATGGCGTGAA GATTGCTTCA GGATTGACTG AGCCCACTTT TCTCGATGAA     300
GATGTTCCCT CCGCGCAACA TACCTACTGC GTAGAAGTAC AGTATCAGGG AGGCGTATCC     360
GACAAAGTAT GCGTGGACGT AGAGGTGAAG GACTTCAAAC CGGTTACCAA TCTACCCGGA     420
ACTGCTTCCA ATGACGAAGT TTCTTTGGAC TGGGACGGTG TGGAAGAGAA AGCTGAAGAG     480
CCGGCAAGTG ATAAAGCAGT CAGCTACAAC GTCTACAAGA ATGGAACCTT GATCGGTAAT     540

```

ACAGCTGAAA	CTCATTATGT	GGAGACCGGT	GTAGCCAATG	GTACATACAT	CTACGAAGTG	600
GAAGTAAAGT	ATCCTGACGG	TGTATCTCCG	AAGGTGGCTG	TAACCGTGAC	CGTGACCAAC	660
AGCTCAATTGA	GCAATGTAGA	TGGACAGGCT	CCTTACACAT	TGCGAGTAGA	AGGCAAGAAG	720
ATTATTGCGG	AAGCCCATGG	TATGATCACG	CTCTACGACA	TCAACGGACG	TACCGTGGCC	780
GTAGCCCCGA	ATCGATTGGA	ATACATGGCG	CAAACCGGTT	TCTATGCAGT	GCGCTTCGAT	840
GTGGGGAATA	AACACCATGT	ATCGAAAATA	CAAGTAAGA			879

(2) INFORMATION FOR SEQ ID NO:167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

ATGATTCTC	TAAGCGAGAG	TTTTGAATCA	GGTATTCCAG	CTATATGGAA	GACCATTGAC	60
GCAGATGGCG	ATGGCTATAA	TTGGATGCAT	TTGACCAATT	TCACGGGACA	GAGTGGTCTC	120
TGTGTCTCTT	CGGCTTCATA	CATAGGCGGC	GTCGGAGCTT	TGACTCCGGA	CAATTATCTG	180
ATAACACCCG	AATTAAACT	ACCCACAGAC	GCGTTGGTGG	AAATAATCTA	TTGGGTATGT	240
ACTCAAGATC	TCACTGCTCC	ATCGGAGCAC	TATGCCGTTT	ATTCTCTTTC	TACAGGCAAT	300
AATGCTGCTG	ACTTTGTAA	TCTCTTATAT	GAAGAGACTT	TGACTGCCAA	ACGATACAA	360
TCCCCCGAGT	TGATCCGCGG	AAATCGGACA	CAAGGTGTTT	GGTATCAAAG	AAAGGTGGTA	420
CTCCCTAACG	ATACTAAATA	TGTTGCTTTC	CGCCATTTTA	ATCCACGGA	TAATTTCTGG	480
CTCAATTGG	ATGAAGTATC	TATCCTGTAT	ACCCCTCTTC	CCCGAAGAGC	TCCGTGTCCG	540
CATCCGGGTG	GTTACACTTA	TCTGTATTC	CGTGATGGAC	AAAAGATAGC	GAGTGGATTG	600
TCGGCATTGG	CATATATCGA	TACGGATGTA	CCGTATGGGA	CTCAAGACTA	TTGTGTCCAA	660
GTCAATTATC	TGCAAGGAGA	CTGTATATAA	GTCTGCAAAA	ATATAGTGGT	GGCAAATTCT	720
GCAAACATCT	ATGGGGCGGA	TAAGCCTTTT	GCGTTGACCG	TGGTTGGCAA	GACCATTGTA	780
GCGAGTGCTT	TCAAAGGAGA	GATCACTCTT	TATGACATTC	GTGGCCGGCT	GATAGCTTCC	840
GGCTGCCGATA	CGCTTAGGTA	CAAAGCGGAA	AATGGTTTTT	ACCTCATTA	AATACAGGTA	900
AACGGAACTG	TCTATACTGA	GAAATCCAA	ATCCAA			936

(2) INFORMATION FOR SEQ ID NO:168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

ATGAAAAAAA	GTTTTCTTTT	AGCCATAGTA	ATGCTCTTTG	GCATTGCCAT	GCAGGGACAT	60
TCTGCTCCGG	TTACGAAAGA	GCGAGCTTTG	AGTCTGGCTC	GGCTGGCTTT	GCGACAGGTA	120
TCCTTGCGAA	TGGGACAAAC	AGCAGTATCT	GACAAGATTT	CCATCGATTA	CGTTTATCGG	180
CAAGGAGATG	CTGAGAGGGG	TATCACATCA	CAAGAGGAAG	GCTCTCCTGC	ATATTTTTAT	240
GTAGCTAATC	GTGGAAATAA	TGAGGGCTAT	GCTCTTGTAG	CAGCAGATGA	CAGAATACCG	300

ACAATTTTAG	CCTATTCACC	CATTGGCCGT	TTGACATGG	ACAGTATGCC	GGACAATCTT	360
CGCATGTGGC	TACAAATTTA	CGATCAGGAA	ATAGGCCTGA	TACTTTCCGG	AAAAGCTCAG	420
CTCAATGAAG	AGATATTACG	TACCGAGGGC	GTACCGGCTG	AAGTACATGC	TCTGATGGAT	480
AACGGTCATT	TTGCCAACGA	TCCCATGCGA	TGGAATCAAG	GTTACCCATG	GAACAATAAG	540
GAACCACTGC	TTCTTAATGG	CAATCATGCC	TATACCGGCT	GTGTTGTCTAC	TGCTGCAGCA	600
CAAATCATGC	GCTACCATAG	CTGGCCGCTT	CAAGGTGAAG	GCTCTTTCGA	TTATCATGCA	660
GGTTCATTAG	TTGGCAACTG	GTCCGGCACA	TTTGGTGAAA	TGTACGACTG	GATCAATATG	720
CCCGGAAATC	CCGACCTTGA	TAATCTGACT	CAATCTCAAG	TGGATGCCTA	CGCCACACTG	780
ATGCGTGTATG	TGAGTGCATC	TGTTTCGATG	AGTTTTTATG	AAAATGGAAG	TGGTACGTAC	840
AGCGTTTATG	TAGTAGGAGC	CTTGCGAAAC	AACCTTCGCT	ACAAGCGTTC	ACTGCAGCTA	900
CATGTACGCG	CCTTATATAC	CTCACAGGAG	TGGCACGATA	TGATCCGCGG	GGAACCTGCC	960
TCCGGAAGGC	CGGTCTATTA	TGCAGGGAAT	AACCAGAGCA	TAGGACATGC	TTTCGTTTGC	1020
GATGGTTATG	CTTCGGATGG	TACTTTCCAT	TTCAACTGGG	GTGGGGAGG	TGTTTCCAAC	1080
GGCTTCTACA	AACTAACACT	CCTCTCGCCG	ACTTCGTTGG	GTATCGGAGG	TGAGGGAATA	1140
GGTTTTACCA	TTTATCAAGA	GAATCATACC	GGTATCGAAC	CGGCTAAGAC	TCCCGCTGAA	1200
GCCGGTACAG	ATGCCTTGCC	GATCTTGCA	CTGAAAGACA	TAGAAGCCGA	GTATAAAAGT	1260
GAATCCGGAT	TGAACGTAGG	GTATTCGATA	TATAATACAG	GTGAAGAGCA	ATCAAATCTT	1320
GACCTCGGAT	ACAGATTGAA	CAAGGCTGAC	GGAGAAGTCA	TAGAGGTGAA	AACCTCATCT	1380
ATCAATATCT	CTTGGTACGG	ATACGGAGAG	CATCCCGAGA	GTTTCTCATT	GGCACCTAAT	1440
CAGTTGTAC	AAGGAATCAA	CACCATCACC	CTACTTTATC	GTCGCACAGG	CACCGAACAG	1500
TGGGAGCCGG	TACGGCATGC	ACAGGGAGGA	TATGTCAATA	GCATTAAAGT	AAATACGACA	1560
GACCCGAACA	ATGTCGTAGT	CACGGTAGAT	AATAACGAAG	GCAAGCTCAG	TATCGTCCCC	1620
AACAGCTTTG	TCGCAGATCT	GAATCTTAT	GAACATAGTA	CGATTACAGT	ACAGTTCAAT	1680
AGCGACAGCC	CTGATGAGAT	CCGTACACCC	GTAGCCTTTG	CTCTATCTAC	AGGAGCTACT	1740
GCGGACGATG	TAATATCTTT	GGGCTGGGTA	ATGGCTGAAG	TTCCGGGCGG	TAGCAGCAAC	1800
TATCCGGTGG	TTTGGTCTAA	AGACGTTCTC	ACTCTCTCGG	AAGGCGACTA	TACATTGTGG	1860
TATAGATTTT	CCATCAACGA	CAAAAAGGAT	GAATGGAAAA	AGATCGGAAG	CGTGTCAGTA	1920
AAAACACCGA	CAGAGTATAC	GCACCCCTTA	TTCGAAGTGG	GCCATAATCA	AACCTTCTACC	1980
TATACGCTGG	ATATGGCACA	CAACAGAGTA	TTGCCCGACT	TTACACTCAA	AAATCTCGGA	2040
TTGCCTTTCA	ATGGTGAGTT	GGTTGTTGTT	TTCCGCCAAA	CACAATCCTC	ATCGGGGTCT	2100
TTATGGGCAG	CTCAAGAAAC	AGTACATATC	AAGCAAGGAG	AAACTTTCGT	ATATAAACCT	2160
GTGTGCGAAG	GCCCTATACC	TGATGGATCC	TATCGTGCGA	CCCTCCATGC	ATTTCGTAAAC	2220
GGACAACAAC	AGTTGTACCT	CAAGGGGAAA	AGGAACTACA	CGGTGAAGAT	CGTCAATGGT	2280
ACAGCGGTAG	AAGCAATAGA	ATCGTCAGAA	GAGATCAGAG	TATTCCCTAA	TCCGGCACGC	2340
GATTATGTGG	AAATATCGGC	ACCTTGCAAT	CCCCAAGAAA	CATCTATCAT	TCTTTTCGAT	2400
CTGTCAGGCA	AGATTGTCTAT	GAAGAATAGT	TTATCAGCGG	GGCATGGCAG	AATGGATGTC	2460
AGCCGACTTC	CTAATGGGGC	CTACATCCTT	AAGGTGGATG	GATATACGAC	GAAAATAAAT	2520
ATAGTGCAC						2529

(2) INFORMATION FOR SEQ ID NO:169

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGAAAAAGC	TATTCTCTC	GCTCACGAGT	CTTGTAATGG	TCTTCGCTGT	TGCAAGTTGC	60
GATATAATCG	ACAAGGATCA	AACCTCTTG	CCGGCTCCGA	CCAATGTGAC	ACCCGATAAT	120
CCGGATGACA	ATCCTTCGGA	GATCGACATT	ACGCAGACGC	ACACAGAAAA	ATATGTTTTG	180
GCTGAAGAAT	TTACCGGCCA	AAAATGTCTC	AACTGTCCGA	AAGGTCATCG	CAAACCTGGC	240
GCTCTCAAGG	AGCAATACGG	TAAGAGATTG	ACTGTTGTCTG	GTATACATGC	CGGCCCTGGA	300
TCTCTCGTGC	CACCTCTTTT	CCGTACAGAA	GCCGGAGACG	CATATTATAG	CAAGTTCGCC	360
AATAATACCC	CTCTCCCTGC	GCTGATGGTT	TCGCGCAAAA	AGTTCCGGCTC	TTCTACGTT	420
TATGATAAGA	GCTACAAAAC	GTGGGACGTG	CCTATTGCCG	AGCAGATGGA	GCAAAAAGCG	480
AAGATCAATA	TCTTTGCCGT	GGCCGAATAC	ACCGATACCC	AAAAGATCAA	GGTGAATGTA	540
AAGGGTAAAA	TACTGGAGGG	GAATACACTC	CCGAAGTCCA	TGGTTCAGGT	GTATCTGTTG	600
GAGGATAAGC	TGATCGCTCC	CGAGGTGGAT	GGCAATACGA	CAGTCGAGAA	TTACGAGCAC	660
AATCACGTGT	TGCGTGGAGC	CGTTAATGGT	ATTGGGGGCG	AAGAATTTGT	GAATCTCAAA	720
GATTATTTGT	ATACCTTACGC	CGTTGAACCG	CTCTCGGGTA	TGTCCTTCGT	AGCCGAGAAT	780
TATTCGATTG	TGGCTTTTGT	ATACGATGTG	CAGACGTTTC	AAGTGTATGA	CGTTGTGCAT	840

(2) INFORMATION FOR SEQ ID NO:170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGAAGAAAT CAAGTGTAGT AGCCTCAGTT TTGGCCGTGG CTCTCGTGTT CGCCGGTTGC	60
GGACTGAAACA ATATGGCAAA AGGCGGCCCTT ATCGGCGCCG GAGTAGGAGG TGCCATTGGT	120
GCCGGAGTAG GTAACGTAGC CGGAAATACG GCTGTCGGTG CCATCGTCGG TACTGCAGTC	180
GGTGGAGCAG CCGGTGCTCT CATCGGAAAG AAGATGGACA AGCAGAAAAA AGAACTGGAG	240
GCCGCAGTAC CCGATGCTAC GATTACAGACA GTAAATGACG GAGAGGCTAT TCTGGTTACT	300
TTCGATAGCG GTATCCTCTT TCGACGAAC TCCAGCACTC TGAGTCCCAA CTCACGCACT	360
GCGCTGACGA AGTTTGCTGC AAACATGAAC AAAAACCCCG ACACGGATAT TCGTATCGTA	420
GGCCATACGG ACAATACCGG CTCCGACAAG ATCAACGATC CTCTGTCTGA GAGACGTGCA	480
GCCAGCGTAT ATTCTTTCTT GAATTCTCAG GGTGTGAGTA TGTGCGCGAT GGCAGCCGAA	540
GGGCGTGGGA GCCATGAACC GGTTCAGAC AATAGCACAG TTGCCGGACG TTCGGCCAAC	600
CGCCGTGTGG AGGTTTATAT CTTGCCGAAT GCCAAGATGA TCGAACAAGC ACAGCAAGGT	660
ACGCTGAAG	669

(2) INFORMATION FOR SEQ ID NO:171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

ATGTCGAAAA AATCGATCCT TCTGCTTTCG TGTCGCTGT GCTTCATTTT TGCTACGAAG	60
GCTGTGACCC CCGTCAGAAA TGTGCGCAAT AGCCAAGTGA ACAGCAAAGC AAAGACCGAA	120
CGTACAAAGC CCTCGGACTC TGTACGGTAC ATTAGCAACA TGATTGCAGA TCGGCTGGAG	180
TTCCGCAACA AGATTTCTTC CGAAAAAGAG GTAAGAAAAG CCGAATATGA AAATCGGCTG	240
GCGATGGAAG CACTCAATTA CCTTGCCATA GATTTATATG GTGAAGATTC TTGGAGCGAG	300
TATGTAAACC CTTTCGTGGG TGCAGGAACC GATGTCGAAA TTCCGAATCT CTATGACATT	360
GATTGCTCTT CGTTCGTGAT GCCCGTCGAA GATAAGCAGG TCACCTCTCA ATTTGGCTAC	420
CGTCGGCGTT TCGGACGGAT GCACTATGGT ATTGATCTTT CAGTGAATCG TGGCGATACG	480
ATACGAGCAG CCTTTGACGG GAAAGTTTCG GTACGCAGCT ATGAAGCGCG TGGCTATGGC	540
TACTACATAG TCTTGCGCCA TCCGAACGGA CTGGAGACTG TGTACGGACA CATGAGTCGC	600
CAATTGGTAG ACGAGAATCA TATCGTTTCA GCAGGACAAC CGATCGGATT AGGAGGCAGC	660
ACGGGTCGAA GCACCGGTCC TCATCTTCAC TTCGAGACCC GCTTCATGGG TATCCCATC	720
AATCCGAGTA CCATTATAGA CTTGCGTAAC GGAGTGCCGC TCCGAGACAT TTACACATTC	780
AAACGAGGGA GCAATTCTCG CTATGCAAAA GCCTCTAAGA CTTCTTCTCG CTATGCAAAA	840

AAAGGGAAGA AAGGCAGACA AGCTTCTTCT CCTATGACCT ATAGAATCAA AAAAGGCGAT	900
ACTTTGGAAA CAATAGCCAA AAGGCACGGC ACTTCTGTTC AGAAACTCTG TGCTACCAAT	960
GGCATTGGCA AGAGTAAAT TTTGACTCCG GGCAAAGCCT TGAGGATCAA A	1011

(2) INFORMATION FOR SEQ ID NO:172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATGGCAAAAA TCAATTTCTA TGCTGAAGGC GTCAGCCTTC CTCGGATCAG AAGACGGATC	60
GTCGGTAAGT GGATAGCCGA AGTATGCAGC CGATATGGGA AAGCGGTGGG AGAAATCTCC	120
TATCTTTTCT GTGATGACGA ATATATCCTG AAAGCCAATC AGGAATTTCT CGATCATGAC	180
TACTACACCG ACATCATCAC CTTCGATTCC TGCGAAGCGG ATACGGTGAA TGGCGACCTG	240
CTTATCAGTC TCGATACCGT ACGCTCGAAT GCCCGTGCTC TTGATCTTCG ATACGAAGAC	300
GAAGTGCATC GTGTCATTAT CCACGGCATA CTGCATCTTT GCGGATTGAA AGACAAGAGC	360
AAAAAGGATG AAGCCCAAAT GCGTGCAGCC GAAGAGAAAG CCCTTGTCAT GCTGCGAGAA	420
ACCATCGGAT CGGAGCTTTC CCTATTGCAT ACA	453

(2) INFORMATION FOR SEQ ID NO:173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

ATGAAGGTAA AGTACTTAAT GCTCACATTG GTTGGAGCAA TTGCACTGAA CGCAAGTGCA	60
CAGGAGAATA CTGTACCGGC AACGGGTCAG TTACCCGCTA AGAATGTTGC TTTTGCTCGC	120
AATAAAGCAG GCAGCAATTG GTTTGTAACA CTGCAAGGCG GTGTTGCAGC GCAGTTCCTC	180
AATGACAACA ACAACAAAGA CCTCATGGAC CGCTTAGGAG CCATAGGTTT TCTTCTGTCT	240
GGAAAGTATC ACAGCCCTTT CTTTGCAACT CGTTTGCAAA TTAACGGAGG TCAAGCCCAC	300
ACTTTCCTCG GAAAAAATGG CGAACAAAGAA ATCAACACCA ATTTTGGTGC AGTCACTTC	360
GACTTTATGT TTGATGTGGT TAACTACTTT GCACCATATC GCGAAAATCG TTTCTTCCAT	420
TTAATTCCAT GGGTAGGTGT TGGCTACCAA CACAAATTCA TCGGTAGCGA ATGGAGCAAA	480
GACAAATGTG AATCACTGAC GGCGAATGTA GGAGTTATGA TGGCTTTCAG ATTAGGAAAG	540
CGAGTAGACT TTGTGATCGA AGCACAAGCA GCTCACTCCA ATCTCAATCT AAGTCGCGCA	600
TACAAATGCCA AGAAAATCTC CGTATTCGAA GATCCCGCAG GACGTATTAT CAATGGATTG	660
CAGGGGATGG CTACAGCAGG TCTTAATTTT CGCCTGGGAG CCGTAGGCTT CAATGCCATT	720
GANCCAATGG ACTACGCACT TATCAATGAT CTGAATGGTC AGATTAACCG TTTGCGCAGC	780
GAGGTCGAAG AACTCTCAAA ACGTCCTGTA TCATGCCCGG AATGTCCTGA AGTAACTCCT	840
GTTACTAAGA CAGAAAATAT ACTGACGGA AAAGCTGTAC TGTTCCGTTT CGACAGCCAC	900
GTTGTGGACA AAGATCAATT GATCAACCTG TATGACGTAG CTCAGTTTGT AAAAGAAACT	960

AACGAGCCGA TTACCGTTGT TGGTTATGCT GATCCTACGG GTAATACTCA ATACAACGAG	1020
AAATTGTCTG AGCGTCGGGC TAAAGCCGTT GTTGATGTTC TGACAGGTAA ATATGGTGTG	1080
CCTTCCGAAT TAATCTCTGT AGAATGGAAG GGCGACTCTA CGCAACCGTT CAGCAAGAAA	1140
GCTTGGAATC GTGTTGTAAT CGTTCGCTCC AAG	1173

(2) INFORMATION FOR SEQ ID NO:174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

ATGACATACA GAATTATGAA AGCTAAATCT TTATTATTAG CACTTGCGGG TCTCGCATGC	60
ACATTCAGTG CAACAGCCCA AGAAGCTACT ACACAGAACA AAGCAGGGAT GCACACCGCA	120
TTCCAACGTG ATAAGGCCTC CGATCATTGG TTCATTGACA TTGCAGGTGG AGCAGGTATG	180
GCTCTCTCGG GATGGAATAA TGATGTAGAC TTTGTAGATC GTCTAAGTAT CGTTCCTACT	240
TTCGGTATCG GTAAATGSCA TGAGCCTTAT TTCGGTACTC GTCTCCAATT CACAGGATTC	300
GACATCTATG GATTCCCGCA AGGGAGCAAG GAGCGTAACC ACAATTACTT TGGAAACGCC	360
CACCTTGACT TCATGTTTCA TCTGACGAAC TATTTCCGGT TATACCGTCC CAATCGTGTC	420
TTCCATATCA TCCCATGGGC AGGTATAGGA TTTGGTTATA AATTCATAG CGAAAACGCC	480
AATGGTGAAA AAGTAGGAAG TAAAGATGAT ATGACCGGAA CAGTTAATGT CGGTTTGATG	540
CTGAAATTCC GCCTATCAAG AGTCGTAGAC TTCAATATTG AAGGACAAGC TTTTGCCGGA	600
AAGATGAACT TTATCGGGAC AAAGAGAGGA AAAGCAGACT TCCTGTAAAT GGCTACAGCA	660
GGTCTAACGT TCAACCTTGG CAAGACAGAG TGGACAGAAA TTGTTCCCTAT GGACTATGCT	720
TTGGTCAATG ACCTGAACAA CCAAATCAAC TCACTTCGCG GTCAAGTGGA AGAGTTGAGC	780
CGTCGTCCTG TTTTCATGCC TGAATGCCCT GAGCCTACAC AGCCTACAGT TACTCGTGTA	840
GTGTTTGACA ATGTGGTTTA CTTCCTATC AATAGTGCAA AGATTGATCG TAATCAAGAA	900
ATCAATGTTT ACAATACAGC TGAATATGCG AAGACCAACA ACGCACCGAT CAAGGTAGTA	960
GGTACGCTG ACGAAAAAAC CGTACTGCG GCCTATAACA TGAAGCTTTC AGAGCGTCGT	1020
GCAAAAGCGG TAGCCAAGAT GCTTGAAAAG TATGGTGTTC CTGCGGATCG CATTACAATT	1080
GAATGGAAGG GCTCATCAGA GCAAATCTAT GAAGAGAACG CTTGGAATCG TATTGTAGTA	1140
ATGACTGCAG CGGAA	1155

(2) INFORMATION FOR SEQ ID NO:175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

ATGGAATTTT TCATGTTATT CATAGCGGCG GTTTCGTTA ATAACGTCGT GCTGTCGCAG	60
TTCTCGGTA TATGCCCATT CTAGGCGTA TCGAAGAAGG TAGACACCTC AATCGGTATG	120
GGTGCAGCCG TGACATTCGT ATTGGCACTG GCTACCTTGG TTACCTTCCT GATTCAGAAG	180

TTCGTTTTGG	ATCGTTTCGG	ATTGGGCTTT	ATGCAGACCA	TTGCATTAT	TTTGGTCATT	240
GCCGCCTTGG	TGCAGATGGT	GGAGATCATA	CTCAAGAAAG	TATCTCCTCC	CCTCTATCAG	300
GCACTGGGTG	TATTCTTGCC	CTTGATTACG	ACGAACTGCT	GTGTGCTCGG	TGTGGCTATT	360
TTGGTTATCC	AGAAGGATTA	TACCTGCTC	CAGAGCTTCG	TCTATGCAAT	ATCCACGGCT	420
ATCGGTTTCA	CCTTGGCAAT	GGTTACTTTC	GCAGGTATTC	GAGAGCAACT	CGATATGACC	480
AATCTCCCCA	AAGCTATGAA	GGGAATACCT	TCGGCACTCT	TGGCTGCCGG	TATATTGGCT	540
ATGGCTTTCA	TGGGCTTCAG	CGGTATCGCC				570

(2) INFORMATION FOR SEQ ID NO:176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

ATGTTATTCA	TAGCGGCGGT	TTTCGTTAAT	AACGTCGTGC	TGTCGCAGTT	CCTCGGTATA	60
TGCCCATTCT	TAGGCGTATC	GAAGAAGTA	GACACCTCAA	TCGGTATGGG	TGCAGCCGTG	120
ACATTCGTAT	TGGCACTGGC	TACCTTGGTT	ACCTTCCTGA	TTCAGAAGTT	CGTTTTGGAT	180
CGTTTCGGAT	TGGGCTTTAT	GCAGACCATT	GCATTTATTT	TGGTCATTGC	CGCCTTGGTG	240
CAGATGGTGG	AGATCATACT	CAAGAAAGTA	TCTCCTCCCC	TCTATCAGGC	ACTGGGTGTA	300
TTCTTGCCCT	TGATTACGAC	GAACTGCTGT	GTGCTCGGTG	TGGCTATTTT	GGTTATCCAG	360
AAGGATTATA	CCCTGCTCCA	GAGCTTCGTC	TATGCAATAT	CCACGGCTAT	CGGTTTCACC	420
TTGGCAATGG	TTACTTTTCGC	AGGTATTTCGA	GAGCAACTCG	ATATGACCAA	TCTCCCCAAA	480
GCTATGAAGG	GAATACCTTC	GGCACTCTTG	GCTGCCGGTA	TATTGGCTAT	GGCTTTCATG	540
GGCTTCAGCG	GTATCGCC					558

(2) INFORMATION FOR SEQ ID NO:177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

ATGAAACAAC	TAAACATTAT	CAGCTTCATC	ATTGCTTTCC	TATTCTTAGG	AACGAGCGCA	60
TCGGCTCAGC	AATCGGGCGG	ATCCGTTACA	GGTACCGTAG	TGGACAAAAG	CTCAAAAGAA	120
CCTATCGCAT	ACGTACAAGT	ATTCTGCAAA	GGAACTACTC	TCGGAACCTC	CACGGATGCA	180
AACGGAAGCT	ACTCGATCAA	GGGAATCCCT	TCGGGTAATC	AAACTATCGT	AGCCCGACTC	240
ATGGGTTACT	CCACTTGCGA	AGAAAAAGTA	CATATAGAAA	AGGGTGGTTC	CCGCCACGTA	300
GACCTCTATC	TGACCGAAGA	GATTCTCTCT	CTCGATGGGG	TAGTGGTATC	TGCCAATAGA	360
AACGAGACTT	TCCGCCGCTA	AGCACCCTCG	TTGGTAACGG	TACTGTCCGC	GGAACTTTTC	420
CTCAAAACCA	ACTCTACCAA	CCTGAGTCAG	GGACTTAAGT	TCCAGCCCGG	TCTGCGCGTG	480
GAGGACAACCT	GTCAAGAACTG	CGGTTTCAAC	CAAGTTCGTA	TCAATGGACT	CGAAGGAGCC	540
TATTGCAAAA	TTCTTATCGA	CAGCCATCCC	ATCTTCAGTT	CGCTTGCCGG	TGTCTATGGC	600

TTGGAGCAGA	TGCCTGCCAA	TATGATCGAA	CGTGTAGAAG	TAATTCGCGG	TGGAGGTTCG	660
GCTCTGTTCG	GCTCTAATGC	TGTGGGAGGC	GTTATCAACG	TAATTACGAA	AGAACCCTTT	720
CGCAATTCCG	CCGAGATCAG	CCATTCTACG	ATGACCTTCG	ACCACGCGAA	AGGGTGGGGG	780
AGCTTCCAAA	ATACGACCCA	GTTCAACGGT	TCTATGCTGA	CGGAAGACCG	CAAAGCCGGT	840
GTCATGGTAT	TCGGCCAAAC	CAACTACCGT	CCCGGACAGG	ATATAGACGG	CGACAACTTT	900
ACCGAACTAC	CCAATCTGCG	CAACCGCTCG	CTCGGTTTCC	GCTCATACTA	TAAGACCCGT	960
CTCTACAGCA	AAGCAACCCCT	CGAATATCAC	AGCATGCAGG	AGTACCGTCG	TGGTGGCGAC	1020
AGACTGGACA	ATCCTCCTTT	CGAAGCCAG	ATAGCGGAAT	ATCTCCAGCA	CTATATCAAT	1080
GGCGGAAGTT	TCAAATTCGA	TCAGGGCTTC	AGCGGTGGCA	AGGATTTCTT	CAGTCTGTAT	1140
GCTTCAGCAC	AAGACGTTC	GCGTCGTAGC	TACTACGGGG	GTGGCGACTA	TACCGAAAAA	1200
CTGCTGAACG	GAGCAGTTCA	GAGTGGGAAG	ACCGAATCGG	ACGAATACAA	CGATGCTTTC	1260
ACGGCTCTTA	CTTCCTACGG	GACTACCAAG	GGATTCGATT	TGCAAGGAGG	AGGTATGTAC	1320
CGTCATACCT	TCGGAGAAAA	CTGGGACTTT	ACCGGCGGAC	TCGAATATAT	CTACGGCCAA	1380
CTCGATGACA	GAAGCGGCTA	CAGACCGAGC	AAAATAGATC	AGAATACCTC	TACTTTTAGT	1440
CAGTACGACC	AGCTCGAATA	TAAGACGGAG	AAGTTAAGTG	CCCTTATCGG	AGCACGTATC	1500
GACTATGTTC	TCTCAATCA	GGATGGCAAA	CGCTATATCG	ATCCGCTCTT	CATTTTCAGT	1560
CCTAGAGCCA	ACGTACGATA	CAATCCCAAT	AAGAATCTCA	GCTTCCGACT	CTCATACAGC	1620
GAAGGATTC	GCGCTCCTCA	GTATTTTCGAT	GAAGATCTGC	ACGTAGAGTT	GGCCGGTGGT	1680
ACTCCTATCA	GCCGTGTCTT	TTCCCCCAAT	CTGAAAGAAG	AACGTTTCACG	AAGCATCAGT	1740
GCTTCTTTTCG	ATTATTACCA	CAGAGCCGAC	GAATGGCAAT	TCAATATCAT	GGGAGAAGCC	1800
TTCTCCACCT	TTATCAGCAA	TCAGTTCAAA	CCATCCGATA	AGGTCGAAAC	CACGAGCGAT	1860
GGCAAAGAAT	GGATCATTCG	TACCATCTAC	AACGACAAGG	ATGGAGTATC	GAAGGTATAT	1920
GGTGTGAATC	TGGAGGGAAG	AATCGCCTAC	AACAAATCGT	TCGACCTCCA	GCTCGGCGGT	1980
ACATGGCAGA	GAAGCCGCTA	CGGAAGCATC	TATACCGCTG	TGGAAGCGGA	CAAAACAACG	2040
GGACAAGCCG	AGATCTCTGT	GAAAGACTAT	GTACGCACTC	CGAATCTGTA	CGGCTATTTC	2100
GTTGTCTACG	TACGTCTCTAC	CGAGCACTTC	GCCATCAATC	TCTCCGGTAC	ATTACAGGGC	2160
AAAATGGATG	TAGTACACGA	AGCCTATGAA	GGCGATATTC	CCGCAGAACA	CATAGCTCCG	2220
GACGGATCGT	TCGACTTTGA	AATGAATGGT	CAGCAATTCA	AAGGTTTGGC	CGAAGGTCAT	2280
GCCAAGCTCG	TCAAGACTCC	GGCCTTCGCC	GATATAGACC	TCAAGCTGAG	CCACGACTTC	2340
CACCTTGCTT	CACTATGAC	CTTGGAATTG	AATGCCGGAA	TACAGAACAT	ATTCAACAGC	2400
TATCAGAAAG	ACACGGACAA	GGGACCGGGT	AGAGCTTCTA	CTTACGTATA	CGGTCCTATG	2460
CAGCCCAGAA	GGATTTTCGT	CGGTACAAAG	ATCAATTTC			2499

(2) INFORMATION FOR SEQ ID NO:178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGTACAAAA	AGATTATTGC	CGTAGCAGCT	CTCTTCTGCG	CCAGCATAGG	GATCCTGAAA	60
GGACAGTCCT	CGGATCTGAC	CCCTCAGGAT	ACTATATATA	GCCCTGAAAT	ATCCTATGCC	120
AAGCCTATT	ATAAGACCAT	AGCATCTATT	GAGATCGAGG	GAATGAGGTC	TTTCGATGAC	180
TTTGTCTTGC	GCAATCTTTC	AGGCTTGGCT	GTAGGTGATG	AAGTCCTGAT	TCCTGGAGAT	240
GCCATGTCTG	CTGCCGTGAA	TAGAATTATG	CGTCAGGGCT	ACTTCTCAAA	TGTGCGAATC	300
ATCGCGGATA	AATATGTCGG	CAATAAAGTC	TATCTGAAAA	TCATTGTCAC	TGAACGTCTT	360
CGCATCAGTA	AGGTTACTTT	TAGCGGGGTA	AAGAAGTCTG	AGAGAGAAGA	TCTTGAAATG	420
AAAATCGGTC	TTGCGGAGGG	GATTGAGATG	ACCAGAAATA	ATGAAGACAA	GGTCAGGCAA	480
ATCGTACAGA	AGTATTTTAG	TGAGAAAGGT	TATCGCGATG	CCAGCATACG	GATAACGCAG	540
GAACCGGATC	TTTCCAAAGA	TGGCTTTGTC	AATGTGCTTA	TCTCGATTGA	GAAGAAAAGC	600
AAAACCAAGG	TGAATGAAAT	TTATTTTCC	GGCAACAAGG	CCCTTAGCAA	TCATAAGCTA	660
AGAATGGCGA	TGAAGAACAC	CAATGCCAAA	TTCAGTCTTA	GAAAGCATAT	TCGCTCATCT	720
TTCTTGAAAC	TTTTTAGTAC	TCATAAGTTT	GTGGAAGAGA	GCTACCGTGA	AGATTTGGTC	780
CGATTGATAG	AGAAGTATCA	GGAATATGGA	TATCGTGATG	CTGAAATACT	GACCGACAGT	840
GTCTGTAAGG	CTCCTGACGG	CAAAAGAGTG	GATATTTATC	TCAACATCGA	AGAGGGGCAG	900
AAGTATTATA	TTAAGGATGT	CAACTTTGTG	GGCAATTCAC	AATATCCATC	GGAGTATTGT	960
GAACGAGTGC	TCGGAATAAA	ATCCGGAGAT	GTGTACAATC	AGAGACGATT	GGCTAAGCGT	1020
CTCAATGAAG	ATGAAGATGC	TGTGGGGAAC	CTGTACTATA	ACAATGGCTA	TATTTTGTGG	1080
TGGGTCGATC	CCGTGGAAC	AAATGTAGTG	GGGATTCTG	TTTCGCTTGA	TATTCGTATA	1140
GCGGAGGGGA	AGCAGGCCAA	TATCAATAAG	GTGATCATCA	AAGGAAATAC	TGTCGTGTAC	1200

GAAGACGTAG	TACGCCGAGA	GCTTTACACA	AAGCCCGGCC	AGCTCTTTAG	TCGCGAGGAT	1260
ATCATTAACT	CTATTCTGCT	CATCAATCAG	CTTGGGCATT	TCGATGCCGA	AAAACTTATT	1320
CCCCGTCCGA	TTCCCAATCC	CGAAACAGGA	ACAGTGGATA	TAGAGTATGA	TTTGGTGCCG	1380
CGTAGCAGTG	ACCAATTGGA	GCTTTCTGTC	GGTTGGAGTC	AGTCCGGACT	TCTGTTCCGA	1440
GGAGCCATTA	AGTTCACGAA	CTTCTCTGTC	GGCAACTTGC	TCCATCCCTC	GATGTATAAG	1500
AAAGGGATCA	TTCCGCAAGG	GGATGGGCAA	ACACTATCAC	TGAGTGCTCA	GACCAATGGA	1560
AAGTACTATC	AGCAGTATAG	TGTCACATTT	ATGGATCCAT	GGTTTGGGGG	CAAGCGGCCG	1620
GATATGTTCA	GCTTCAGTGC	ATTCTATTCC	AAGACTACGG	CGATTGACTC	CAAGTTCTAC	1680
AATAGCAATG	CCGGCAACTA	CTATAATGCC	TACTATAATA	GCTACTACAA	CAACTATAAT	1740
AGTTATTACA	ACGGTATGTC	GAACTATACC	GGCGACCTCT	ATACTCAGGC	CAGCGATCCG	1800
GATCGTTTCG	TTCAGATGTT	AGGTACTTCG	ATCGGTTACG	GTAAGCGTTT	GACTTGGCCG	1860
GACAATTGGT	TCCAGATTTA	TACTTCTCTG	AACACACCT	ACTATAGACT	GCGAAATTGG	1920
AGCTACAATA	CCTTCCAAAA	TTTCCATCAT	GGCTCGGCTA	ATGATCTCAA	CTTGAGCTG	1980
CGTCTCTCTC	GTAATTCCAT	CGATAATCCT	ATTTATACCA	GAAGCGGATC	GGATTTTCATG	2040
GTTTCTGTTG	CTGCTACTCT	TCCTTATTCT	TTGTGGGACA	ATCATGACTA	TGCCAGCCAG	2100
AACTTCAGCG	TAAGCGATCG	TTACAGATTT	ATCGAGTATC	ACAAGTGGAA	GTTTAGAGGA	2160
CGAGTTTTTA	CTCCATTGCT	CAATCCTGCT	ACGCATAAAT	ATACACCGGT	GCTCATGAGT	2220
CGAGTGGGAA	GAGCAGTTCT	TGTTTCGTAT	AATTCCAATA	AGAAATCTCC	TTTCGGTACT	2280
TTCTATATGG	GAGGTGATGG	TATGTCCAGC	TATTATGGTG	GCTACATGAA	TGAGACTATA	2340
GGTTTGCGTG	GTTATAAGAA	CGGATCTATT	GCCGGTAATA	ACTACGACTA	TGCATATGCT	2400
TATATGCGGC	TTACGATGGA	ACTACGTTTC	CCGATTCTGT	TTGAAAATC	ATTCAATGCG	2460
TGGCTCTTAG	CTTTTGCCGA	AGCAGGCAAT	GCGTGGCGCA	GTATCGACAA	TTATAATCCC	2520
TTTAACCTGA	AGCGATCGGC	CGGTGTAGGA	TTGCGTGTAA	CGTTACCGAT	GGTCGGAATG	2580
CTCGGTATCG	ATTGGGGATA	TGGCTTTGAC	CGTCCGGACA	ATTCTCTACA	GCGAGGAGGA	2640
AGCAATGTCC	ACTTTGTGCT	CGGACAGGAG	TTC			2673

(2) INFORMATION FOR SEQ ID NO:179

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...522
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

ATGAATGGCG	ATATGAAACG	GTTTTTGATT	TTGATCGGCT	TTGCACTGGC	GGTAGCTTTC	60
TCCGGTTTTT	CCCAAAAGTT	CGTTTTGGTA	GATATGGAAT	ATATCCTCAG	GAATATTCCCT	120
GA CTATGAGA	TGATGAACGA	ACAGCTGGAA	CAGGTGTCCA	AGAAATGGCA	AAATGAAATC	180
GAAGCTCTCG	AAATGAAGC	CCAATCTATG	TATAAGAAAT	ATCAGAGCGA	TCTCGTATTC	240
TTGTCTGCTG	CACAGAAGAA	AACCCAAGAA	GAGGCTATCG	TAAAGAAAGA	GCAGCAAGCA	300
TCCGAGCTCA	AGCGGAAGTA	TTTCGGCCCG	GAGGGGGAGC	TGTATAAGAA	ACGCTCCGAT	360
CTGATGAAGC	CTATTCAGGA	TGAGATTTGG	AATGCTATCA	AAGAGATTGC	CAAGCGTAAC	420
AACTATCAGA	TGGTGCTTGA	TAGAGGTACG	TCCGGAATTA	TCTTTGCCAG	TCCGTCTATT	480
GACATTAGCG	ACCTTGCTACT	GAGCAAGATG	GGCTTTAGCA	AG		522

(2) INFORMATION FOR SEQ ID NO:180

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

```
ATGAAACGGT TTTTGATTTT GATCGGCTTT GCACTGGCGG TAGCTTTCTC CGGTTTTTCC      60
CAAAGTTTCG CTTTGGTAGA TATGGAATAT ATCCTCAGGA ATATTCCTGA CTATGAGATG      120
ATGAACGAAC AGCTGGAACA GGTGTCCAAG AAATGGCAAA ATGAAATCGA AGCTCTCGAA      180
AATGAAGCCC AATCTATGTA TAAGAAGTAT CAGAGCGATC TCGTATTCTT GTCTGCTGCA      240
CAGAAGAAAA CCCAAGAAGA GGCTATCGTA AAGAAAGAGC AGCAAGCATC CGAGCTCAAG      300
CGGAAGTATT TCGGCCCGGA GGGGGAGCTG TATAAGAAAC GCTCCGATCT GATGAAGCCT      360
ATTCAGGATG AGATTTGGAA TGCTATCAAA GAGATTGCCA AGCGTAACAA CTATCAGATG      420
GTGCTTGATA GAGGTACGTC CGGAATTATC TTTGCCAGTC CGTCTATTGA CATTAGCGAC      480
CTTGTAAGTA GCAAGATGGG CTTTAGCAAG                                     510
```

(2) INFORMATION FOR SEQ ID NO:181

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 489 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

```
ATGAAGAAAT TTTTCTCAT GCTTCTGATG GCTCTTCCTT TGAGCCTCTT GGCACAAAAG      60
GTGGCAGTGG TAAACACTGA GGAGATCATT TCCAAATATG CGGAACAAGT AGCTGCTACC      120
AAACAGCTCA ACGAATTGGC CGAAAAGTAT CGCCTTGATC TCAAGAGTAT GGACGATGAG      180
TTTGCCAAAA AGACAGAAGA ATTTGTAAAG GAAAAAGACT CTCTACTGGA GAACATCCGC      240
AATCGTCGTC AGCAGGAACT TCAGGATATT CAAACTCGTT ATCAGCAGTC ATACCAAACG      300
ATGCAGGAGG ATTTGCAAAA GCGCCAACAA CAGCTTTTGT CTCCTATCCA ACAAAGGTG      360
GCTGATGCCA TCAAGAAAGT GGGTGACGAA GAAAACTGTG CCTACATCAT GGAGGCCGGT      420
ATGATGCTTT ACACCGGAGC TACTGCTATT GACTTGACCG CAAAGGTAAA AGCGAAACTC      480
GGAATCAAG                                     489
```

(2) INFORMATION FOR SEQ ID NO:182

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

```
ATGAAGGAAG CTATTCCTCG AAAGAACAAG TATATAAAGC TCAACGGTAT ATACAGATTG      60
TCATTCATTC TGCTATGCTG CCTGCTATGC TCTCAGGCAG CTATGGCACA AGGCGTCAGG      120
```

GTATCGGGCT	ATGTGCTCGA	CCGTGGGGAA	AAGCCGATCC	CGTTCGCCGG	AGTCAAAGTG	180
CGTGGTACGG	GGACAGGCGC	AACGACGAAT	CTGAAAGGAT	ACTACGAGTT	TCGGATGAAG	240
GCCACGACGG	ACAGCATCAC	GATCGAGTTC	AGCTCCATGG	GGTACCAAGG	GGTAAGTCGC	300
AGCTTTCCGT	CTCTGACCAA	GGACACTCGG	CTGAATGTTC	GTTTGGCAGA	GGCCGAGATG	360
GAGCTTTCGA	GCGTGACGGT	ACAGGCCACA	AAACGCAGAC	TCAACACGAT	GGAGCGCGTC	420
AATACCCGAG	ACCTTCGTGT	CAATGCAGGG	CCTACGGGAG	GGGTGGAATC	GCTCATCAGT	480
ACCTACGCAG	GAGTAACGCA	GAACAATGAA	CTAAGCTCGC	AATACTCGGT	TCGCGGAGGA	540
AGCTACGATG	AGAATATGGT	CTATGTAAAC	GGAGTGGAGG	TTTATCGCCC	GCTGCTGGTT	600
CGCTCTGCAC	AGCAGGAAGG	TCTGAGCTTC	GTCAATCCGG	ATCTGACACA	ATCCGTACAG	660
TTCTCCCGCG	GAGGGTTCAC	GGCCGACTAT	GGCGACAAGA	TGTCTCCCGT	ACTGGATATT	720
CGCTACAAGC	AACCGCAGGA	GAAGGAAGGA	GCGGTACTCC	TCGGGATGCT	ACAATCGAGT	780
GCCTACTATG	GCAGCAGTGC	CGGAGCCTTC	AGCCAAATCA	CGGGTGTACG	CTACAAGAGT	840
GCCAAATCGC	TCTTGGGCAC	TACGGACACG	AAAGCCGAAT	ACGATCCGAT	CTATGCGGAC	900
GGACAGACAT	TCATGACGTA	CCGTTTCAGC	CCCAAGCTGT	CGGTTAGTTT	CCTCGGCAAT	960
ATTTTCGAAA	CTCGCTACAA	GTTTGTCCCT	CAGACCCGTG	AGACGAGCTT	CGGTACACTG	1020
AGCGATGCCA	AAAAGTTGAA	GATCTTTTTC	GACGGTCAGG	AACAAGATCG	TTTCCTGACC	1080
TACTTCCGTG	CCTTCAGCAT	GAACTTCGTG	CCGGACGACA	AACAGCGGCA	TACGGTTACG	1140
CTTTCGGCCT	TCAACAGTAA	CGAACGGGAG	ACCTACGATA	TTCAGGGAGA	ATACTTTCTG	1200
AACGATGTGC	AGTTCGGGCG	GCTTCGATGG	CTTCGGGCTC	AGAGAACTCC		1260
AACGGCTTGG	GCATCGGGCG	CAATCACGAG	CATGCGCGCA	ACAGGCTGAG	CTACCGCGTG	1320
CTGAACATGG	GTTACAGAGG	GGAGATGAAG	CTGAACGAGA	AGCATCGCCT	GCAAGCCGGC	1380
GTATCGGCAC	AGATGGAGAA	AATAGCCGAC	CATATCAGCG	AATGGGAACG	GAGGGATTTCG	1440
GTAGGATACA	ACCTACCTCA	CTGAGAGACC	GTATTGCTGA	TGTACAATAA	CCTATATGCC	1500
GATACGCAGA	TGAGGGGAAC	GCGCTTGTCT	GCATTTCGTAC	AGGATCGATT	CAACTTCAGC	1560
ATGGGAGGAG	GTACATTTTC	TCTCATTCGG	GGTATCAGAG	CTTCGTGGTG	GAGCTTCAAC	1620
AAGGAGTTTG	TCGTACAGCC	ACGTATCAGC	GTGGGTATT	CTCCCCGAAAG	CAACCCGGCT	1680
TTGGTACTGC	GTGCAGCCGC	CGGACTTTAT	TATCAGGCAC	CGTTTTACAA	AGAGCTAAGG	1740
CAGACGCATA	AGGATGCCGA	AGGCAATAAC	GTGGTTGTCC	TCAACGAGAA	GATCCGCTCT	1800
CAGGGAGCTT	TTCACATTCT	CGCAGGAGCA	GACTATACCT	TCGAAATGGG	GGGGCGAAAA	1860
TACAAGTTTA	CGGCAGAGGC	TTACTACAAG	AGCCTGTTC	ACATCAACCC	GTATATAATA	1920
GAGAACGTGA	AGATCCGCTA	TCTGGGCGAA	AACATCGGTT	CGGGTTATGC	TGCGGGTATC	1980
GATCTCAAGC	TCTTCGGCGA	ACTGGTACCC	GGAGTGGATT	CGTGGCTGAC	GGCTTCCATT	2040
ATAAAAGCCC	GTCAGAAACT	GGATGGCTAC	GGTTCTTTAC	CACTGATGAA	CGCACCCACT	2100
TACAATTTCT	CCTTCTCTCT	TCAGGAGTAC	GTGCCGGGCA	ATAAACGCAT	CACAGCCACC	2160
CTGCGGGCTG	CATAAGCGG	AGGATTGCCC	CAGCTCAATC	CGAGCAAAGG	GCTTAGCTCG	2220
CCGGCCTTTA	CCGCACCGGC	CTATAAGCGT	GTCGATCTGG	GGGTAATGTA	CAAATGGCTC	2280
GACCCGGATG	ACTCCTTTGC	CGGCCGAAGC	AAATGGCTAA	TGGGAGTAAA	AGGGGCCTAC	2340
ATAGGGGCTG	ACCTCTTCAA	TCTGTTTCGAC	ATGACCAACG	TCAATTCTTA	CTACTGGGTG	2400
TCGGATGCCT	ACCAACAGCA	ATACGCCGTA	CCGAACCTACC	TGACACGCCG	CCAATTCAAC	2460
CTGCGTCTCC	TCGTCAATT	C				2481

(2) INFORMATION FOR SEQ ID NO:183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

ATGTACAGCG	GACATCATAA	AATCCATTAT	CCTTTTCTTA	TCCTGTTGGT	ATGCCTTGCT	60
TTTGCTGCCT	GCAAGAGCGT	GAAGTTGAAA	GATGCGGAGA	AGGCACATGA	TCGCCAAGAG	120
TATACCAAGG	CTGCCGATAT	GTACAATACA	TTATACAGGC	GTACCCGACG	AAAGCAGGTG	180
GAGATGAAAG	CTTATACGGC	TTCGGATCC	GGTGAAACT	ATCGTGCCGC	CGGCAGACAA	240
GCCAAAGCTT	TGCGTGGCTA	TCTGAATGCC	AGACGCTACG	GGTATCCGGA	TTCTGTGGTA	300
CTGCTCCGTT	TGGCACAGAC	TTATCAGCAA	GGAGGTAAC	ATAAGGAAGC	CGAGGTACTC	360
TTCCGTGGAT	ATCTGGAAGC	TTATCCGAAA	AGTTATTTTG	CAGCTATCGG	TTTGGAGGGG	420
TGTCTCTTTT	CCGCCAGCA	AAAGGAATAT	CCTACACGTT	ACCGGATACG	GCGAGCTGCC	480
GAGTGAATT	CGGCACGGG	CGACTTCGGC	CCGGCCTATG	CACCCGATGC	TTCGGCTCTC	540
TATTTACAT	CGAGCAGAAG	CAAAGACGAC	GTTTGGATA	ATAGCAGCAT	AACGGGACTG	600
AAACCCAACG	ACATTTATAT	CATCAAACGA	GATGCACAAG	GACGATGGGG	ACGTCCCGAT	660
AGCGTGTCCG	GAGGAATCAA	CCTCCATGG	GATGAAGGCG	TGCCAACGAT	CACGCCCGAT	720

GGTAGTACCA	TATATTATAC	GTTGGCGCAG	CAAGGAGCCG	ATTACGACCG	TACGGTACAG	780
ATCTATTCCG	CCGCTCGGAG	CGGAGAAGGC	GGTTGGAGCA	ACGGTTCGCT	CGTGGACATT	840
ATGCGCGATT	CGCTCCGTAT	GGCTGCTCAT	CCCTCTATGT	CGGCATCCGG	CGATTACCTG	900
TATTTCGTCA	GCAATATAGG	CGGTAGCTAT	GGCGGCAAGG	ATATTTATCG	TGTCAAGGTG	960
TCGGATCGTT	CTTATGGTTC	ACCGGAGAAT	TTGGGGCCTG	ATATCAATAC	GCCGGGGGAC	1020
GAAATGTTTC	CCTTCATAGA	TGGGGATAGT	ACCCTTTTCT	TCGCTTCGGA	CGGACACGCC	1080
GGTCTGGGAG	GACTGGATAT	TTTCAAAGCC	ACGCTGGACT	CTACCGGCCA	ATGGCATGTA	1140
GTCAATATGG	GACAACCGGT	CAATTCCTCT	GCCGATGATT	TCGGCTTGGC	TGTGGAGCCT	1200
AAAGGCAAAA	ACAAAGAAGA	AGCTTTGCCG	GACAACGGAG	TCAAAGGTGT	ATTTTGTTCC	1260
AACCGAGGCG	ATGCACGCGG	ATGGCCGCAC	CTCTTCCATT	TCGAACTGCC	GGCTATCTAC	1320
ACCGAGATTG	AAGGTTATGT	GATGGACAGA	GAAGAAAATC	CCATAGCCGG	AGCCACTGTC	1380
AGGATCGTAG	GCGAACGCGG	CCCCGTAGGA	CAGGGATTTCG	TGACTACTCG	TGACGATGGC	1440
TCCTATAAGA	TGAGCGTGCA	GGGCGATACT	CGCTATGTAA	TGCTTGCCGG	AGCATCGGGT	1500
TATTTGAATC	AGTACGTAGA	ACTCAAGACC	GATACCGCCA	AGCAGAGTGA	GACCTACTAT	1560
TGGGACTTTT	TCCTTGATC	GCGTGAGAAA	GCCGAGGGCT	TGCAAAATAT	TTTCTATGAT	1620
TTCGATAAAG	CTACTCTTCG	CCCCGAAAAGC	ATGAAGAGCT	TGGACGAACT	GATTTCGTATC	1680
CTCACGGACA	ATCCGGATAT	TCGGATCGAA	TTGGGTTCGC	ATGCCGACAG	GAAAGGCCCC	1740
GATGCTTACA	ACCTCGGACT	ATCTGACCGC	AGAGCCAAAT	CCGTGGTGGA	TTACCTCACG	1800
AGTCGTGGCA	TACGGGCCGA	CAGGCTTACG	TGGAAAGGCT	ACGGTAAGTC	TGTCCCAAG	1860
ACGGTGACAG	CCAAAATTGC	CGAACGGCAC	GATTTCTCTGA	AGGAAGGCGA	TGTGCTCACC	1920
GAGGAATTCG	TAGCACCTTT	GACCGAGGAG	CAGCAGTCAG	TCTGCGACCA	ACTGAACCGT	1980
CGTACCGAGT	TCCGTGTGAT	CGAAGAAGAG	TTGCGT			2016

(2) INFORMATION FOR SEQ ID NO:184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

ATGAAAAAGT	TTTTCTTCGC	GCTACTATCG	ATTGGTATTT	CAGCGCAGGC	TTTTGCCAAG	60
ACGGACAACG	TCCCGACAGA	TTCGCTACGA	GTACACAATC	TTCAGACCGT	CACGGTCTAT	120
TCTACACGCA	CGGCCGTACC	TCTGAAAAAG	ATACCGGCCA	AGATGGAACT	CATCTCATCG	180
CGCAACATCA	AGCAGTCCGG	CTTTAACAA	ATGACCGACA	TCCTCAAGAC	GCAAAGTTTCG	240
CTCGATGTCA	TACAATACCC	GGGCTTTAGT	TCGAACATCG	GTATCCCGCG	TTTCAAGCCC	300
TCCGGCAAGT	ATGTAACCGT	ATTGGTAAAC	GGCATCCCTG	CGGGAACGGA	CAATATCTCT	360
ACGCTCAACA	CGAGCAACAT	CGAACAAATC	GAGATCCTCA	AAGGCCCGTT	CTCTTCCATC	420
TACGGCACCA	ATGCCATGGG	CGGTGTGGTG	AACATCATCA	CCCAACAATC	CAAGGACAAG	480
ATCCATGGCA	ACGTTTCTCT	CTTCGGCGGT	AGCTACCAGA	CCATGGCCGG	ATCATTCAAC	540
TTGGGTGGCC	GCTTCGAGGA	TATTTTCTCA	TTCGATCTTA	GTCTGGGCTT	GGACAAGCAG	600
AACAAGGACT	ATAAGACCGG	ATCAAAACAAT	TTCTATCCCC	TGAGCAAACCT	GGAAGAAGCT	660
ATAGTAGATG	TAAATGCTAC	CAAAAACAAG	AAAATGAAGG	GGAGCGACTA	TACTGTAGCA	720
ACGGGACGTC	TGCGTTTCGG	TATCGACTTC	ACGCCCCGAAT	GGTCGCTGAA	TCTGTATCAA	780
AACGTATTCC	TCGGAGATGC	GATCCCCGTA	GGAGGATCTA	TATGGGGCGT	TTACGGAGAA	840
TCCAAAAAAA	ATCTGAATCG	TTCTTCGACC	TCTTTTCGAGC	TGCTCGGCAA	ACATGGCTGC	900
CACACGCTTC	AATTTCTCCC	CTACTTCAAC	ATAGAGAAAT	CGGAGAACTA	TAACAATGCC	960
GATCCCAACG	GTTTTCATCAA	CTACAAAAGC	GACTACTACA	CCTATGGTGC	CCTACTCCAG	1020
GACAAGATTT	CCTTTGGAGG	ACAAAATATC	GTAATCGGTG	TCGACAGCCG	AAACATGACG	1080
ATGGAGTCAG	AAAGATTCTGA	GCAGGCAGGA	GTGAATACAA	AGCCATACAA	CCCCGGATAT	1140
GCCACGAACA	ATATCGGTTT	GTTCCGACAG	GCCAATTCTT	ACCTGCTGAA	CGATGCTCTA	1200
TCGATATCTG	CCGGTGCACG	TGCCGACTTC	ATGTTCTTTG	ACCTGAAAGC	GAACGAGTAT	1260
CTCAACAATG	AAGCCAAACA	GGAACTCAT	AACGTAATCA	ATCCGAATGT	CGGAATCAAA	1320
TATGAGTTTG	TGAAAGGCCT	TACAGCTCAT	GGTACATTTC	GTAGTGCAAT	CAGTGCTCCC	1380
GATGCTTTCC	AAAAAGCAGG	CCAATACGTA	GGCCCCGTTTC	GCACGACCAT	AGGCAATCCT	1440
GACCTGAAAC	CCGAAAAGTC	CATGACCTGG	GACTTCGGTA	TCGGATACAG	CAATGCACGC	1500
TGCGGGATCC	AAGCCGACGT	AACCTTAACC	TATTTCCACA	CCGACCACAA	AGATCTGATC	1560
TTGTCCAGCC	CTGACTATGC	TAATAATATC	ACCACATACA	TCAATGCCGA	CAAGGCTCGT	1620
ATGAGCGGTA	TCGAGGCCCT	TTTGTCTTAT	GACTTCGGCA	GCCTCTTGTC	CAACAAGTTC	1680
TCTCTCCGCG	CATTTGCGAA	TGCCACGATC	ATGCTCAATT	CCGAGATGAA	GAAAAGCCAG	1740
ACCGATGCCC	CTTGAGCGGA	AATGTACTAC	GTTTCGAAGC	AGAACATCAC	CTTCGGTATC	1800

GAATATCGTG	GCAAAGAAGG	ACTTGAAGTG	ATGCTCAACG	GTCGCTTCAT	GGGACGCAGG	1860
ATCGAGCAAA	ACTGGTATGC	TTACTACCCC	GAAGTTCGCC	CCGAACTCCA	GCAACTGCTT	1920
GCAGCAGAAG	AGCCTGAATT	GGCTGCTCAG	GGACTGCTCC	GTCATCCGCA	AGCAATGGTG	1980
TTCAATGCCT	CTGCTTACTA	CCACATGAAC	AAGTATCTCA	CCTTCGGTGT	GAAC TTGAAC	2040
AACATCTTGG	ATGAGCTTTA	TACGGAGAAA	GACGGCTACC	ACATGCCCCG	ACGTAACATC	2100
ATGGGTAAAG	TTATGGTCAA	CTTC				2124

(2) INFORMATION FOR SEQ ID NO:185

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

ATGAACAGGT	TTTCAAATCA	TTGGCCCTGC	ATCCTCGTGG	GGTTTGTACT	CTGGTTTGTA	60
TCGGCGAGTC	GGACTGTGGC	ACAAAACGCC	TCCGAAACGA	CGGTATCGTA	CGATACGGAT	120
ACCGCCGTAC	TCTCCGAAGC	CGATGTGCTT	CGGATCGCTC	TTAGTGAGAA	TGCCACAGTG	180
AAAGTGGCCG	ATATGGATGT	GCGCAAACAG	GAATATGCAC	GTAGGGCAGC	ACGTGCCGAT	240
CTCTTCCCGA	AAGTAGACCT	CAATGGCGTT	TACAGCCATA	CGCTAAAGAA	GCAGGTCTTA	300
TATATAGATA	TGCCCCGTTT	CAGCAGTAGC	GAAGGTATCG	AAATGGGGCG	TACACACAAT	360
ACGCAAGGAG	GGGTGAACGT	CTCCATGCCA	TTGGTGTCCG	CACAGCTTTG	GAAAAGCATT	420
GCCATGACCG	GAGAACAGCT	CGATCTGGCT	CTGGAGAAAG	CTCGCAGCTC	CCGAATCGAT	480
TTGGTGGCAG	AGGTGAAGAA	GGCTTACCTC	AGTGTATTGT	TGGCCGAGGA	CTCTTATGGC	540
GTATTCAAGC	GCAGCTATGA	CAATGCTCTG	GCCAATTATA	AGAACATATC	CGACAAGTTC	600
GATCGTGGAC	TTGTGGCCGA	GTATGATAAG	ATTCGAGCCA	ATGTACAGGT	ACGCAACATC	660
GAGCCTAACC	TCTTGCAAGC	GCAGAACTCC	GTAGCCCTTG	CTCTCTGGCA	GCTCAAGGTC	720
CTGATGAGCA	TGGAAGTGGA	AACTCCGATC	AGACTCTCCG	GTTCAATTGC	CGACTATAAA	780
GAACAAGTCT	ATACCGGCTA	TTTTGCCGCC	GATACGCTTA	TTTCCAACAA	CTCCTCCCTG	840
CGTCAGCTCG	ATATACAGCG	TCGTCTGGCT	GTCAAGTGAG	ACAAGCTGAA	CAAGTACAGC	900
TTCTTGCCCTA	CACCTCAATCT	GGGAGGGCAG	TACACCTATT	CGCTCAACAG	CAACGACATC	960
AAATTCTGGG	GCGAGGGACA	ACGCTGGACG	CCTTTCTCCA	CCATATCGCT	CAGCCTGTAC	1020
ATTCCTATAT	TCAATGGAGG	CAAACGTCTG	TACAACGTGA	AGCAAAGTGC	TTTATCGATC	1080
CGTCAGATCG	ATCTGCAACG	ACGCCACATA	GAGCAATCCA	TCCGAATGGG	AATCAAGAAC	1140
CAAAATGACC	GTCTGCGTAC	CTGTATGCAG	AGATTTGTGG	CCTCGGAAGA	GGCTGTCCGA	1200
AGTGCAGAAA	AGGGCTATCA	GATAGCAGAG	AAACGCTATC	AGACAGGCGA	AGGCACTCTC	1260
GTCGAGCTCA	ACGATGCCGA	TGTGGCTCTT	TTGCAGGCTC	GACTCAATTA	TAATCAGGCC	1320
ATATTCGACT	TTATGACCGC	AAAGGCCGAA	TTGGACAAGA	TGAACGGCAT	GGGGATTCCC	1380
GAACAA						1386

(2) INFORMATION FOR SEQ ID NO:186

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

```
ATGTGGGGGG ACAGCCATGG AGTGGCGCCG AACCAAGTGC GCCGAACGCT GGTGAAGGTA      60
GCCTTAAGTG AATCCCTTCC TCCGGGTGCA AAACAGATTG GTATCGGATT CTCTCTCCG      120
AAAGAAACGG AGGAAAAAGT CACCGCCCTA TATCTCCTTG TGAGTGATTG TTTAGCGGTG      180
CGCGACTTGC CGGACTACAA AGGGCGAGTC TCTTACGATA GCTTCCCGAT CTCAAAGGAA      240
GATCGTACCA CAGCCCTTTC TCGGATTTCG GTAGCCGGAC GCCGCTTCTT TTATTGGCT      300
GCGGATATAG GGCCTGTTGC TTCTTTTCC CGATCCGATA CGCTGACTGC CCGTGTGGAA      360
GAGGTGGCTG TCGATGGCCG CCCTTTGCCG TTGAAAGAGC TGTGCGCTGC CTCCCGTCGT      420
CTGTATAGGG GGTATGAGGC CCTCTTTGTA CCCGGTGATG GCGGATCGCG GAACTATCGT      480
ATCCCGGCCA TTTTGAAGAA GGCTAATGGA AACTCATAG CGATGGCCGA CAGACGAAAA      540
TATAATCAGA CGGATCTGCC GGAGGATATA GATATAGTCA TCGGCGCAG TACGGACGGA      600
GGGAAATCGT GGAGCGATCC CAGGATTATC GTACAGGGAG AGGGGCGCAA TCATGGCTTT      660
GGCGATGTAG CCTTGGTGCA AACCCAAGCA GGAAAGCTCC TGATGATCTT TGTGGGTGGA      720
GTAGGCCTGT GGCAGTCTAC CCCCATCGT CTTTATATATC GGAAAGTCGG      780
GACGAAGGAC TGACTTGTGC GCCTCCTCGG GATATAACCC ATTTTCATCTT CGGCAAGGAT      840
TGTGCCGATC CGGGACGCGG TCGCTGGTTG GCCTCCTTTT GTGCTTCGGG ACAAGGGCTT      900
GTGCTGCCAT CCGTCTGAT GAGTCTTGTG GCTGCCATCC GCGAATCAGG GCAGGAGTAC      960
GTCCTGAACA ACTATGTCTT CTATAGCGAC GATGAGGGCG ATACATGGCA GCTTTCCGAC     1020
TGTGCATACC GCCGTGGCGA TGAGGCAAAG CTTTCATTGA TGCCCGATGG CAGGGTACTG     1080
ATGAGCATAA GCAATCAGGG ACGGCAGGAG AGCCGACAGC GTTCTTTCGC TCTCTCCTCC     1140
GACGATGGCC TTACTTGGGA GAGAGCCAAG CAGTTCGAGG GCATCCATGA CCCCAGCTGT     1200
AATGGAGCTA TGCTTCAAGT GAAAAGGAAC GGAAGGGATC AAGTGCTGCA CTCCTGCCT     1260
CTCGGCCCGG ATGGGCGTCG CGATGGAGCT GTCTATCTCT TCGATCATGT CTCCGGCCGC     1320
TGGTCCGCTC CCGTTGTTGT CAATTCAGGA TCGAGTGCCT ACTCGGATAT GACTCTGCTG     1380
GCGGATGGAA CGATCGGTTA TTTGTCGAA GAGGGCGATG AGATCTCATT GGTTTTCATT     1440
CGGTTCGTCC TTGACGATCT CTTGATGTC CGGCAA                                1476
```

(2) INFORMATION FOR SEQ ID NO:187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

```
ATGAAAAAAG AAAAAGTTTG GATTGCGATC GTCGCCGGTT TGGCTTTCGT ATTGGGCCTT      60
TATGCTCTTG GCCGCAAGTG CGCTCAGCTA CGCCGCTCTC AGCCTTCGGT GACTGTGACC      120
GGTATGGCCG AGCGTAATTT CAAATCCGAT CTGATCGTTT GGAAGTCTTC GTACCGAGTC      180
CAGATGATGG ATCTCGAATC GGCCTACAAG GCTTTGAAGG AAAACAGAT ATTGGTAGCA      240
GACTATTTGA AAAACAAGCA GCTGCCGAT TCGTCTTATA TCTTCTCAAG CGTAGCCATC      300
TCTAAAGAAT ACAACTACTA TTACGATCCT CGGCAGGAAC AAAACGTCAG GACCTTTGCC      360
GGGTATCTGC TCAGCCAGAC AGTTACGGTG ACCTCACAGG ACATCGAACA TGTGGAGAAA      420
ATATCTCGCG ATATAACGGA GCTGATCAAT CAGGGGGTAG AGATTACCTC CGACCGTCCG      480
GCCTATTACT ACACCAAGCT CAATGATCTG AAGGTGGAGA TGCTGCGCAA TGCCTCCGAA      540
GACGCTTTCA ATCGTGCTTC GGTCAATGCG GAGGGGAGCG GTTCCTCCGT GGGTAAGATG      600
CTATCTTCTT CGATGGGCGT GTTCCAGATA GTGGGGCTCA ACTCGAACGA AGATTATAGC      660
TGGGGAGGTT CGTTCAATAC GTCTTCCAAG ATGAAGACGG CAAGCATAAC GGTAAAGGCT      720
TCTTTCGCTT TGAAG                                735
```

(2) INFORMATION FOR SEQ ID NO:188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

ATGAAAAAAA	CAATTGCAAT	TATCGCCTCA	GCCCTCTTGG	CTTTAGGAGC	CGTCGGCTGT	60
AAGAAAAATG	CTGACACTAC	CGCTGTGAGT	GAAAAGGATA	GCATAGCCTT	GTCCATGGGT	120
ATTTTGTACG	GACAGGATTT	TGCCAATCAG	TTCGAAATGT	CCCGCTTGCA	AGGCCAGCCG	180
ATTGATTCGG	TAGCTTTCTT	GGACGGTTTC	AAATATGGTA	TCGATACGAC	GCGCTTCTCG	240
TACAATCTGG	GAGCCATCTA	TGCTTCCAAT	ATAGCTCGTC	AGCTGGCTCA	TGATTCCATC	300
GATATCGACA	AGTTCTATGC	AGCCATGCGT	GCGGCTCTTC	TTAAAGACAC	CGTATCTATC	360
GCCATGAAGC	CTGCAGATGC	ACAGGCTTTC	ATGCAACGAA	TCCAAGCCAA	AAAGCAGCGA	420
GAAAACAATA	TGAAGCAGTT	TGGCCAGAAC	ATCGAAAAGG	GTAATGAATA	CATCGATACC	480
TTTAAAAAAG	AAGATGGTGT	AACTGTTACG	ACAACTGGTC	TGGCATACAA	GACTCTTCAG	540
GAAGGTACGG	GAGCTACTCC	CTCTTTGGCC	GATACTGTAC	GTGTCAAGTA	TGTGGGTACT	600
CTGGTCGATG	GTAAAGAGTT	CGACAAAAAC	GAAGAAGGAA	TCGAATTTCG	CGTTACCGGT	660
GTGATTAAAG	GCTGGACGGA	GATGCTCCAA	CTCATGAAGG	TCGGTCAGAA	AGTTCGCGTG	720
GTAATCCAC	AGGAGCTGGC	TTATGGGGAG	ACCGGCAACT	ATACCATCGA	ACCGTTCTCT	780
ACCCTGACGT	TCGAGATGGA	ACTTATCGGG	ATCAAGCCCG	GGAAAAAG		828

(2) INFORMATION FOR SEQ ID NO:189

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ATGAAAGTAT	TACGGCAAGT	ATTCTCTCCC	ATCCTTTTTG	TCCTACTGAC	AGGTGCCTGC	60
TCCACCACAA	AGAATCTGCC	GGAAGGCGAA	CAGCTGTATA	TCGGAATGGG	CAAGACACAG	120
ATACTCCGGC	AGGACAAGAG	CCACGCCGGC	CAACAGGCTC	TGACCGAAGT	GGAGAGTACA	180
CTGAAAGTTA	CACCCAATGG	AGCTATTTTC	GGCAGTGCAA	GTGCCTCCTT	ACCCAAGATA	240
CCATTCCGGC	TATGGCTATA	CAACAGCTTC	GTGGGGGATT	CCACTGTGAT	TTCGAAATGG	300
ATATTCGACA	AGTTTGACG	CAAGCCGGTT	TTCATCAGTC	AGGTCAAATC	CGATAGCCGG	360
GCTAAGGTGG	CGACGAACAT	CCTCCGCGAA	CACGGGTACT	TCGATGCTAA	AGTAAAAAGC	420
AGTGTGACCA	CTCTGAAAAA	GGACTCGCTC	AAAGCCAAAA	TCTCCTATAC	GGTGGATATG	480
GCCTCTCCTT	ATCATTACGA	CAGCATCATT	CCCTTACCGA	TCAGCACTTT	CCCCGACAGC	540
ATTCTGGCTT	ACAGGCAGAC	TCCGTCTTTG	ATCAGGAAAG	GAGACCAGTT	CAATTTGGCA	600
AAGCTGCACG	AAGAGCGTCA	GACCATCAGT	GCCTTGCTGA	GAGACAATGG	TTACTACTAC	660
TTCCGCCCCAC	AGGATATTAT	CTACGAAGCC	GATACCCTCC	TCGTAAGAGG	TGCCGTATGC	720
CTGCGAGCCA	AGCTCTCGGA	AGATACTCCA	CCCCAAGCCA	TGCGCCCGTG	GAGGATAGGG	780
AAACGGACAG	CAGTCTGTCT	CGGAATGAAC	GGAGAAAGCC	CGACAGACTC	GCTCGAAGTG	840
GAGGATATGA	AAGTCTTTTA	CTATCGTAAA	ATGCCGGTTC	GCCCCAAGAT	TTTGCCAAA	900
CGCTTTCGTT	TCTTCTCCGG	CAATCTGTAT	CGGCAGAAAG	ACGATGAGAC	GACACGCAAA	960
TCCTTGGGTC	GTTTGGGAGC	CTTCTCCGTT	ATCGATCTCA	ATTTTTCGCA	ACGCGATTCC	1020
ATTTCCGGCC	TTTTGGATGT	GCGACTGCTA	ACCACCCTCG	ACAAACCTTG	GGATGCATCA	1080
TTAGAGACCT	TGTTACAGAG	CAAAAGCAAT	GACTTCATCG	GTCCCGGACT	GAATTTTGCT	1140
CTTGCTCGGC	GCAATGTATT	CGGCGGAGGA	GAAAATCTTT	CTTGGAATAT	CGGTGGATCG	1200
TATGAGTGGG	AGACCGGCAA	TCGTCCCGAA	AATAGCAGCA	ATCGGCTGAT	CGATATAAAT	1260
TCGTACAACA	TGAATACGGC	CGTGAACCTC	TCGTTTCCCT	CGATTGTATT	TCCGGGCTCG	1320
CTGGATAAAT	ACTATTACTA	CCCCACGACT	ACGACTTTTC	AGGCTTCTGC	CACCGCGCTG	1380
AACAGGGCAC	ACTACTTTAG	CATGTACTCT	TTCGGCTTTT	CGACCACCTA	CGAATTTTCAG	1440

CCCTCCAAGG	AACACCGGCA	TGCTATTTTC	CCGCTCAAGC	TCAACTACAA	CCTCCTGGGG	1500
CATCAGACAG	AAACTTTTCCA	GGCCATTACG	GCGAACAAATC	CGCCCCTGCT	GCTCAGCCTT	1560
CAGAGTCAGT	TCCTTGGTCA	AATGGGGTAT	ATCTATACGT	TCAACAAATC	CGTTTCAGAG	1620
AAAAGTCCTC	ATCATCTTTG	GATGCAATTC	GGACTATCCG	AGGCAGGCAA	TCTCCTGAAT	1680
CTGATCTATC	TGGCAGCCGG	CAAGAAGTAC	AGCGACACCA	AGAATTTTCGT	CGGCGTCCCC	1740
TTCTCTCAGT	TCATCAAAGC	CACGGGAGAA	CTGCGCTATT	CCTATACCAT	AGACCGCAAT	1800
CAGTCACTGG	CAACCCGTTT	CGGGACAGGC	GTGATATATA	GCTATGGCAA	TATGCGAGTG	1860
GCACCCTATA	GCGAGCAGTT	CTATGTAGGC	GGTGCCAATA	GTATCAGAGC	TTTCACCGTC	1920
CGTAGCATCG	GCCCCGACG	GTTCAATCCG	GATTCCGACA	ATCAGTATTC	CTATTTGGAT	1980
CAGGTGGGCG	AATTCAAAC	CGAAGCCAAC	GTGGAATATA	GAGGCAAGCT	TTTCGGGGAT	2040
CTCCACGCAG	CGTTTTTCCT	CGATGCGGGC	AACGTTTGGC	TCTTGAGGGA	GGATTCTTCC	2100
CGTCCGGGCG	GTGCTCTGTC	CGAAGTGGA	TCGGTGAGCA	ATTTCTTGAA	TAGCATCGCT	2160
CTCGGCACCG	GTGTCGGCCT	TCGCTACGAT	CTGGCATTTT	TCGTGGTTCG	TGTCGATGTC	2220
GGCTTCGGTC	TCCACCTTCC	TTACAATACG	GGTAAGAAAG	GTTACTACAA	TATCCCACGC	2280
TTTAAGGATG	CCATCGGTTT	CCATTTGGCT	GTGCGCTATC	CCTTC		2325

(2) INFORMATION FOR SEQ ID NO:190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

ATGTCCTCGC	ATTCCGTTTC	GATCTAATC	GGCATTGCCG	GCTGCTTGCT	CCTCATGCTT	60
GCTTCCTCCT	GCTCGGTCAC	CCGTTATGTG	CCGGACGGTA	GCAGACTATT	AGACAGGGTA	120
ACGATCGCAA	GCGAAACGGG	CAGTATCGCT	CTGCCGGAAG	ATATTCCGGA	CTATACCCTC	180
CAGCAACCCA	ATTACAGACT	GTTCCGGATG	ACTCGCTGGC	TACTGCGCGT	CTATAGCAGC	240
TCGAATCCGA	ACAGCAACAG	CTGGTGGAAC	CGTTCGCTCC	GGAAAATGGG	CGAACCGCCT	300
GTCTCATCG	ATTCTGTCTC	CACCGATCGT	ACTGCCAACC	GTCTGGCAAA	GGCGATGGCC	360
GGCGATGGCT	TTCTCGATGC	TACTGCTCGT	GCCGTGGTAG	ACACCGGCTT	GTACAAGAAA	420
GCTCGCATTA	CTTATCTGAT	TCAGCCCGGA	AGCCGTTATT	ATATACGCAA	TATGGCTTTG	480
GATGTGAAGA	ATCCACTCCT	TCCTCCCCTT	GCGCTTGGA	ATTCGCTTCC	TTCGGCATAC	540
AAGGTCGGGA	TCAGCGAGGG	TTCTCCCTTG	TCGCCCATCG	TACTCGATGA	AGAGAGAAAG	600
GCGATAGCTC	GTCATATGCG	CAACAACGGC	TTCTGGAAGT	TCTCCGCCGA	GGATGTTTAT	660
TATGAAGCAG	ATACTACCGT	TTCAGGAGGA	TCGGGTACGA	AATCTGCCGA	TCTGAAATTA	720
GTGGTCAATG	GCATCGGGCG	TTATCCATAT	CGGATCGGCA	GGGTATTCTT	TCATGCCGAT	780
TATGATCCTC	TCGAATCGGA	CTTCAGAGTT	CAGGAGCTGC	CACGTATCGA	TTCGATTTCG	840
CGTGGCGATT	ACACTGTTTA	CTATGGGAGT	AGGGGACGTT	ATATCCGGGC	ATCGGCTCTC	900
ACGCGGTCCG	GTCCCGTTAC	ACCGGAGCT	TTTTTCTGCG	AGGATGATGT	GGAACGCTCT	960
TATATCAAGC	TGAATGCGCT	CCCTATCGTT	CGGAACGTGA	ATATCCGATT	TGTGGAGCAC	1020
AATGGTAAGG	ATGAGATTGC	TCTGGCGGAT	AGCTCTCGCC	TTGTGGACTG	CTATATTCTT	1080
ACCGTTCCGG	CCAAGAGCAA	ATCGTTTCGAA	GCCGAAGTCC	TCGGCACCAA	TTCCGCTGGA	1140
GACTTCGGGG	CGGCTTTGTC	TCTCGGTTTC	ACCGATCGCA	ATTTGTTTCG	TGGGGCGGAG	1200
ATGTTCAATA	TCAAACCTCA	GGGTGCTTAC	GAAGCCATTC	GCAAGGGTTC	GCACAGCTTC	1260
ATGGAATATG	GGGTGGAAG	CTCGCTCCGT	TTCCCTCGTC	TCCTCTTCCC	ATTCATTCTT	1320
GACGAAACGC	GCCGGCGGCT	ACGGGCATCC	ACGGAATGGA	AGATCGGGTA	TAATTACCAG	1380
ACACGTCCGG	AGTTTGATCG	GGTGATTCTC	TCCGCTCAAC	TCAATTATTC	ATGGCAGACC	1440
TACCTGCACA	ATCGTCTGCG	TCATACGATC	CGCTGCTGG	ATGTCGATTA	TCTCCATCTC	1500
CCGTACATCG	ATCCCGACTT	CGCCCAATCC	CTTCCGCTCA	CGACTGCACT	GTATAACTAC	1560
ACGGAGCAGT	TTATCCTCGG	CTCGGCATAT	ATACTGAACT	ATACCACGGC	TTCGTCCATG	1620
GAGCGTAGCG	TATCCAATCC	TTTTACGGCA	CGGTTTCAGTA	TCCAGACAGC	CGGCAACCTG	1680
CTGCAAGCCA	TTTCTTATCT	GACCGATTCT	CCGAAAGACG	AACACGGGTT	GTATAAAATG	1740
TTCGGTCGTC	ACTATGCTCA	GTTCTGTCAG	CTCGATCTCG	ATCTGGCTAA	AACCGTTCTT	1800
CTCGAAAAGG	ACAATACTTT	GGCACTGCAT	CTGGGTTTCG	GACTGGCTTT	CCCTTATGGC	1860
AATGCTCGCC	ATATACCCTT	TGAGTTACGT	TACTTTGCCG	GAGGATCGAA	CAGCGTTTCGC	1920
GGCTGGAGTG	TCCGTACCTT	CGGCCCGGGG	AGTATGAAGA	TGACTCCGGA	CAAGACCTTC	1980
TTCGATCAGA	TGGGTGATAT	TCGTCTGGAT	CTGAATGTCT	AATACAGGAC	AAAGCTGTTC	2040
TGGAAGTTTC	GCGCAGCAGC	TTTTGTCTGAT	GCCGGCAATG	TCTGGACGAT	AAAGGAGTAT	2100
GAGAATCAGG	AGGACGGTCT	TTTTCGTTTC	GATCGCTTCT	ACAAGGAAAT	AGCTTTGGCC	2160
TACGGTCTGG	GGCTTCGTCT	CGACTTCGAT	TATTTCTCTG	TGCGGCTGGA	TGCCGACTG	2220

AAAGCCTACG ATCCTCAGCA GACAGGGCGT TACAAATGGG CTATCACACG CCCAAACCTT 2280
TCTTCCAATT TCGCTTGGCA CATTGCAGTA GGCTATCCGT TC 2322

(2) INFORMATION FOR SEQ ID NO:191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

ATGAGAAAAA	GAATTCTACA	ACTTTTCTCG	ACCGCATTGC	TGCTGGCATT	AGGCTCCTCT	60
CTCGCCATAG	CGCAAACAGT	GGTGACCGGT	AAGGTGATCG	ATTGAGAAAC	GTCCGAACCG	120
CTCATCGGTG	TATCCGTAAAG	CACCGGTGAG	GGAGCATCCC	TCCGCGGTGT	AACCACCGAT	180
ATGGATGGTG	GCTTCCGATT	CGAAGTACCG	GCCAAATCTG	TCTTGACTTT	CCGTTGCGTA	240
GGTTATGCTA	CCGTAACTCG	CTCTATAGGC	AGAGGTTCTC	AAGAAGACCT	CGGTACGATT	300
CTCCTCGATC	CCCAGGCCAT	CGGCTTGGAT	GAGATTGAGG	TAATAGCCTC	TGTGGTGCCC	360
AAAGACCGTA	TGACGCCGGT	ACCCGTTTCC	AATATCCGTG	TGGCTGATAT	TCAGGCAGCA	420
TCGTTGAATG	TGAATTTC	CGAAGTGGT	AAATCCACTC	CCTCTACCTA	TACGACAAAA	480
GGAAACCGAG	GTTTCGGTGA	TGGTCGTACC	AATGTGCGTG	GATTTCGACAC	TTACAACCTC	540
GGTGACTCA	TCAACGGAGT	TCCTGTCAAT	GGTATGGAAG	ACGGGAAAGT	ATATTGGAGC	600
AATTGGAGTG	GTCTGATGAA	TCAAGCCAGT	ACCATTGAGA	TTGAGCGCGG	ACTCGGAGCC	660
TCCAAGCTCG	GTATCAGCTC	GGTAGGTGGT	ACGATGAACA	TTATCACGAA	GACTACGGAC	720
GCCAACACCG	GTTTCTCCGA	ATATTCTGTA	ATGGGTAAATG	ATGGATTGCA	CAAAGAATCG	780
TTCTCCATTT	CTACGGGTAT	GAACGACGGT	TGGGCTATCA	CCATTGCAGG	CTCCCATATG	840
ACGGGTCTGG	GTTATGTGAA	GGGGCTGAAG	GGACGTGCAT	TCTCTTACTT	CTTCAACGTT	900
TCGAAGAAGT	TCAATGAACG	TCATACCTCT	TCTCTTACCG	GATTCGGTGC	ACCACAATGG	960
CACAACCAAC	GTTCTTCCAA	ATATTCTGTA	GCCGACTATG	ACAAATACGG	CATCCGTCAC	1020
AATCAATCCT	TCGGCTATCT	GCGAGGCGAA	CTGACTCCTA	CGGCTTATGC	TTACAATACG	1080
TACCACAAGC	CCCAGTTCTC	GCTGAACCAC	TTCTGGAAGA	TGGATGAAAA	TACCTCTCTT	1140
TATACcgCAN	CCTACGCATC	TTTGGCTACC	GGTGGAGGTC	ATCGCGCTTA	TGGAAAGAAC	1200
AGTAAGTGGG	TATTGATCAA	TACAACACCC	GGACAACCTT	ATGAACAAAC	AAAGGTGACT	1260
CCCGATGGAC	TTATCGACTA	CGATGCCGTA	CTGGCTGCCA	ATGCTGCGGC	GAGCAATGGC	1320
TCGGAAGCAA	TTTTTGCCCT	TGGCTCCAAC	TCTCACAAAGT	GGTTCGGTCT	ACTCTCTTCA	1380
TTCAAGAAGA	AACTTAATAG	TTGCTGACT	TTGACAGCCG	GATACGATGG	GCGTTACTAC	1440
CGTGGCGACC	ACTATGACAA	GATCACCGAT	CTGCTCGCGG	GTAGCTACTA	CATAGAGGAT	1500
CCCAAGACAA	AGCTCGCATA	CCATGCGGAA	GGTCAGCAAC	TGAAAGTGGG	TGACATTGTA	1560
AATCGGGACT	ACACAGGCGA	AATCATGTGG	CACGGCCTCT	TCGCACAGAT	GGAGCATTCG	1620
TCCGAATGGA	TCGATGCATT	CGTATCAGGA	TCTATCAACT	ACGAACATA	CCGCAATCAC	1680
AACTATGGCG	GTAGCAAGTC	CACCGGCTAC	CTGCCCAGCG	TATCGCCGTG	GAAAAGCTTC	1740
CTTCCGTGGA	GTGGCAAGGC	AGGTCTGAGC	TACAAGTTCTG	CACAGGGACA	CAATGTATTC	1800
GCCAATGGCG	GTTTCTTCAC	ACGTGCACCA	CTCTTTGGCA	ATATCTATGC	TGCGGGGGCT	1860
ATCATTCCCA	ATGACAAAGC	CAATATGGAA	AAGGTGCTTA	CAGGAGAGGT	CGGCTATGGA	1920
TTACGAAATC	ACAAAAACTT	CGAGTTCAAT	ATCAACGGAT	ACTATACGAA	GTGGATGGAT	1980
CGCGTGACCT	CGAAGAGAAT	CGGAAACGAG	TATGTTTATC	TCAATGGCGT	TGATGCTGTT	2040
CACTGTGGGG	TAGAGGCTGA	GGTCAGCTAT	CGTCCTATTC	GTGAGATCGA	CCTTCGCGGT	2100
ATGTTCTCTC	TCGGTGACTG	GACTTGGCAA	AACAATGTAA	GTTACACTTC	TTACGACGAA	2160
GCCGGCAATG	AGACAGGCGA	GGATATAACC	TATATCAAGG	GTCTTCACGT	CGGAGATGCA	2220
GCACAGATGA	CGGCTGCTGT	ATCGGCAGAC	ATAGAGCTGT	TCAAGGGTTT	CCATGTCTATA	2280
GGTAAGTACA	ACTTCCTTGG	CAAGAACTAT	GCAGGATTCA	ACCCCGCAAC	GCCTAATGCA	2340
CAGCAGTACG	AAGCGGATGG	CAAAGAAATC	GTGGAATCAT	GGAAGTTGCC	CGATGTAGGT	2400
CTGTTGATC	TGTTCTGCATC	CTACAATTTC	AAGCTTGGTT	CACTCAGCAC	CACATTCTAT	2460
TTCAACATGG	ACAACGTAGC	CGACAAGCGA	TATGTGAGCG	ATGCCGACGA	CAATATCATC	2520
GGTAAGAAAC	ACGATGAGGC	TTCGGCTCTC	GTATGGTACG	GTTTCGGCGC	CACTTGGTCT	2580
ACCGGTATTC	GTGTAAACTT	C				2601

(2) INFORMATION FOR SEQ ID NO:192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

```
ATGAAGTTT CAATCCGCCT TTCTCTCTGC ATCATCTTTC TCCTCTCTGC ATTTATCCTG      60
CCTGCTCTCG GACAAAAATC CAAGCAGGTA CAGCGACTTG AGAAGCAACG TAAGGAGGCC      120
CTCAAAGCCA TCGAAAAAAC CGATCGCGAA CTACGAAATA CCAAGAAAGA CAAGCAAGAC      180
AAACAAAGC ATCTCAACCT CCTGAACAAG CAGGTTGCTC AACGCAAGCA GATGGTACAA      240
CTCTTGGACA ATGAGGTCAA AGAGTTGCAA TCCGACATTG ATTCCATGAC GGGTGTATGT      300
CATCAGCTCT CTGTAGAAGA GAAAGCCCGA TCCGATGAAT ATGCCCAAGC TCTACAGTCT      360
ATGCAAAAGC GGAAACGCTC GTTGGATCGC ATCCTTTTCA TTTCATCGGC CAAGAGCTTT      420
GACGAAGGCA TCGCAGGAT GCGTTTCTTG GAACAATACG CTTCTGCATA CAAGCTGGCA      480
TCTGTCCGGC TCGCGGATAC AGCTAGCAAG TTGGAGACTG AACGTGCGAC TGTAGAAGAC      540
GCCAAAAGG AGAAAGGACA TCTCTTAGTC ATCAGAGAAG AGGAAAAAAA GAAACTCGAA      600
GGACAGCAAG CCGAGCAACG TCGGCAGGTG CAGGCTTTGG GAGCCAAACA AAAAGACTTG      660
GAAGCGCAGC TCGGAAAGCA GAAAAAGCAA GCCGAAGCTC TGAACAGAAA GATCGAGAAA      720
CAGATTGCCA AGGAAATAGA AGCTGCCGAA CGTCGTGCTC GAGAAGAACG TGAACGGTTG      780
GCACGCGAAG CCAAAGCCAA GGGTAAGCCG GTTCCTGCCG AACCGGAACG GAAGGCGGAG      840
ACCAAAGCGG GCTATGCTAT GGATGCCTCT GAGCGTGCTC TCTCGGGCAG CTTTGCACAG      900
AACAAAGGTC GCCTGCCCGG CCCCGTTCGC GGCAGATACC GAATCGTAAG CGACTTTGGC      960
GTGCATCAGC ACAGTGAGCT GAAAAAGTA CAAGTTAATA ATGGAGGTAT CGACATCGCT     1020
GTAGCAACAG GATCCGATGC TACCAGCGTA TTCGATGGTG TAGTGTCAG TGTATTCTGT     1080
ATACCCGGTT ATAATTCGGC CGTAATGGTT CGTCACGGTA ACTATATCAC GGTTTATGCG     1140
AATCTGAGCA AAGTGTATGT AAATTCGGC ACTCGTGTTA AAACGGGTCA GGCTCTTGTT     1200
CGTGCCTATA CGGATCCCTC CAACAACAG ACCATTATC ACTTCGAAAT CTGGAAAGAA     1260
CGCAGCAAAC AAAACCCAAG ACTATGGTTA CGA                                     1293
```

(2) INFORMATION FOR SEQ ID NO:193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

```
ATGAAAAAGT ATTTGTTATA TGCCTCGTTG CTAACGAGTG TTTTGCTCTT TTCCTGTTCA      60
AAGAACAAATC CTAACGAGCC GGTGGAAGAC AGATCCATCG AAATTTCTAT AAGGGTAGAT      120
GATTTACCA AAACGGGTGA GGCAGTACGC TATGAAAGGA ATCAAGGAAG TGCTGCCGAA      180
AGGCTCATTA CCAATCTTTA CCTCTTGTG TTCGATCAGT CAGGGGCGAA TCCGGCGAAA      240
TACTATATTA CCGGTAACAC TTTCACCGGA GGGACCTGGC TTCCTGACGA TATGAAGGTG      300
AAGTTGGATA TGACACAATC CGAGGCCGGA GAGCGCAAAG TATATGTCGT AGCCAATGTT      360
GATAATGCGG TTAACACGGC TCTTGATGCT GTCGCTAACG AAAGCGATTT GCAGACTGTA      420
AAGAGGACGA CTGCAATGCC GTGGTCGACC GATATAGCCT CTCCTTTCTT GATGTCCGGA      480
AACAAAGACAC ACGACTTCTT GGCCAATCGT CTTTGGACA ATGTGCCCCT TGTGCGTGCC      540
ATTGCCAAGG TGGAGCTGAA TATCTCGCTG AGTGAGAAAT TTCAGATTBT GCCGATAATT      600
GTCAATGGTA GTTTGAGTGA GTTCAAGTTC AGATACGTAA ACTTCGACAA GGAGACCTAC      660
```

GTAGTGAAGC	CAACGACCAA	GCCGGACAAT	CTCATTAGTT	CTGCTAATGG	TGTTTGGCCT	720
CAGATTACAG	ATTGGACTGT	ATGGGGTGCT	TCCTTAAATA	CTTCTCCTGC	TCCGGATGCG	780
GGCACAGGTT	ATACATTGGA	TGCAAATGGC	AAGGTAACGG	CACTACGGAT	TGTTACCTAT	840
CTGAATGAGC	GCGATAGCAA	AGGGGCTACG	GTAGAGGTCG	CATTGCCTCG	TGTGGATGAT	900
GGCACCCCTT	CTCCTCCGGA	ATTGCGTCCG	GAGCTTTATC	GTTTGCCTTT	GCCGGACAAG	960
ATCTTGC GCA	ATCATTGGTA	CAAGTATGAA	GTCGAGATT			999

(2) INFORMATION FOR SEQ ID NO:194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGATCAGAA	CGATACTTTC	ACGATATGTA	TCCTCGAACT	TTTGGAGTCG	GGGAGCTACC	60
TTTTTTTTTCA	CGATTTTCCC	GGCCTTCATC	CTCGCCGCTA	CTGCTTTGCC	GGCTTG TGGA	120
GGGGGTACTG	CTTCAGGCTC	CGATCGTACG	CTGGCTGTGA	CCATCGAGCC	ACAGAAATAC	180
TTTCATCGAGT	CCATTGCGGA	TAAGTCGGTG	CAGGTGGTGG	CATTGGTACC	GGCCGGCAGC	240
AATCCGGAGG	AATACGACCC	TTTCGCCTACC	GTGATGAAGC	GTTTGTCCGA	AGCAGATGCC	300
TACTTCTATA	TAGGAGGACT	GGGGTTCGAG	CAAAGAAATC	TCGCTGCCAT	TCGGGACAAT	360
AACCCTAAGC	TCCCTCTTTT	CGAAATGGGC	AAAGCCTTGG	CGGATGCCGG	AAGTGCAGAT	420
CTCCACGGCT	CCTGCACAGA	TCATTCTCAT	ACAGACCTGC	ATGCCCATGA	TCCGCACTAT	480
TGGAGCAGTG	TGGTAGGGGC	AAAGGCACTC	AGTCGTGCTG	CATACGACGC	GCTTGTGGAG	540
CTTTATCCGA	ACGAGAAAGA	CAAAATGGGAC	AAAGGGCACG	ACCGTCTCAA	CGGACGTATC	600
GACAGCGTGA	AGAGACTCGT	CGATACCATG	TTTGCCAATG	GCAAAGCAGA	CAAAGCCTTC	660
GTATATATAT	ACCCATCGCT	CAGCTTTTTT	GCCCAAGAGT	TCGGCCTGCG	GCAGATCGTC	720
ATAGAGGAAG	ATGGGAAAGA	GCCTACGGCT	GCCCACCTTC	GTCGTGTGAT	CGATCAGGCA	780
CGTGCCGATG	GTGTCAGAAT	CGTATTTATC	CAACCCGAAT	TTGAAACGCG	TCAGGCGGAG	840
GACATCGCAC	GCGAGATCGG	TGCTCGTCCG	GTAAGGATCA	ATCCTCTGCG	CAGCTCGTGG	900
GAGGAGGAAA	TTTTACATAT	TGCTCGCGCT	TTGGCTCATG	AACGG		945

(2) INFORMATION FOR SEQ ID NO:195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGATCGGAA	AAAAAATCTT	TTTTATCCTG	CTGGCGCTCA	TTGCGTTCAG	TGGGCTGAAC	60
GCAGCGACAG	ACACTGAGTT	CAAGTACCCG	ACCGATGCCA	ATATCATCGG	TCACGTCAA	120
GACAGCAAGA	CGGGTGAACA	CCTTGTCGGT	ATCACTATTG	CTATCAAAGG	CACTACCTTT	180
GGTACATCTA	CAGATGCAAC	GGGGCACTAC	TATCTTCGTA	ACTTGCCTCC	GGGTGAGATC	240
ACTTTGATTA	TGCGTGGCAT	GGGCTATAAG	AGCCAGGAGC	GCGTAGTCCG	CGTAGAAAAG	300

GACAAGACTA	TCGAGGTGAA	TTTCGAAGCA	GAAGAGGATG	CCATCAATCT	GGACGAAGTC	360
GTGATTTCCG	CCAACCGCGA	ACTGACGCTT	CGCCGTCTTG	CTCCTACTCT	GGTAAATGTA	420
TTGAACGAAA	AAGTCTTCTC	GCAAGTCAAT	GCTTCTAACC	TGGCTCAAGG	CTTGTCATTC	480
CAGCCGGGAG	TTCGTGTAGA	GAACAACGTG	CAGAAGTGTG	GTTTCAATCA	AGTTCGTATC	540
AATGGACTGG	ATGGTCGTTA	TGCACAGATC	CTCATCGACA	GCCGTCCCAT	CATGAGTGCC	600
CTTGCCGGTG	TTTACGGTCT	GGAGCAGATC	CCTGCCAATA	TGATCGAACG	TGTGGAGGTA	660
GTACGTGGTG	GAGGATCGGC	CTTGTACGGT	TCTTCTGCTA	TTGCCGGAGT	GGTGAATATC	720
ATCACCAAGG	AACCTTCTCA	CAATTCTTTC	ACATTCAATG	AATCTCTGAG	CTTTACCGGT	780
TTCAGCAAGC	TGGATAACAA	CACGAAC TTC	AATGCCTCCA	TCGTCAGCGA	TGACAACCGT	840
GCCGGTGCCA	TGGTATTCGG	GCAGGCTCGT	TACCGCAACC	ATTGGGATGC	TAACAATGAC	900
GGTTATTCCG	AATTGGGTAA	AATAGATGCC	CGCTCGCTGG	GAGCGCATTC	TTATTTGCGC	960
TTGAGCGACT	GACCAAAATT	GACGGGAGAG	TTTCACACGA	TCAGTGAATT	CCGCCGTGGT	1020
GGCGATCGTA	TCGATTTGCC	TCCTCACGTA	GTGGGTGTAG	CTGAACAAAC	TGACCATAGC	1080
GTATTTAGCG	GAAACTTGAA	ATACGATCTC	TTCTCTTCCA	ACTATAAACA	CCACTTCCAG	1140
GCTTATACTT	CCGGACAGAT	CGTAAATCGC	AAGAGCTATT	ACGGAGGTAT	CGGAGAGATT	1200
GACGTCAATG	GCCACCCCGG	TGGTACGGAA	GGCTACCCTA	TCCTCAAGA	TCAATACGGC	1260
AATAATTATG	GCGTGACCAA	AGGCAAGACA	TATATGGGCG	GTATCCAGTA	CAGCTACGAC	1320
TTGGACAAAT	TCCTCCTCAT	GCCTTCGCAA	CTTTTGTTTCG	GAGCCGAATA	TACGCGTGAT	1380
GAACTCAATG	ACGTGATGCC	CATCCTTTCA	TGGCAGACCG	GCGAGGATGC	CAATGGGAAT	1440
ACCATTCCCC	TCTATCCCGA	ATTGGATCAG	AATATCAACA	ACTACAGCCT	ATTCGGTCAG	1500
AACGAATGGA	AAAATGACAG	ATGGAGCATC	CTTGTTGGCG	CTCGTTGGA	CAAGCATAGC	1560
GAAGTCAAGG	ATATGATTCT	GAGTCCTCGT	ACCACACTGC	GTTTCAACGT	GAATCCGGAC	1620
ATCAACCTGC	GCGCTACATA	TGCAAAAGGG	TTCCGCGCAC	CGCAGGTATT	CGATGAAGAC	1680
TTGCACGTAG	GGTTGTAGG	CGGTGAGGCA	CAGAAAGTAT	TCAACGATCC	GAACCTCAAG	1740
CCTGAAATTT	CTCATGCATT	CAGTTTGAGT	GCCGATATGT	ATCATCGTTT	CGGTAACGTC	1800
CAGACCAACT	TCCTTGTTGA	AGGCTTCTAT	ACTCGTTTGC	TGGATGTATT	CACCAACGAG	1860
GAGCAGCCTG	ATCAGCACGA	TGGCATCAAA	CGCTACACGC	GTATCAACGG	TAGCGGAGCC	1920
AAAGTATTCT	GTCTCAATCT	GGAAGGTAAG	GTGCGATACA	AGTCCTTCCA	GCTCCAAGCC	1980
GGTCTTACCC	TGGCCAGCAA	CAAATACGAC	GAAGCACAGG	AGTGGGGTCT	GAATACGGTG	2040
AAAGACACCA	ACGGAGCTTT	TGTTACCGAG	GCCAATGCAA	ATGGACAACA	GGAATACAAG	2100
AACGAATCCA	TGACGGATAC	GCAGATCACC	CGTACCCCA	GCGTATACGG	TTATTTTACT	2160
TTGGCCTACA	ATCCTGCTCA	CTCATGGAAC	ATAGCCCTTA	CGGGAGCATA	TACCGGTCAG	2220
ATGTATGTAC	CCACGCTAT	CGAATATGGT	GTGAAGTCTG	CCGAAGTGA	TATTATGCAG	2280
AACAATCCTG	AGATTACCGA	CGAAACCGGA	AAGGCTCCCC	GTATTGATGA	GCTGAAGAAG	2340
ACACCTGCAT	TCTTCGATTT	GGGCTTGAAA	GTGGGTTATG	ACTTCCACGT	ATTCCAGGCT	2400
ACTGAGGTTT	AATCTATATG	AGGTATGAAC	AATATCTTCA	ACTCTTTCCA	GAAGGACTTC	2460
GATCGTGGAG	CTGCACGTGA	CAGCGGATAT	ATCTATGGTC	CTACGCAGCC	GCGTACAGGC	2520
TACATGGGCT	TGGTAGTGAA	GTTC				2544

(2) INFORMATION FOR SEQ ID NO:196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

ATGACAGTAA	AGCGCGCAGT	GCGAATAGCA	CTTCTCACGC	TGATAGGCAT	TCTTTTTTCC	60
TCACCTTCTC	TTGTTCGGGC	GCAAAGTCTT	TTCAGCACCG	AACATGTCTT	GCAACTATAC	120
AACAAGATAC	TCATATGGAGA	GTCGGCGGCG	GATACCGTCG	CAGAGAAAAC	GGCAGGTGAG	180
TCGGCATTTC	CTTTTATAGA	CAAATCATC	AATCTCGGCC	GCATTTTCCT	CGGCAAACCA	240
TATCGCTATC	GCGGTCTTTC	CCCATGGCCG	ATGGACTGCT	CGGGCTATGT	GTCTTACCTC	300
TACTCCAAAT	TCGACATCAA	ACTCCACGTC	GGTGGCGGCG	CACAGAGCCA	ATATACGAAT	360
CCTATCGAGC	GCGAGGATGT	TCGTCCGGGC	GACCTCCTTT	TTTTCAAAGG	CCGCAATGCA	420
CGCAGCAACC	GTATCGGGCA	TGTAGCTTTG	GTCTGATCTG	TCGATGAAGA	TGATATTACC	480
ATGATGCACA	CCCGCAATTC	GCGAGGGATC	GTGATCGAAA	AATCAATCG	CAGTGCATAC	540
TTCTCCCGTC	GCTTGGTGAG	CTATGGCAGG	GTACCCGGAG	CCAAGAGAGT	GATCCACGA	600
AAAAAGT						606

(2) INFORMATION FOR SEQ ID NO:197

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1365
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGAAACGGA	CAATCCTCCT	GACGGCACTG	ACCGTCCTAT	CTTCGCTCTC	CTTGCTTCGT	60
GCACAAAATG	AATCCGAAGC	ATCAACCAAT	CCGATGTCAG	GCCTCTCCCT	GGAAGACTGT	120
ATCCGGATAG	CCAAGGAGCG	CAACCTGAAT	CTGCGCAGAC	AGGAGATCGA	ACAAGAAAAC	180
CGAATCATTA	GTCTCGATGC	AGCACGACAC	AGTTTCCTGC	CCTCGGTCAA	TGCAGGCATC	240
GGACACAACT	ATAGCTTCGG	ACGTTTCGAAA	GACAAAACGG	GAGTAACCGT	AGATCGCTCC	300
TCGATGAATA	CCAATCTCAG	CATCGGAGCT	TCGGTGGGAA	TATTCAGCGG	CACACGTCGT	360
CTGCACGACC	TCAAGCAGCA	AAAGTACAAC	GTGGAGGATG	GTATAGCCCG	ACTTCAAAAA	420
GCGCGTGAA	ACCTCAGCCT	GCAAAATCGCG	GCTCTCTATA	TCAATTTGCT	CTTCCGTCAG	480
GAAATGACTC	GTACGGCAGA	AACACAGTTG	GCACTGATTC	GCGAGCAACG	CAATCGCACG	540
GCCGAAATGG	TTCGCGTAGG	TAAATGGGCA	GAGGGTAAGC	TCCTCGACAT	AAATGCCCAG	600
ATGGCCAAGG	ACGAACAACT	TCTCGTACAA	TATCGTTTCGG	AGGAGGAGCT	GGCTCGTCTG	660
GACTTGGGGC	AAGCCCTCGA	ACTGGAGCAC	CCCGAAAGCA	TTGCAGTCAA	GGCTCCCAGC	720
ACAGACGTTT	TCGTAGCAGA	AAGGTTGGGA	TCTCTCCTTG	CTCCCGAAGA	GATCTATCGC	780
ACGGCTCTCG	GCTTGAAACC	GGCACTGCAT	TCGAGCGAGC	TGCAAATAGC	TTCCGGCACGC	840
GAAGGTCTGG	CCTCGGCTCG	TGCGGCATAC	TTCCCGACGC	TCAGCCTCTC	TGCCGGATAC	900
AGCAACGGTT	ACTTCCGCGA	CCTCGGCAAG	GAGTATGCCG	CCATCAACCC	CTCCTTCTCC	960
GAACAGTGA	AGAACAACGG	CAGCTACAGT	ATCGGACTCT	CTTGGAATAT	CCCATCTTTC	1020
TCTGCCATGC	AAACGCAAGA	TGCGGTTTCGG	AGCAGTCGCC	TGCAAATACG	CTCAAGCGAG	1080
CTTCGACTCG	TCGAAGAGAA	AAAAGCCCTC	TATAAAGAGA	TCAGGCAAGC	ATACAGCAAT	1140
GCCGTGGGAG	CCGATAAGGC	CATCGCAGCA	GCCGAAAACA	GCAAGGCCGC	TACGCTCAAG	1200
GCATACGAAT	ACGCTCGCGA	CAGCTTCGAG	GCAGGGCGCT	TGTCTGCCTA	CGAATATGCC	1260
GAGGCAAAAA	CAAAATACGC	CCTCAGCCAA	GTGGAAGAAC	TTCTGTCCAA	GTATGACTTC	1320
ATATACAAAG	CCAAAGTTTT	GGATTTCTAT	CAGGGCAAAG	ACTTC		1365

(2) INFORMATION FOR SEQ ID NO:198

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1332
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGCGTTTCC	AACATTATCT	CATCTGTACG	GCTGCCGTAG	CGGCTTTGGC	TGCGAATCCC	60
CTTACGGGGC	AATCGAATAT	GACCTCGAA	GAGTGCATAG	ACTATGCACG	CCGGCACAGT	120
TCGGCCGTGG	CGCTGTCCGC	TGCGGAACTG	GAGCAGTCCA	AGGCCGATTA	CCTTCAGGCC	180
GTCGGCAATT	TTCTGCCCCG	TGTATCGGCC	GGAAACGGTG	CTTCGTGGAA	TTTCGGACGC	240
GGATTGGATG	CCGAGACGAA	TACCTACACC	GACATCAACA	GCTTCAACAA	TTCTGTACAGC	300
ATACATGCCA	CGATGACCCT	TTTCGACGGT	TTGCAGAGTG	TCTATCGACT	GCGGATGGCG	360
CATGCACGCC	GGGAGGCTTC	GCGCCTCTCC	GTTCGCGAGC	AGCAGGAGCT	GGCAGCTCTC	420

GGCACCACGG	AGGCCTACTA	CGACCTCGTC	TATGCGCGCC	AAATGCAAGA	GCTGGCCATG	480
CAGAAGTACG	AGGAGAGCAG	CCGCCTCCAC	CGGCAGACGG	CTCGAATGGA	AGAGCTGGGG	540
ATGAAGAGTC	GTCCCGATGT	CCTCGAGATG	CAGTCGCGAA	TGGCCGGTGA	CCGTTTGGCC	600
CTGACTCAAG	CGGACAATCA	GTGCATCATC	GCTCTGATCC	GGCTCAAAGA	AAAAATGAAC	660
TTCCCCATCG	ATGACGAACT	CGTCGTAGAC	GATATGCCGG	CTGACAGTCT	CTCCGCCGAC	720
ATGGCCGAAT	CGGACAGCTC	GGCCGGCGTC	TTCGCCCGTG	CTGCCCATCA	TCATCCCGTC	780
CTCCTCCGTG	CCAAACTCGA	CGAGCAGGCT	GCCACCGACC	GTTTGCAGGC	CGCGCGAGGT	840
GCATTCCGTG	CGAGTGTGTC	GGTATCCGGA	GGATGGAACA	CGGGATTCTC	ACGCTTTTGT	900
AATGGATCGG	ACTATACGCC	CTTCAGCGAG	CAGTTTCGGA	ACCGTCGGGG	GGAATACGTC	960
AGTCTGAATC	TGAGTATCCC	CATCTTTTCG	GGATTACGCC	TTGTGAGCCA	TCTGCGTCAG	1020
GCGCGTGCCG	AACGCAGGGC	GGCAATCGTC	CGACGGGGCG	AAGCGGAGCG	CAGGCTCTAC	1080
AGCGAGATCG	CCCAAGCCAT	GGCCGACCGG	GATGCCGCTC	TGGCTTCCTA	CCGCCAGGCG	1140
AAGGAGCATA	CCGACGCCAT	GCAAACCGCT	TACGAAGCCG	TCTTGACGCG	TTATGAGGAG	1200
GGGCTGAATA	CGGCCATCGA	CCTGACCACT	CAGGCCAATC	GGCTCCTGGA	TGCCCCGTGTG	1260
CAGCGACTGA	GAGCGGCCAT	GACCTACCGG	CTCAAATGCA	AACTCATAGC	CTATTACGGC	1320
TGCCTTTTCGG	AC					1332

(2) INFORMATION FOR SEQ ID NO:199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

ATGAACAAAT	TTTACAAATC	ACTTTTGCAG	TCAGGACTGG	CTGCCTTCGT	GTGATGGCA	60
ACTGCACTGA	CCGCTTCTGC	ACAGATTTCG	TTCGGAGGGG	AACCCTTGAG	TTTCTCTTCA	120
AGATCCGCCG	GAACGCATTG	ATTTCGACGAT	GCAATGACTA	TCCGCCTTAC	TCCGGATTTC	180
AATCCGGAAG	ACCTGATCGC	ACAGAGCCGT	TGGCAATCGC	AAAGAGATGG	CCGGCCCCGT	240
CGGATAGGAC	AAGTAATACC	GGTGGATGTG	GACTTTGCAAT	CCAAGGCTTC	GCACATCTCT	300
TCCATCGGAG	ACGTAGATGT	ATATCGCCTG	CAATTCAAGT	TGGAAGGAGC	CAAAGCCATT	360
ACGCTTTTAT	ACGATGCATT	CAATATTCCG	GAGGGCGGAC	GCCTCTATAT	CTATACCCCC	420
GACCATGAAA	TTGTGTTGGG	AGCATATACG	AACGCCACTC	ATCGCCGCAA	CGGAGCTTTT	480
GCCACAGAGC	CGGTACCGGG	GAGTGAGCTT	ATTATGGATT	ATGAAGTGTC	TCGCGGAGGG	540
ACTTTGCCTG	ACATCAAGAT	CTCCGGTGCG	GGTTATATAT	TCGACAAAGT	CGGCGGACGC	600
CCCGTAACCG	AATACCATTA	CGGGATCCGT	GAGGACGATT	CCGATTTCGA	TTGCGAGATC	660
AACATCAATT	GTCTGAAGG	TGCAGACTGG	CAGGCAGAGA	AGAACGGTGT	GGTGCAATATG	720
ATCATGGTAA	AAGGACAGTA	TATCTCAATG	TGCTCAGGCA	ACCTGCTCAA	TAATACGAAA	780
GGAGACTTTA	CTCCGCTGAT	CATTTCTGCC	GGACACTGTG	CTTCCATAAC	AACCAATTTC	840
GGTGTAACGG	AATCCGAGTT	GGATAAGTGG	ATCTTCACTT	TCCACTATGA	AAAAAGAGGA	900
TGCAGCAATG	GTACATTGGC	CATCTTCCGT	GGCAACAGTA	TCATCGGAGC	TTCCATGAAG	960
GCTTTCCTCC	CGATCAAAGG	TAAATCCGAT	GGTCTCTTGC	TGCAACTCAA	CGATGAAGTC	1020
CCTCTGCGCT	ATCGTGTCTA	TTACAATGGA	TGGGACAGTA	CGCCCCGATAT	TCCCTCGAGC	1080
GGTGCCGGTA	TTCATCATCC	GGCCGGAGAT	GCCATGAAGA	TTTCCATCCT	AAAGAAGACT	1140
CCGGCTCTGA	ATACATGGAT	CTCCTCCAGT	GGTTCCGGAG	GGACTGACGA	TCATTCTAT	1200
TTCAAATACG	ATCAAGGTGG	TACGGAAGGA	GGATCGTCCG	GTTCTTCTCT	CTTCAATCAG	1260
AATAAGCACG	TGGTCGGCAC	ACTGACCGGA	GGTGCCGGCA	ATTGTGGCGG	GACGGAGTTC	1320
TACGGCAGAG	TGAACAGTCA	TTGGAACGAG	TATGCATCCG	ATGGCAATAC	GAGCCGATG	1380
GACATCTATC	TGGATCCCCA	AAACAATGGC	CAGACGACCA	TCCTCAACGG	AACGTATCGT	1440
GACGGTTATA	AGCCTTTGCC	CTCTGTGCCC	CGGTATTGTG	TGCAGTCTAC	AGGCGATCAG	1500
GTCGAATTGA	ATTGGACGGC	TGTTCTTGCC	GATCAATATC	CATCATCTTA	TCAGGTCGAA	1560
TACCACATAT	TCCGAAATGG	AAAGGAAATA	GCTACGACAA	AGGAGTTGTC	CTATTTCGGAT	1620
GCCATCGACG	AAAGTATTAT	CGGTAGCGGT	ATCATTGATG	ACGAAGTAAG	CGCACGCTTC	1680
ATTTATCCCT	CGCCGTTGGA	TGGAGTGGAA	TCTTATAAGG	ATACGGACAA	GACTTCTGCC	1740
GACCTTGCCA	TAGGAGACAT	TCAGACCAAG	CTGAAGCCGG	ACGTAACACC	TCTCCCCGGA	1800
GGAGGAGTAT	CATTAAGCTG	GAAAGTTCTC	TTCTTAAGCC	AGTTGGTTTC	CCGATTTCGGA	1860
GAAAGCCCCA	ATCCTGTGTT	CAAAACCTTT	GAAGTGCCCT	ATGTTTCTGC	CGCAGCCGCA	1920
CAAACCCCCA	ATCCTCCCGT	TGGCGTAGTC	ATTGCAGACA	AGTTTATGGC	CGGTACATAT	1980
CCCGAAAAGC	CTGCTATCGC	TGCCGTTTAT	GTAATGCCAT	CCGCTCCGGA	CTCTACTTTC	2040
CACCTCTTCC	TGACAGAGCAA	GACAAACAGA	AGATTGCAGA	AGGTGACAAC	TCCCTCCGAT	2100
TGGCAGGCCG	GAACATGGTT	GAGGATCAAT	TTGGATAAGC	CGTTCCCGGT	GAATAATGAC	2160

CATATGCTTT	TTGCCGGTAT	CAGAATGCCT	AATAAGTACA	AGCTCAATCG	TGCTATCCGT	2220
TATGTAAGAA	ATCCCGGATA	CCTTTTCTCC	ATTACCGGTA	AGAAGATTTC	ATATAACAAC	2280
GGAGTCTCTT	TCGAAGGCTA	CGGAATACCC	TCGCTCTTGG	GCTATATGGC	TATCAAATAT	2340
CTGGTGGTAA	ATACCGGATC	TCCGAAGATC	GATATGTCGC	TTGTACAGGA	GCCTTATGCT	2400
AAGGGAACGA	ATGTGGCTCC	ATCCCCGAA	TTGGTCGGCA	TATATGTCTA	TAAGAACGGA	2460
ACATTTATCG	GCACACAGGA	TCCATCCGTC	ACAACCTATT	CGGTTTCAGA	CGGAACAGAG	2520
AGCGATGAAT	ACGAAATAAA	ACTGGTATAT	AAGGGATCGG	GCATTTGCAA	TGGCGTTGCT	2580
CAGATTGAGA	ATAACAATGC	TGTCGTTGCA	TATCCGCTCG	TTGTAACAGA	TCGTTTCAGC	2640
ATTAAGAACG	CTCATATGGT	TCACGCTGCC	GCCCTCTACT	CATTGGATGG	CAAGCAGGTT	2700
CGTCTTGGA	ACAACCTCCG	CAATGGCGTG	ACATTCACTG	TTCAAGGACT	TACGGCCGGT	2760
ACTTATATGC	TCGTTATGCA	GACGGCAAAC	GGCCCTGTGA	GCCAAAAGAT	CGTGAAGCAG	2820

(2) INFORMATION FOR SEQ ID NO:200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

ATGAAATATC	TTATCAGACT	CTTCTTATCA	TTGATGTTAC	TCTCTCTCTG	GACGGGCTGT	60
ACACACGAGG	AGCTCTCTAT	TTGCGATGGC	GAGAATACGC	TTGTTTTTACG	CGTAGAGACC	120
GGTAAAGCCC	CAATGCTCG	TGCCACAGAA	CCCGGTCAGG	GCATATACAA	TGAGAATAAA	180
GTAGGCTCCA	TTTCTGTGCT	CTTCTATTTA	GAGGGACAAC	TTCGTTGGCA	GGTGAAGTCT	240
ACAGACTATC	AAATCCATGA	AGGGGCCTAT	ATCATTCCGG	TCAAAGAGCA	AATGCGACCA	300
CTATTCAATG	GCAACAACAA	CTTCAGCATC	TATGTAGTGG	CCAATCTCGA	TTTCAATGCT	360
CCGGCCACAG	AAGCTGCGCT	TTTCAATTT	GTGGTAGAGA	AATCTATTGA	AGTCTCTTCT	420
ACGACAGCCC	CTGCCGATT	CGTAATGCTT	GCTCATGGCA	ATAAGCAGAT	CAATATGGCT	480
ACGACAGAAG	GGAAACTGTT	GGGGGATTAT	AAACTCAAAC	GAGTGGCAGC	AAAGATTTCG	540
ATGATAAAAC	CCACCATCAA	TGTGCAAGGA	TATGAAGTGG	TCGGAAATAT	ACAGGCAAAG	600
TTTCGCAATT	CGGTAACGAA	GGGGTTCCTT	ACCACAGAAG	CTCAAGAGAT	CCCAGCTGCT	660
GCATCCTATA	AGACATCGGA	ATATCTTGAT	ATTGCAGAGT	CGGCACCTGC	CAATTCTATC	720
CATTTCTATT	CTTACTATAA	CAAATGGACA	CTCTCCACAC	CGGAGAAGCG	ACCGGAATTC	780
TTCATCATGG	TCAAATTCAA	AAAGACAGGA	CAGCCGGACA	ACACAGCCAA	ACCGTACTAC	840
TACAGAGTGC	CCCTCGAATC	TCAGGACAAT	CAGGTCAAGA	GCAATGTCCT	CTATAATCTG	900
AATGTGAAAA	TCGAAATCTT	GGGTTCTTTA	CAAGAGCCGG	AAGCTGTTTC	TGTAAACGGC	960
AACTCGCAA	TAGAAGAATG	GATTCTCCAT	CAGGATGCAT	TCAATCTGCC	TGCCACCAAT	1020
TACTTGATAG	TGGAACAGCA	CGAAATCTTC	ATGAATAACG	TGAACACATA	CTCGGTGAAA	1080
TATCAAACCT	CGCAGAAACC	AATCAGCATT	AGCATACAGT	CAGTTACCTT	TAGCTACGTC	1140
TCTTCTGATG	GCACTCAGCA	CAATGATCTT	GTAGCAAGTA	GTAGCGACCA	GTATCCTACG	1200
ATTACAAGCG	ATAATACAAG	CATCATAATC	ACTTCCAAGA	TACCGGTTAA	TAACGTACCA	1260
AAGAAGATCG	TTTTTGAGGT	AACTAATGGG	GTAGCCGGTT	TGAAAGAGAC	TGTCACAGTA	1320
CTCCAATATC	CTGCACAATT	TATTGTCAAT	ACACTTGGCA	CAGCATCGGC	ATGGAGACCA	1380
GACGGATCTT	TGGCTCCGGG	GCTTAACAAT	AAAGCGATT	ACCATGTCGT	AGTACTGGTT	1440
CCACCCGAGA	ATTTATTTGA	AGATGGGACA	CAGACAATCA	TCGGTTATCC	CCCCACTGAA	1500
ACAATTTCTT	TTCATAAGAA	AGAGAACAAT	ACCTATCCGA	TAGTATGGTC	TGACACAAAT	1560
ACGACAAAAC	AGGACCTTGA	GACATCAAGA	ATGATTTTAC	CTTCCTTTGA	GTTAGCCTCC	1620
CAACTTGGGG	CTACTCTCCC	GATGCCCTAT	CTCGAGTATT	GGCCAGGGAC	ATCATATCTC	1680
CTTGACTATT	CGGGAAACTA	TAATAATAAG	AGATACGCCT	TGTTTAATTG	CGCTTTTTAC	1740
TGGGAGAAAA	GAAAAGTTAA	TAACGAAGAA	ATTAAATTCG	ATGACTGGCG	TTTGCCGACA	1800
GAAGCTGAGA	TCAAATTGAT	AGATAAGCTG	CAACATAATG	AGCAGAGTGC	TGTCCAAGCT	1860
ATCATGACAG	GGAAATTATTA	TTGGGATAGT	TACTCTGCAA	ATGGGTCTTA	TAAAATGCAA	1920
GGAGGAGGGG	GCCAAGGAAA	TTCTTCCAAA	GCCTATGTTC	GTTGCGTGCG	GGATGTGAAA	1980
AAGCCGATTC	GTGACAAGAA	GTCAGGTAAG				2010

(2) INFORMATION FOR SEQ ID NO:201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3846 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

ATGCGAAAAA	TTTTGAGCTT	TTTGATGATG	TGCTCTCTGC	ATTTAGGTCT	ACAATCTCAG	60
ACTTGGCATG	GAGATCCGGA	CTCAGTGGCA	GCCCTACCTT	CTATCGGTAT	TCAAGAGTCA	120
AGTTGTACCC	GAATCACGTT	CGAGGTTGTT	TTCCCCGGAT	TTTATAGTGT	GGAAAAACGA	180
GAAGGCAACC	AAGTCTTTCA	GCGCATTTC	ATGCCGGGTT	GTGGCTCGTT	TGGGAATCTG	240
GGCGAAGCTG	AATTGCCTGT	TTTGA AAAAG	ATGATAGCCG	TTCCGGAATT	TTCAACAGCT	300
AACGTTGCTG	TAAAAATCAA	AGAGACGGAG	ACATTGACACA	ATTATAATAT	CTATCCTAAT	360
CCTACCTATG	TCGTAGAGGA	GTTGCCTGAG	GGGGGGACTT	ATCTGGTAGA	GGCTTTTCGCG	420
ATAACAATG	ACTATTATAG	CCAAAATGTA	AGCCTCCCTT	CTACTCACTA	TGTCTATTCT	480
CAAGACGGGT	ATTTTCGCTC	ACAAAGATTT	ATCGAAGTTA	CCCTGTATCC	TTTTCGATAC	540
AACCTGTGCC	GACAAGAAAT	TCTATTTGCA	AAAAAAATCG	AGGTTACAAT	AACCTTCGAT	600
AATCCTCAGC	CACCTTTTACA	AAAAAACACC	GGCATATTTA	ACAAAGTAGC	CTCCTCTGCA	660
TTTATTAATT	ATGAAGCTGA	TGGCAAAATCG	GCGATAGAAA	ATGATATGGT	GTTCAGTCGT	720
GGTACAACAA	CGTACATAAG	CGGAAATGTT	GCCAGCAACC	TCCCTCAGAA	CTGTGACTAC	780
TTGGTTATTT	ACGATGATAT	GTTCAACGTA	AATCAACAAC	CACACGACGA	AATCAAACGG	840
CTGTGCGAAC	ATAGAGCCTT	CTACAACGGC	TTTGATGTAG	CTGCTGTAAG	TATAAAGGAC	900
GTATTGAATA	GCTTCCCATC	AAATGCCACC	TCATACATCA	ACGAAACTAA	ACTGAAAAAT	960
TTCATTGCTC	CAGTTTACAA	CCAAAGCAAT	GCGAAGAGGA	CTTAGATGG	CAAACCTGGA	1020
TACGTGCTAC	TGATCGGAAA	ACCATTGAGC	AAATATTTGG	CTGACACTGA	TAATACAAAA	1080
GTCCCAACCT	CTTTTATTCA	TAATGTCTCC	TTAATTCCAA	GTCATCCAAC	TTTGGTTTCC	1140
ATATGCGCCT	CCGACTATTT	TTTtagTGT	GTTCGCCCC	TTGATACTGT	CGGCGATTGT	1200
TTTATCGGTC	GATTTAGCGT	CACCAATGCT	CATGAATTGC	ACAATCTGAT	TGAAAAGACT	1260
ATCAACAAAG	AAATCTCATA	TAATCCTATT	GCACACAAAA	ATATTCTTTA	CGCAGAAGGG	1320
AAAGGCTGCG	ATGCTCCAAT	CTTACGTTTA	TTCTTAAAAG	AAATCGCCTC	TGTTTACACA	1380
GTCAACTCTA	TCTTAAAAATC	TAATCAGGTC	TCTGCAATAG	ACTCGATATT	TGACTGCTTG	1440
AATAATGGTT	CCCATCATTT	TTATTTTAAAC	ACTCATGGAA	TGCCGACTGT	TTGGGGGATA	1500
GGGCAGGGAC	TGCACGTCAA	TACTCTAACA	GCCCGATTGA	ACAATACATC	TTGCGAGGGA	1560
TTATGTACGA	GTCTATCATG	TAGTTCGGCT	GTAGCAGATT	CAACTATTAG	ATCGCTTGGA	1620
GAAGTCTCTA	CCACATACGC	ACCTAACAAAG	GGATTCTCGG	CTTCTTAGG	AGGAAGCAGA	1680
GCCACCCAAT	ATGCCGTTTA	TTTAGAAGGC	CCCTGTCTCT	CGTCAGAATT	TTATGAATAT	1740
TTACCTTATT	CTTTATATCA	ACTGTCTCTG	ACTGTTGTTG	GCGAAATGTT	GCTATCATCC	1800
ATTATCAATA	CTAATTCTGT	TGATACGTAT	TCGAAATTCA	ACTTCAATTT	GCTTGGCGAC	1860
CCTGCACTAA	ACATTATGGC	TCATGGCATG	GAGGTTAGTA	ATTGTATTAC	ACTACCAAAC	1920
AACACCATTA	TAAGCAGTCC	GATAACAATA	AAAAATGGTG	GCTGCCTAAA	AATACCGGAA	1980
AAAGGAGTTT	TGCATTTTCA	TAATAATGGC	TCCATACAAG	TCATGTCCGG	AGGAACTCTG	2040
GAAATAGGCA	ATCAGGCTAA	AATATCCGGA	GAGACCGGTG	CTAACCCAC	CTTATTATACC	2100
GTTTACGGCG	ATGCTCTTGC	GATTAAACAAG	CAGGTAGAGA	TAGACAATAT	AGACCGACTT	2160
AACTTGTTTT	CTACGCATTC	GGTCATGCCC	AAATTTCAAT	TTGACAGTGT	GAAATTCAAC	2220
AGTGCCCCCG	TGTATACAA	GAACGTGATT	GTGGAGATAA	GCAATTGCGA	ATTTACCAAT	2280
CGAAGTGACA	TTATTTCAAA	GAATTGTGAC	CTAAGCGTTG	AAAACAGTAT	GTTTAGCAGT	2340
TCGGGGATAA	CGGTATTCAA	GCCTATGGCT	ACAAGCTCCA	TCACCGGATT	ATCTACAAAA	2400
GCAAAGATTA	CCGACAATAC	TTTTTTTGCG	ACAGGAAACT	TCGCCTACCA	TATCACAAC	2460
ACGCCAGGCT	TAACAGCAAC	CTCCAATGCT	GCCATCAAGT	TAGACAATAT	TCCTGAGTAT	2520
TACATTTCCG	GTAATAAAAT	AGTCAATTGC	GATGAGGCTC	TTGTACTAAA	TAATAGTGCG	2580
AACAGAACGA	ACAGACTCCA	CAATATCACA	CGGAATGTGA	TAAAAAATG	TAGGATTGGG	2640
AGCACGCTTT	ATAATTCTCTA	TGGTATTTAC	AACCGAAATA	AGATCAGTAA	CAATCATATA	2700
GGAGTACGTC	TCCTCAACAA	CAGTTGTTTT	TATTTTCGATA	ATGCTCCTGT	AATCAATGAA	2760
GAAGATAAGC	AGACGTTTAT	TTCTAATAGG	ACTTGGCAGC	TCTATTATC	AAACGGTACA	2820
TTCCCTCTCA	ACTTCCATTA	CAACAGCTTG	CAGGGGGGAG	ATACAGATAC	ATGGATTTAC	2880
AACGACACGT	ATACGAATCG	CTATATTGAC	GTTTCAAATA	ATCACTGGGG	CAACAATGAT	2940
TTGTTTGATC	CGAATCAGGT	TTTCAATACG	CCAGACTTGT	TCATTGGAT	ACCTTTTGG	3000
GATGGATTGC	CAAATGGGAG	ATCGGGCAAT	AGCTCTGCTG	AAGCAGTAGA	ATTCCAAACA	3060
GCATTGGACT	GTATTGGCAA	TAGCGATTAT	CTTTCGGCAA	AAGTGGCTCT	CAAGATGATG	3120
GTTGAAACCT	ACCCGGAATC	CGACTTTGCA	ATAGCTGCTT	TGAAGGAATT	GTTCAAGATA	3180
GAGAAAATGT	CAGGCAACGA	TTACGAAGGC	TTGAAAGATT	ATTTCAAGATC	CAATCCAACC	3240
ATCATCTCTT	CCCAGAACTT	GTTCCCGACA	GCTGATTTCC	TGTCTGCGCG	ATGCGATATT	3300
GTGTGTGAAA	ACTATCAGTC	TGCCATCGAT	TGGTACGAAA	ATCGCTTGAA	TAGTGAAATC	3360
TCCTATCAGG	ACAGTGTGTT	TGCGATCATT	GACCTTGGTG	ACATTATTG	GAATATGCG	3420
TTAGACTCAC	TCAGAGGGAC	TGGTATAGAT	TTGAACATAC	TTTCTGTGTA	ACAAAGGAAA	3480
TCGCTCGAAA	GCCATCAAAA	TGTAAAAAAT	TATTTGTTGT	CAACTCTTCC	GAAATCAACA	3540

GGTACTCTCC	TGCTCCATT	AGAATGCAAC	AAATCAAGCC	TTGATAAATC	CAAGATAATC	3600
TCTATTTTCG	CCAATCCGGC	GAAAGCTGTT	GTAAACAATA	TCTACTATAC	CGATAACCTT	3660
TCCTGTTCTG	TAATAAAAAAT	ATATGGAATA	AATGGAGCCT	CGGCTGATAT	AACCGGGTTG	3720
CCCAAACATC	TATCCGAAGG	TTATTACAGC	ATACAGTTCA	ATACATCCAA	CTTTGATCCC	3780
GGTTTCTACC	TGTAACGCT	AAATGTTGAT	CAGAAAAATTA	TAGATACGGA	AAAATTACGA	3840
ATCAAA						3846

(2) INFORMATION FOR SEQ ID NO:202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

ATGATGTGCT	CTCTGCATTT	AGGTCTACAA	TCTCAGACTT	GGCATGGAGA	TCCGGACTCA	60
GTGGCAGCCC	TACCTTCTAT	CGGTATTCAA	GAGTCAAGTT	GTACCCGAAT	CACGTTTCGAG	120
GTTGTTTTTC	CCGGATTTTA	TAGTGTGGAA	AAACGAGAAG	GCAACCAAGT	CTTTCAGCGC	180
ATTTCATGCG	CGGGTTGTGG	TCTGTTTGGG	AATCTGGGCG	AAGCTGAATT	GCCTGTTTTC	240
AAAAAGATGA	TAGCCGTTCC	GGAATTTTCA	ACAGCTAACG	TTGCTGTAAA	AATCAAAGAG	300
ACGGAGACAT	TGACAATTA	TAATATCTAT	CCTAATCCTA	CCTATGTCGT	AGAGGAGTTG	360
CCTGAGGGGG	GGACTTATCT	GGTAGAGGCT	TTCGCGATAA	ACAATGACTA	TTATAGCCAA	420
AATGTAAGCC	TCCCTTCTAG	TCACTATGTC	TATTCTCAAG	ACGGGTATTT	TCGCTCACAA	480
AGATTTATCG	AAGTTACCCT	GTATCCTTTT	CGATACAACC	CTGTCCGACA	AGAAATTCTA	540
TTTGCAAAAA	AAATCGAGGT	TACAATAACT	TTCGATAATC	CTCAGCCACC	TTTACAAAAA	600
AACACCGGCA	TATTTAACAA	AGTAGCCTCC	TCTGCATTTA	TTAATTATGA	AGCTGATGGC	660
AAATCGGCGA	TAGAAAAATG	TATGTTGTTC	AGTCGTGGTA	CAACAACGTA	CATAAGCGGA	720
AATGTTGCCA	GCAACCTCCC	TCAGAAGTGT	GACTACTTGG	TTATTTACGA	TGATATGTTC	780
AACGTAATTC	AACAACCACA	CGACGAAATC	AAACGGCTGT	GCGAACATAG	AGCCTTCTAC	840
AACGGCTTTG	ATGTAGCTGC	TGTAAGTATA	AAGGACGTAT	TGAATAGCTT	CCCATCAAA	900
GCCACCTCAT	ACATCAACGA	AACATAAAGT	AAAAATTTC	TTGCTCTCAG	TTACAACCAA	960
AGCAATGCGA	AGAGGACTTT	AGATGGCAAA	CTGGGATACG	TGCTACTGAT	CGGAAAACCA	1020
TTGAGCAAA	ATTGCGTGA	CACTGATAAT	ACAAAAGTCC	CAACCTCTTT	TATTCATAAT	1080
GTCTCCTTAA	TTCCAAGTCA	TCCAACTTTT	GGTTCCATAT	GCGCCTCCGA	CTATTTTTTT	1140
AGTTGTGTTT	CGCCCCTTGA	TACTGTGCGG	GATTTGTTTA	TCGGTTCGAT	TAGCGTCACC	1200
AATGCTCATG	AATTGCACAA	TCTGATTGAA	AAGACTATCA	ACAAAGAAAT	CTCATATAAT	1260
CCTATTGCAC	ACAAAAATAT	TCTTTACGCA	GAAGGGAAG	GCTGCGATGC	TCCAATCTTA	1320
CGTTTATTTCT	TAAAAGAAAT	CGCCTCTGGT	TACACAGTCA	ACTCTATCTT	AAAATCTAAT	1380
CAGGTCTCTG	CAATAGACTC	GATTTTGAC	TGCTTGAATA	ATGGTTCCCA	TCATTTTAT	1440
TTTAACACTC	ATGGAATGCC	GACTGTTTGG	GGGATAGGGC	AGGGACTCGA	CGTCAATACT	1500
CTAACAGCCC	GATTGAACAA	TACATCTTCG	CAGGGATTAT	GTACGAGTCT	ATCATGTAGT	1560
TCGGCTGTAG	CAGATTCAAC	TATTAGATCG	CTTGAGAGAG	TCCTGACCAC	ATACGCACCT	1620
AACAAGGGAT	TCTCGGCTTT	CTTAGGAGGA	AGCAGAGCCA	CCCAATATGC	CGTTTATTTA	1680
GAAGGCCCTT	GTCCTCCGTC	AGAATTTTAT	GAATATTTAC	CTTATTCTTT	ATATCACAA	1740
CTCTCGACTG	TTGTTGGCGA	AATGTTGCTA	TCATCCATTA	TCAATACTAA	TTCTGTTGAT	1800
ACGTATTGCA	AATTCAACTT	CAATTTGCTT	GGCGACCTCG	CACTAAACAT	TATGGCTCAT	1860
GGCATGGAGG	TTAGTAATTG	TATTACACTA	CCAAACAACA	CGATTATAAG	CAGTCCGATA	1920
ACAATAAAAA	ATGGTGGCTG	CCTAAAAATA	CCGAAAAAAG	GAGTTTTGCA	TTTTACTAAT	1980
AATGGCTCCA	TACAAGTCAT	GTCCGGAGGA	ACTCTGGAAA	TAGGCAATCA	GGCTAAAAATA	2040
TCCGGAGAGA	CCGGTGCTAA	CCCCACCTTT	ATTACCGTTT	ACGGCGATGG	TCTTGCGATT	2100
AACAAGCAGG	TAGAGATAGA	CAATATAGAC	CGACTTAAC	TGTTTTCTAC	GCATTGCGTC	2160
ATGCCCAAAT	TTCATTTTGA	CAGTGTGAAA	TTCAACAGTG	CCCCGCTGTA	TACAACGAAC	2220
TGTATTGTGG	AGATAAGCAA	TGCGGAATTT	ACCAATCGAA	GTGACATTAT	TTCAAAGAAT	2280
TGTGACCTAA	GCGTTGAAAA	CAGTATGTTT	AGCAGTTCGG	GGATAACGGT	ATTCAAGCCT	2340
ATGGCTACAA	GCTCCATCAC	CGGATTATCT	ACAAAAGCAA	AGATTACCGA	CAATACTTTT	2400
TTTGCGACAG	GAAACTTCGC	CTACCATATC	ACAAACACGC	CAGGCTTAAC	AGCAACCTCC	2460
AATGCTGCCA	TCAAGTTAGA	CAATATTCCT	GAGTATTACA	TTTCCGGTAA	TAAAATAGTC	2520
AATTGCGATG	AGGCTCTTGT	ACTAAATAAT	AGTGGCAACA	GAACGAACAG	ACTCCACAAT	2580
ATCACACGGA	ATGTGATAAA	AAACTGTAGG	ATTGGGAGCA	CGCTTTATAA	TTCTATGGT	2640
ATTTACAACC	GAAATAAGAT	CAGTAACAAT	CATATAGGAG	TACGTCTCCT	CAACAACAGT	2700
TGTTTTTATT	TCGATAATGC	TCTGTAAATC	AATGAAGAAG	ATAAGCAGAC	GTTTATTTCT	2760

AATAGGACTT	GGCAGCTCTA	TTCATCAAAC	GGTACATTCC	CTCTCAACTT	CCATTACAAC	2820
AGCTTGCAGG	GGGGAGATAC	AGATACATGG	ATTTACAACG	ACACGTATAC	GAATCGCTAT	2880
ATTGACGTTT	CAAATAATCA	CTGGGGCAAC	AATGATTGTG	TTGATCCGAA	TCAGGTTTTC	2940
AATACGCCAG	ACTTGTTCAT	TTGGATACCT	TTTTGGGATG	GATTGCCAAA	TGGGAGATCG	3000
GGCAATAGCT	CTGCTGAAGC	AGTAGAATTC	CAAACAGCAT	TGGACTGTAT	TGGCAATAGC	3060
GATTATCTTT	CGGCAAAAGT	GGCTCTCAAG	ATGATGGTTG	AAACCTACCC	GGAATCCGAC	3120
TTTGCAATAG	CTGCTTTGAA	GGAATTGTTC	AGGATAGAGA	AAATGTCAGG	CAACGATTAC	3180
GAAGGCTTGA	AAGATTATTT	CAGATCCAAT	CCAACCATCA	TCTCTTCCCA	GAACCTGTTC	3240
CCGACAGCTG	ATTTCCTGTC	TGCGCGATGC	GATATTGTGT	GTGAAAACCTA	TCAGTCTGCC	3300
ATCGATTGGT	ACGAAAATCG	CTTGAATAGT	GAAATCTCCT	ATCAGGACAG	TGTTTTTGCA	3360
GTCATTGACC	TTGGTGACAT	TTATTGGAAT	ATGCAGTTAG	ACTCACTCAG	AGGGACTGGT	3420
ATAGATTTGA	ACATACTTTC	CTGTGAACAA	AGGAAATCGC	TCGAAAGCCA	TCAAAATGTA	3480
AAAAATTATT	TGTTGTCAAC	TCTTCCCAG	TCAACAGGTA	CTCTCCTGCC	TCCATTAGAA	3540
TGCAACAAAT	CAAGCCTTGA	TAAATCCAAG	ATAATCTCTA	TTTCGCCCAA	TCCGGCGAAA	3600
GCTGTTGTAA	CAATAATCTA	TACACCGAT	AACCTTTCCT	GTTCTGTAAAT	AAAAATATAT	3660
GGAAATAAATG	GAGCCTCGGC	TGATATAACC	GGGTGCCCCA	AACATCTATC	CGAAGGTTAT	3720
TACAGCATAC	AGTTCAATAC	ATCCAACCTT	GATCCCAGGT	TCTACCTGGT	AACGCTAAAT	3780
GTTGATCAGA	AAATTATAGA	TACGGAAAAA	TTACGAATCA	AA		3822

(2) INFORMATION FOR SEQ ID NO:203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

ATGGCTATCA	TGATGAAAAG	TATTGTTTTT	AGAGCATTTC	TAACGATTTT	GCTCTCGTGG	60
GCAGCGATCA	CGAATCCGAC	TGTCGAAGAG	ATCTCAGGCA	TGAATGCATC	CTGTCTGGCT	120
GCTCCGGGTC	AACCGGATAC	TATCTTATAT	GAAAGTTTTG	AGAATGGACC	TGTTCCCAAT	180
GGCTGGCTTG	AGATAGATGC	TGATGCTGAT	GGTGCCACTT	GGGGAAGCCC	ATCAGGCTCT	240
TTCTCTGTAC	CTTACGGACA	CAATGGCCTT	TGCACCTACT	CCCATATACG	TTCCGGTATC	300
TCAACAGCGG	GCAACTATCT	GATTACACCC	AATATAGAAG	GAGCCAAACG	GGTCAAGTAC	360
TGGGTATGCA	ATCAGTATAG	TACCAATCCG	GAACATTACG	CAGTAATGGT	ATCGACAACG	420
GGGACTGCCA	TTGAAGACTT	TGTTTTGTG	TTTGATGATT	CCATAACAGG	GAAACCGACT	480
CCTCTTGAT	GGCGTAGACG	AATCGTGGAC	TTACCGGAAG	GGACCAAATA	TATTGCATGG	540
CGACATTACA	AAGTCACCGA	CTCACACACA	GAATTCTTGA	AATTGGATGA	TGTCACTGTG	600
TATAGGTCGA	TCGAAGGGCC	CGAACCTGCT	ACCGACTTCA	CAGTAATCAA	TATTGGTCAG	660
AATGTGGGAC	GATTGACTTG	GAACTATCCG	GAGGATTATC	AACCGGAAGG	AAAGGGGAAT	720
GAAGAGTTGC	AGCTTAGCGG	CTACAACATC	TATGCGAACG	GTACACTACT	GGCACAATA	780
AAAGATGTCT	CCATACTGGA	GTATGTGGAC	AGCACTTACT	CTTGCGGAGA	CAATCCCCTG	840
CAAGTGGAGT	ACTGCGTTAC	AGCCGTTTAC	GATGAAAGCA	TAGAATCTTC	GACCGTATGT	900
GGCACGCTGC	ATTACGCCAC	GGATGCCATC	CTTTATGAAA	ATTTTGAGAA	TGGACCTGTT	960
CCCAATGGTT	GGCTTGTGAT	AGACGCTGAT	GGAGATGGAT	TTAGCTGGGG	ACACTATTTG	1020
AATGCATACG	ACGCTTTTCC	CGGCCATAAT	GGAGGCCATT	GCTCCTTGTC	GGCTTCTTAT	1080
GTTCGGGGTA	TAGGCCCGGT	GACTCCCGAC	AACTATCTGA	TTACCCCCAA	GGTTGAAGGA	1140
GCCAAACGTG	TCAAAGTACT	GCTAAGCAGC	CAGGATGCCA	ATTGGGCAGC	GGAAACATTAC	1200
GCGGTGATGG	CTTCGACAAC	GGGGACTGCT	GTCCGAGATT	TCGTCAATAT	GTTTGAAGAA	1260
ACCATGACAG	CGAAGCCGAC	CGGCGCATGG	TATGAAAGAA	CCATCAACTT	ACCTGAAGGG	1320
ACTAAATACA	TCCATCTGGC	GCATTACAAC	TGTACCGATA	TATATTTCTT	GAAGTTGGAC	1380
GATATCACTG	TATTCGGGAC	CTCTGCATCA	GAGCCCGAAC	CTGTTACCGA	TTTCGTTGTC	1440
TCGCTTATTG	AAAAACAACAA	GGGACGATTA	AAGTGAATT	ATCCTAACCG	CTACGAACCC	1500
GATAAGACTG	ATGATAAAGA	CCCATTGCAG	CTTGCCGGCT	ACAATATCTA	TGCAACCGGC	1560
TCGCTCCTTG	TTACATACAT	AGACCCGACT	GTTTTGGAGT	ATATCGATGA	GACTTATTCT	1620
TCACGAGACG	ATTACGGTGA	ATTGGGAATAT	TGTGTCACCT	CCGTTTATAA	CGACAATATC	1680
GAGTCCCAAT	CGGTTTGCGA	TAAGCTGATT	TATGATTCTC	AATCGGACAT	TATCTTATAT	1740
GAAGGCTATT	AGGCCGGAAG	TATTCCTGAA	GGCTGGTTGT	TGATTGATGC	TGATGGCGAC	1800
AATGTTAATT	GGGACTATTA	TCCTTGGACT	ATGTATGGAC	ATGACAGTGA	GAAGTGTTAT	1860
GCATCCCCTT	CGTACTTACC	GATGATTGGC	GTTTAACTC	CGGATAACTA	TTTGGTTACA	1920
CCCAGACTCG	AAGGAGCCAA	GCTTGTCAAG	TATTGGGTAA	GTGCGCAAGA	TGCTGTTTAT	1980
TCGGCTGAGC	ATTATGCTGT	GATGGTTTCT	ACTACGGGAA	CTGCTGTTGA	AGATTTTGTC	2040

CTCTGTTCG	AAGAGACAAT	GACCGCTAAG	GCTAACGGTG	CATGGTATGA	GCGAACTATT	2100
ACATTGCCTG	CAGGAACAAA	ATATATTGCC	TGGCGGCATT	ATGATTGCAC	CGATATGTTT	2160
TTCTTGCTCT	TGGATGACAT	TACGGTTTAT	CGTTCTACTG	AGACTGTTCC	CGAGCCTGTT	2220
ACTGATTTTCG	TTGTCTCGCT	TATTGAGAAT	AACAAGGGTC	GCCTGAAATG	GAATTATCCT	2280
AACGGCTACG	AACCCGATAA	GACTGATGAT	AAAAAACCAT	TGCAGCTTAC	CGGCTACAAC	2340
ATCTATGCAA	ATGGCTCGCT	CCTTGTTCAC	ATACAAGACC	CGACTGTTTT	GGAGTATATC	2400
GATGAGACTT	ATTCTTTCAG	AGACGGTCAG	GTGGAAATGG	AATATTGTGT	CACTGCCGTT	2460
TATAACGACA	ATATCGAGTC	CCAATCGGTT	TGCGATAAGC	TGAACTATAC	TATCACATCC	2520
TTGGATAATA	TTCAATCTGA	TACAAGCTTG	AAAATATATC	CTAATCCGGC	ATCGTATGTG	2580
GTAAGGATAG	AGGGATTGAG	TCGGAGCAAG	TCGACAATCG	AGTTGTATAA	TGCGCTGGGA	2640
ATTTGCATAT	TAAGGGAAGA	GACTCATTCA	GAGAAAACGG	AAATCGATGT	TTCACGTCTC	2700
AATGACGGAG	TCTACTTGAT	TAAAGTAGTC	GGTGAAATA	AAACAACAAC	CGAAAAGGTA	2760
GAGATAAAGA	GGCCG					2775

(2) INFORMATION FOR SEQ ID NO:204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2766
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

ATGATGAAAA	GTATTGTTTT	TAGAGCATTT	CTAACGATTT	TGCTCTCGTG	GGCAGCGATC	60
ACGAATCCGA	CTGCTCAAGA	GATCTCAGGC	ATGAATGCAT	CCTGTCTGGC	TGCTCCGGCT	120
CAACCGGATA	CTATCTTATA	TGAAAGTTT	GAGAATGGAC	CTGTTCCTCA	TGCTGGCTT	180
GAGATAGATG	CTGATGCTGA	TGGTGCCACT	TGGGGAAGCC	CATCAGGCTC	TTTCTCTGTA	240
CCTTACGGAC	ACCAATGGCTT	TGCACTTAC	TCCCATATAC	GTTCGGGTAT	CTCAACAGCG	300
GGCAACTATC	TGATTACACC	CAATATAGAA	GGAGCCAAAC	GGGTCAAGTA	CTGGGTATGC	360
AATCAGTATA	GTACCAATCC	GGAACATTAC	GCAGTAATGG	TATCGACAAC	GGGACTGCC	420
ATTGAAGACT	TTGTTTTGTT	GTTTGATGAT	TCCATAACAG	GGAAACCGAC	TCCTCTTGTA	480
TGGCTTAGAC	GAATCGTGGA	CTTACCGGAA	GGGACCAAAT	ATATTGCATG	GCGACATTAC	540
AAAGTCACCG	ACTCACACAC	AGAATTCTTG	AAATTGGATG	ATGTCACTGT	GTATAGGTCG	600
ATCGAAGGGC	CGGAACCTGC	TACCGACTTC	ACAGTAATCA	ATATTGGTCA	GAATGTGGGA	660
CGATTGACTT	GGAACTATCC	GGAGGATTAT	CAACCGGAAG	GAAAGGGGAA	TGAAGAGTTG	720
GAGCTTAGCG	GCTACAACT	CTATCGCAAC	GGTACACTAC	TGGCACAAAT	AAAAGATGTC	780
TCCATACTGG	AGTATGTGGA	CAGCACTTAC	TCCTTGGCAG	ACAATCCCTT	GCAAGTGGAG	840
TACTGCGTTA	CAGCCGTTTA	CGATGAAAGC	ATAGAATCTT	CGACCGTATG	TGGCACGCTG	900
CATTACGCCA	CGGATGCCAT	CCTTTATGAA	AATTTTGAGA	ATGGACCTGT	TCCCAATGGT	960
TGGCTTTGTA	TAGACGCTGA	TGGAGATGGA	TTTAGCTGGG	GACACTATTT	GAATGCATAC	1020
GACGCTTTTC	CCGGCCATAA	TGGAGGCCAT	TGCTCCTTGT	CGGCTTCTTA	TGTTCCGGGT	1080
ATAGGCCCGG	TGACTCCCGA	CAACTATCTG	ATTACCCCCA	AGGTTGAAGG	AGCCAAACGT	1140
GTCAAGTACT	GGGTAAGCAC	GCAGGATGCC	AATTGGGCAG	CGGAACATTA	CGCGGTGATG	1200
GCTTCGACAA	CGGGGACTGC	TGTCGGAGAT	TTCGTCATAT	TGTTCGAAGA	AACCATGACA	1260
GCGAAGCCGA	CCGGCGCATG	GTATGAAAGA	ACCATCAACT	TACCTGAAGG	GACTAAATAC	1320
ATCGCATGGC	GGCATTACAA	CTGTACCGAT	ATATATTCTT	TGAAGTTGGA	CGATATCACT	1380
GTATTCCGGA	CTCCTGCATC	AGAGCCCGAA	CCTGTTACCG	ATTTCGTTGT	CTCGCTTATT	1440
GAAAACAACA	AGGGACGATT	AAAGTGAAT	TATCCTAACG	GCTACGAACC	CGATAAGACT	1500
GATGATAAAG	ACCCATTGCA	GCTTGCCGGC	TACAATATCT	ATGCAAACGG	CTCGCTCCTT	1560
GTTACATAGC	AAGACCCGAC	TGTTTTGGAG	TATATCGATG	AGACTTATTC	TTCACGAGAC	1620
GATCAGGTGG	AAGTGAATA	TTGTGTCACT	GCCGTTTATA	ACGACAATAT	CGAGTCCCAA	1680
TCGGTTTGGC	ATAAGCTGAT	TATGATTCT	CAATCGGACA	TTATCTTATA	TGAAGGCTTT	1740
GAGGCCGGAA	GTATTCCTGA	AGGCTGGTTG	TTGATTGATG	CTGATGGCGA	CAATGTTAAT	1800
TGGGACTATT	ATCCTTGGAC	TATGTATGGA	CATGACAGTG	AGAAGTGTAT	TGCATCCCTT	1860
TCGTACTTAC	CGATGATTGG	CGTTTTAACT	CCGGATAACT	ATTTGGTTAC	ACCCAGACTC	1920
GAAGGAGCCA	AGCTTGTCAA	GTATTGGGTA	AGTGCGCAAG	ATGCTGTTTA	TTCGGCTGAG	1980
CATTATGCTG	TGATGGTTTC	TACTACGGGA	ACTGCTGTTG	AAGATTTTGT	CCTCTTGTTT	2040
GAAGAGACAA	TGACCGCTAA	GGCTAACGGT	GCATGGTATG	AGCGAAGTAT	TACATTGCCT	2100
GCAGGAACAA	AATATATTGC	CTGGCGGCAT	TATGATTGCA	CCGATATGTT	TTTCTTGCTC	2160
TTGGATGACA	TTACGGTTTA	TCGTTCTACT	GAGACTGTTC	CCGAGCCTGT	TACTGATTTC	2220
GTTGTCTCGC	TTATTGAGAA	TAACAAGGGT	CGCCTGAAAT	GGAATTATCC	TAACGGCTAC	2280
GAACCCGATA	AGACTGATGA	TAAAAAACCA	TGTCAGCTTA	CCGGCTACAA	CATCTATGCA	2340

AATGGCTCGC	TCCTTGTTC	CATACAAGAC	CCGACTGTTT	TGGAGTATAT	CGATGAGACT	2400
TATTCTTCAC	GAGACGGTCA	GGTGGAAATG	GAATATTGTG	TCAGTCCCGT	TTATAACGAC	2460
AATATCGAGT	CCCAATCGGT	TGCGATAAG	CTGAACATA	CTATCACATC	CTTGGATAAT	2520
ATTCAATCTG	ATACAAGCTT	GAAAATATAT	CCTAATCCGG	CATCGTATGT	GGTAAGGATA	2580
GAGGGATTGA	GTCGGAGCAA	GTCGACAATC	GAGTTGTATA	ATGCGCTGGG	AATTTGCATA	2640
TTAAGGGAAG	AGACTCATTC	AGAGAAAACG	GAAATCGATG	TTTCACGTCT	CAATGACGGA	2700
GTCTACTTGA	TTAAAGTAGT	CGGTGGAAAT	AAAACAACAA	CCGAAAAGGT	AGAGATAAAG	2760
AGGCCG						2766

(2) INFORMATION FOR SEQ ID NO:205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

ATGAAAAGTA	TTGTTTTTAG	AGCATTCTA	ACGATTTTGC	TCTCGTGGGC	AGCGATCAGC	60
AATCCGACTG	CTCAAGAGAT	CTCAGGCATG	AATGCATCCT	GTCTGGCTGC	TCCGGCTCAA	120
CCGGATACTA	TCTTATATGA	AAGTTTTGAG	AATGGACCTG	TTCCCAATGG	CTGGCTTGAG	180
ATAGATGCTG	ATGCTGATGG	TGCCACTTGG	GGAAGCCCAT	CAGGCTCTTT	CTCTGTACCT	240
TACGGACACA	ATGGCCTTTG	CACCTACTCC	CATATACGTT	CCGGTATCTC	AACAGCGGGC	300
AACTATCTGA	TTACACCCAA	TATAGAAGGA	GCCAAACGGG	TCAAGTACTG	GGTATGCAAT	360
CAGTATAGTA	CCAATCCCGA	ACATTACGCA	GTAATGGTAT	CGACAACGGG	GACTGCCATT	420
GAAGACTTTG	TTTTGTTGTT	TGATGATTCC	ATAACAGGGA	AACCGACTCC	TCTGTATGG	480
CGTAGACGAA	TCGTGGACTT	ACCGGAAGGG	ACCAAATATA	TTGCATGGCG	ACATTACAAA	540
GTCACCGACT	CACACACAGA	ATTCCTTGAA	TTGGATGATG	TCAGTGTGTA	TAGGTCGATC	600
GAAGGGCCCG	AACCTGCTAC	CGACTTCACA	GTAATCAATA	TTGGTCAGAA	TGTGGGACGA	660
TTGACTTGGA	ACTATCCCGA	GGATTATCAA	CCGGAAGGAA	AGGGGAATGA	AGAGTTGCAG	720
CTAGCGGCT	ACAACATCTA	TGCGAACGGT	ACACTACTGG	CACAAATAAA	AGATGTCTCC	780
ATACTGGAGT	ATGTGGACAG	CACTTACTCT	TTGCGAGACA	ATCCCTTGCA	AGTGGAGTAC	840
TGCGTTACAG	CCGTTTACGA	TGAAAGCATA	GAATCTTCGA	CCGTATGTGG	CACGCTGCAT	900
TACGCCACGG	ATGCCATCCT	TTATGAAAAT	TTTGAGAAATG	GACCTGTTCC	CAATGGTTGG	960
CTTGTTGATAG	ACGCTGATGG	AGATGGATTT	AGCTGGGGAC	ACTATTTGAA	TGCATACGAC	1020
GCTTTTCCCG	GCCATAATGG	AGGCCATTGC	TCCTTGTGCG	CTTCTTATGT	TCCGGGTATA	1080
GGCCCGGTGA	CTCCCGACAA	CTATCTGATT	ACCCCAAGG	TTGAAGGAGC	CAAACGTGTC	1140
AAGTACTGGG	TAAGCACGCA	GGATGCCAAT	TGGGCAGCGG	AACATTACGC	GGTGATGGCT	1200
TCGACAACGG	GGACTGCTGT	CGGAGATTTC	GTCAATTTGT	TCGAAGAAAC	CATGACAGCG	1260
AAGCCGACCG	GCGCATGGTA	TGAAAGAACC	ATCAACTTAC	CTGAAGGGAC	TAAATACATC	1320
GCATGGCGGC	ATTACAACCTG	TACCGATATA	TATTTCTTGA	AGTTGGACGA	TATCACTGTA	1380
TTCCGGACTC	CTGCATCAGA	GCCCGAACCT	GTTACCGATT	TCGTTGTCTC	GCTTATTGAA	1440
AACAACAAGG	GACGATTAAA	GTGGAATTAT	CCTAACGGCT	ACGAACCCGA	TAAGACTGAT	1500
GATAAAGACC	CATTGCAGCT	TGCCGGCTAC	AATATCTATG	CAAACGGCTC	GCTCCTTGTT	1560
CACATACAAG	ACCCGACTGT	TTGGGAGTAT	ATCGATGAGA	CTTATTCTTC	ACGAGACGAT	1620
CAGGTGGAAG	TGGAATATTG	TGTCACTGCC	GTTTATAACG	ACAATATCGA	GTCCCAATCG	1680
GTTTGCAGTA	AGCTGATTTA	TGATTCTCAA	TCGGACATTA	TCTTATATGA	AGGCTTTGAG	1740
GCCGGAAGTA	TTCTGGAAGG	CTGGTTGTTG	ATTGATGCTG	ATGGCGACAA	TGTTAATTGG	1800
GACTATTATC	CTTGGACTAT	GTATGGACAT	GACAGTGAGA	AGTGATTATG	ATCCCTTCG	1860
TACTTACCGA	TGATTGGCGT	TTTAACTCCG	GATAACTATT	TGGTTACACC	CAGACTCGAA	1920
GGAGCCAAAG	TTGTCAAGTA	TTGGGTAAGT	GCGCAAGATG	CTGTTTATTC	GGCTGAGCAT	1980
TATGCTGTGA	TGGTTTCTAC	TACGGGAAC	GCTGTTGAAG	ATTTTGTCTT	CTTGTTCGAA	2040
GAGACAATGA	CCGCTAAGGC	TACCGGTGCA	TGGTATGAGC	GAAGTATTAC	ATTGCCTGCA	2100
GGAACAAAAT	ATATTGCCTG	GCGGCATTAT	GATTGCACCG	ATATGTTTTT	CTTGCTCTTG	2160
GATGACATTA	CGGTTTATCG	TTCTACTGAG	ACTGTTCCCG	AGCCTGTTAC	TGATTTCTGT	2220
GTCTCGCTTA	TTGAGAATAA	CAAGGGTCGC	CTGAAATGGA	ATTATCCTAA	CGGCTACGAA	2280
CCGATAAAGA	CTGATGATAA	AAAACCATTC	CAGCTTACCG	GCTACAACAT	CTATGCAAAT	2340
GGCTCGCTCC	TTGTTACAT	ACAAGACCCG	ACTGTTTTGG	AGTATATCGA	TGAGACTTAT	2400
TCTTCACGAG	ACGGTCAGGT	GGAATGGA	TATTGTGTCA	CTGCCGTTTA	TAACGACAAAT	2460
ATCGAGTCCC	AATCGGTTTG	GATAAGCTG	AACTATACTA	TCACATCCTT	GGATAATATT	2520
CAATCTGATA	CAAGCTTGAA	AATATATCCT	AATCCGGCAT	CGTATGTGGT	AAGGATAGAG	2580
GGATTGAGTC	GGAGCAAGTC	GACAATCGAG	TTGTATAATG	CGCTGGGAAT	TTGCATATTA	2640

AGGGAAGAGA CTCATTGAGA GAAAACGGAA ATCGATGTTT CACGTCTCAA TGACGGAGTC 2700
TACTTGATTA AAGTAGTCGG TGGAAATAAA ACAACAACCG AAAAGGTAGA GATAAAGAGG 2760
CCG 2763

(2) INFORMATION FOR SEQ ID NO:206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

ATGAACAGCA	TCATGAAATA	TCAATTATAT	ACGGCCGTCA	TAATGGCTCT	CTCTGTATCA	60
TCCGTTTTCG	GTCAAACCCC	ACGAAATACA	GAAACCAAAC	GCCCCGACAC	GCTGCGCAGG	120
GAGCTTACTA	TCGTTAATGA	CCAGACTGTG	GAGATGGAGC	ATGCGGATCC	GCTTCCGGCT	180
GCATACAAGG	CCATCGAACC	TCGATTAAAA	CCTTTCCGTC	CGGAATATAA	CAAGCGTACA	240
TTCGGATTTC	TCCCTGAAGT	TTCTCTTTCA	GGCAGGAACA	ATCTTCCGAA	TATCCTGCCG	300
ACGGAAGGTC	ATATGAAGCA	CCGGGGGTAC	CTGAATATCG	GTATCGGCCA	TACGCTAAAC	360
CAGCGAATGG	ATGCCCGGCT	TCGTCTGATA	GATGCAGAGC	AGGAGAGACT	GAATCTTTTC	420
CTCTCCTATC	GTGGGATGAA	ATCGGCTTTC	AATACCGGTG	ACTTCGACGG	CGACAGAAAG	480
GATAGACGAA	TGATGGCAGG	AGTGGACTAC	GAGCAGCGCA	GGCCTTCCTT	TGTGCTTGCT	540
ACCGGCTTGT	ATTATTCGAA	CCATTATTTT	AATAACTACG	GACGGGGAGC	TACCACCAAT	600
GTGGGCAGCA	TCCCTCAGCT	ATCGACACCT	GTACTCCTC	AGATGGACAA	CGGGACCCAC	660
AACGTCCGTG	TATACTTGGG	TGCAAAAAAT	GATGTGATCG	ATGCCAGGAT	CGACTATCGT	720
TTCTTCCGTT	CTATTCCCTA	TCGGGTACCC	GATCCGATGA	AGGCTCTCAC	AGAACATACG	780
CCTGAAGTGA	ACGTGACGAT	GAGTAATGAG	TTGTCCGATG	ATATTAAGCT	CGGTGTGCGA	840
GTTCGTACGG	GAGGATTGTT	TTTGTCCAAA	AACAGCGAAA	TGATTCAAAC	GGGCGTTCTG	900
TCCGAAACCG	ACCGCAACCT	GTATTATGTG	GAGGGCGCGC	CCACAATCGG	ATTTGTGCGA	960
GACTCGGACA	ATATGCAATG	GAACATACAG	GCCGGAGTAG	GGATTTCTTC	CCATTTCCGA	1020
GCCAAAGGGA	GGTTGTTTTT	CTGGCCTAAA	CTGGATGCTT	CGCTTAGTAT	CTTCCCTTCA	1080
TGGCGTGTGT	ATGCGAAAGC	CTTCGGCGGT	GTGATTTCGAA	ATGGTCTCGC	CGATGTTATG	1140
CAAGAGGAGA	TGCCCTACCT	GATGCCCAAT	ACGATTGTAC	TCCCTTCGCG	CAATGCTTTG	1200
ACCGCCCAAT	TAGGGGTGAA	GGGGAATATA	GCCGATGTGG	TACGTATGGA	GGTTTATGGC	1260
GACTTCTCCA	AGCTGACAGG	TGTGCCTTTC	TATACTCCGA	CTCTACCCTT	ATATAATCCA	1320
TCCGACTTGT	ATCAGTATAA	TGTGAGTTTC	TTGCCGATAT	ATGCCGACGG	CAGCCGCTGG	1380
CGCGCAGGTG	GTAAGCTGGA	ATACTCTTAT	CGCGATATGC	TCCGCTTTCT	GGTAGACGCA	1440
TCCTATGGCA	AGTGGAATTT	GGATGGAGGA	CTGTGCGCCT	CCATGCAGCC	CGATCTTATA	1500
TTGAAGGCAG	AAGTAGGTGT	TCATCCCATT	GCCCCATTGG	ATGTCAGACT	CCGGTATACA	1560
CAGCTGAACG	GACGGTATCG	GATTCTTTTC	GGCTCGGCTG	GCTCGGAAGC	CTTGGGTATC	1620
GGTAATGTAC	ATCTTCTTAG	TGCGGATGTT	TCATACAAGC	TGAAAAAGAA	CTTGAGCCTT	1680
TATCTCAAAA	TCGATAATAT	GCTGGCGGAA	ACGACAGAGC	TTATCGGTTA	TTATCCTATG	1740
CAGCCGTTC	ATTGTTTCGC	CGGTTTTAGC	TGGACTTTTC			1779

(2) INFORMATION FOR SEQ ID NO:207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

```
ATGAAATATC AATTATATAC GGCCGTCATA ATGGCTCTCT CTGTATCATC CGTTTGCGGT      60
CAAACCCAC  GAAATACAGA AACCAAACGC CCCGACACGC TGCGCAGGGA GCTTACTATC      120
GTTAATGACC AGACTGTGGA GATGGAGCAT GCGGATCCGC TTCCGGCTGC ATACAAGGCC      180
ATCGAACCTC GATTAATAAC TTTCGGTCCG GAATATAACA AGCGTACATT CGGATTTGTC      240
CCTGAAGTTT CCTCTTCAGG CAGGAACAAT CTTCCGAATA TCCTGCCGAC GGAAGGTCAT      300
ATGAAGCACC GGGGGTACCT GAATATCGGT ATCGGCCATA CGCTAAACCA GCGAATGGAT      360
GCCGGCTATC GTCTGATAGA TGACAGAGCAG GAGAGACTGA ATCTTTTCTT CTCCTATCGT      420
GGGATGAAAT CGGCTTTCAA TACCGGTGAC TTCGACGGCG ACAGAAAGGA TAGACGAATG      480
ATGGCAGGAG TGGACTACGA GCAGCGCAGG CCTTCCTTTG TGCTTGCTAC CGGCTTGAT      540
TATTCGAACC ATTATTTCAA TAACTACGGA CGGGGAGCTA CCACCAATGT GGGCAGCATC      600
CCTCAGCTAT CGACACCTGT TACTCCTCAG ATGGACAACG GGACCCACAA CGTCCGTGTA      660
TACTTGGGTG CAAAAATGA  TGTGATCGAT GCCAGGATCG ACTATCGTTT CTTCGGTTCT      720
ATTCCCTATC TGGGTACGAG CGAGTAGGG  ATTCTTCCC  ATTTGCGAGC CAAAGGGAGG      780
GTGACGATGA GTAATGAGTT GTCCGATGAT ATTAAGCTCG GTGTCGAAGT TCGTACGGGA      840
GGATTGTTTT TTGCCAAAAA CAGCGAAATG ATTCAAACGG GCGTTCTGTC CGAAACCGAC      900
CGCAACCTGT ATTATGTGGA GGGCGCGCCC ACAATCGGAT TTGTCGGAGA CTCGGACAAT      960
ATGCAATGGA ACATACAGGC CGAGTAGGG  ATTCTTCCC  ATTTGCGAGC CAAAGGGAGG     1020
TTGTTTTTCT GGCCTAAACT GGATGCTTCG CTTAGTATCT TCCCTTCATG GCGTGTGTAT     1080
GCGAAAGCCT TCGGCGGTGT GATTGCAAAT GGTCTCGCGG ATGTTATGCA AGAGGAGATG     1140
CCCTACCTGA TGCCCAATAC GATTGTACTC CCTTCGCGCA ATGCTTTGAC CGCCCAATTA     1200
GGGGTGAAGG GGAATATAGC CGATGTGTA  CGTATGGAGG TTTATGGCGA CTTCTCCAAG     1260
CTGACAGGTG TGCTTTCTA  TACTCCGACT CTACCCTTAT ATAATCCATC CGACTTGTAT     1320
CAGTATAATG TGAGTTTCTT GCCGATATAT GCCGACGGCA GCCGCTGGCG CGCAGGTGGT     1380
AAGCTGGAAT ACTCTTATCG CGATATGCTC CGCTTCTTGG TAGACGCATC CTATGGCAAG     1440
TGGAATTGG  ATGGAGGACT TGTCGCCTCC ATGCAGCCCG ATCTTATATT GAAGGCAGAA     1500
GTAGGTGTTT ATCCCATTCG CCCATTGGAT GTCAGACTCC GGTATACACA GCTGAACGGA     1560
CGGTATCGGT ATTCTTTTGG CTCGGCTGGC TCGGAAGCCT TGGGTATCGG TAATGTACAT     1620
CTTCTTAGTG CGGATGTTTC ATACAAGCTG AAAAAGAACT TGAGCCTTTA TCTCAAAATC     1680
GATAATATGC TGGCGGAAAC GACAGAGCTT ATCGGTTATT ATCCTATGCA GCCGTTCAT      1740
TGTTTCGCCG GTTTTAGCTG GACTTTTC                                     1767
```

(2) INFORMATION FOR SEQ ID NO:208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

```
ATGATGGAAA AATGTATCTT TGCTCACTAT CCACATAACC TTGTGTTTAT GATTGCAAG      60
CATTTTCGTA TCATTTTGGG ATTTCTTTCT CTGTGTTTTT CGGCAGGTGC TCAACAAGAG      120
AAGCAGGTGT TTCATTTTCT GAACCTTCCG GCTACTGCAC AGGCTTTGGC TGCCGGAGGC      180
AAAGCTATCA CCATCGTAGA CGACAATCCC GGACTGGCTT TTGAGAATCC GGCTCTGCTC      240
GGATATGAAT CCGGTGGCCG CGCCTTTCTT TCCTATTTAT ATTATATGAG TGGTTCGCAT      300
ATGGGCAATG CCGTTTATGC CTCGTCCGTC GGAGAGCGTG GCATGTGGGG TGTGGCATG      360
CGTTTCTGTA ACTACGGGTC TATGCAAGGA TACGATCAGA ATGCGATTGC CACCGGCTCT      420
TTAGTGCTT  CGGATATAGC TGTACAAGGA TTTTACAGCC ATGAACTGAG CAACCACTTC      480
CGCGGTGGAG TCAGCCTAAA AGCATTTGAT TCTTCTATCG AGACGTATAG TTCCTTTGGC      540
CTGGGTGTTG ATGTCGGTAT CAGTTATTAC GACGATGACA AAGGATATTC CGCTTCCGCT      600
CTGTTCAAGA ACGTAGGGGC GCAACTGAAA GGCTATAATG AAGAACGGGA ACCGCTCGAT      660
TGGGATTTC  AGCTCGGCTT TTCCCGCAGT TTTATCAATG CTCCGTTTCG CTGACATC      720
ACGTTGTTCA ATCTGAATCC GCATATTTC  AAGCGTCTTG TACCACGCGA TCTGTCCAAG      780
ATGCAAAAGT TCCTCCGACA CTCTCGATA  GGAGCAGAAT TTACTCCTTC CGAGAGGTTT      840
TGGGTCCGGC TGGGATATAC GCCACAGATT GCACAGGATT TCGAGGTGGA AGGCGGCAAC      900
AAATGGGGAG GTCTTTCCGG CGGCGTCGGT TTCACCTCAG GTGTAGTACG TGTAGGCGTA      960
```

TCTGCTGCCA CCTATCATCC TGCAGCTCTT TCGTTCATGT GTTCGGTAGG TATCCGTTTG 1020
GACGATAAGA GCATCTTC 1038

(2) INFORMATION FOR SEQ ID NO:209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

ATGGA AAAAT	GTATCTTGC	TCACTATCCA	CATAACCTTG	TGTTTCATGAT	TCGCAAGCAT	60
TTCCGTATCA	TTTTGGGATT	TCTTTCTCTT	GTGTTTTTCGG	CAGGTGCTCA	ACAAGAGAAG	120
CAGGTGTTTC	ATTTTCTGAA	CCTTCCGGCT	ACTGCACAGG	CTTTGGCTGC	CGGAGGCAAA	180
GCTATCACCA	TCGTAGACGA	CAATCCCGGA	CTGGCTTTTG	AGAATCCGGC	CTGCTCGGA	240
TATGAATCCG	GTGGCCGCGC	CTTCTTTCC	TATTTATATT	ATATGAGTGG	TTCGCATATG	300
GGCAATGCCT	GTTATGCCTC	GTCGTCGGA	GAGCGTGGCA	TGTGGGGTGT	TGGCATGCGT	360
TTCTGAACT	ACGGGTCTAT	GCAAGGATAC	GATCAGAATG	CGATTGCCAC	CGGCTCTTTT	420
AGTGCTTCGG	ATATAGCTGT	ACAAGGATTT	TACAGCCATG	AACTGAGCAA	CCACTTCCGC	480
GGTGGAGTCA	GCCTAAAAGC	ATTGTATTCT	TCTATCGAGA	CGTATAGTTC	CTTTGGCCTT	540
GGTGTGGATG	TCGGTATCAG	TTATTACGAC	GATGACAAAG	GATATTCCGC	TTCCGCTCTG	600
TTCAAGAACG	TAGGGGCGCA	ACTGAAAGGC	TATAATGAAG	AACGGGAACC	GCTCGATTGG	660
GATTTCCAGC	TCGGCTTTTC	CCGCAGTTTT	ATCAATGCTC	CGTTTCGCTT	GCACATCACG	720
TTGTTC AATC	TGAATCCGCA	CTATTTCAAG	CGTCTTG TAC	CACGCGATCT	GTCCAAGATG	780
CAAAAGTTCC	TCCGACACTT	CTCGATAGGA	GCAGAATTTA	CTCCTTCCGA	GAGGTTT TGG	840
GTGGGGCTGG	GATATACGCC	ACAGATTGCA	CAGGATTTCG	AGGTGGAAGG	CGGCAACAAA	900
TGGGGAGGTC	TTTCGGCCGG	CGTCGGTTTC	ACTTCAGGTG	TAGTACGTGT	AGGCGTATCT	960
GCTGCCACCT	ATCATCTTGC	AGCTCTTTCG	TTCATGTGTT	CGGTAGGTAT	CCGTTTGGAC	1020
GATAAGAGCA	TCTTC					1035

(2) INFORMATION FOR SEQ ID NO:210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

ATGATTTCGCA	AGCATTTCGG	TATCATTTTG	GGATTTC TTT	CTCTTG TGT	TTCCGCAGGT	60
GCTCAACAAG	AGAAGCAGGT	GTTTCATTTT	CTGAACCTTC	CGGCTACTGC	ACAGGCTTTG	120
GCTGCCGGAG	GCAAAGCTAT	CACCATCGTA	GACGACAATC	CCGGA CTGGC	TTTGTAGAAT	180
CCGGCTCTGC	TCGGATATGA	ATCCGGTGGC	CGCGCCTTTC	TTTCTATTAT	ATATTATATG	240
AGTGGTTCGC	ATATGGGCAA	TGCCTGTTAT	GCCTCGTCCG	TCGGAGAGCG	TGGCATGTGG	300
GGTGTGGCA	TGCCTTTCCT	GAAC TACGGG	TCTATGCAAG	GATACGATCA	GAATGCGATT	360
GCCACCGGCT	CTTTTAGTGC	TTCGGATATA	GCTGTACAAG	GATTTTACAG	CCATGA ACTG	420

AGCAACCACT	TCCGCGGTGG	AGTCAGCCTA	AAAGCATTGT	ATTCTTCTAT	CGAGACGTAT	480
AGTTCTTTTG	GCCTTGGTGT	GGATGTCGGT	ATCAGTTATT	ACGACGATGA	CAAAGGATAT	540
TCCGCTTCCG	CTCTGTTCAA	GAACGTAGGG	GCGCAACTGA	AAGGCTATAA	TGAAGAACGG	600
GAACCGCTCG	ATTGGGATTT	CCAGCTCGGC	TTTTCCCGCA	GTTTTATCAA	TGCTCCGTTT	660
CGCTTGACAC	TCACGTTGTT	CAATCTGAAT	CCGCACTATT	TCAAGCGTCT	TGTACCACGC	720
GATCTGTCCA	AGATGCAAAA	GTTCTCTCGA	CACTTCTCGA	TAGGAGCAGA	ATTTACTCCT	780
TCCGAGAGGT	TTTGGGTCGG	GCTGGGATAT	ACGCCACAGA	TGACACAGGA	TTTCGAGGTG	840
GAAGGCGGCA	ACAAATGGGG	AGGTCTTTTCG	GCCGGCGTCG	GTTTCACTTC	AGGTGTAGTA	900
CGTGTAGGCG	TATCTGCTGC	CACCTATCAT	CCTGCAGCTC	TTTCGTTTCAT	GTGTTTCGGTA	960
GGTATCCGTT	TGGACGATAA	GAGCATCTTC				990

(2) INFORMATION FOR SEQ ID NO:211

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...972
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

ATGTGCCTCG	AACCCATAAT	TGCTCCGATT	TCATCCGAGT	TGCTCGAGCA	GGAGCTGACT	60
GCCGATCGTT	TTCTGCGGAT	GACAAACAAA	GCCGGCAATG	AGATCTATGT	TTTACGGCC	120
GAAGAAGCTC	CGCATTGCAT	GAAAGAAGTA	GGCCGACTGC	GAGAAGAAGC	CTTTCGGCAT	180
TATGGCGGAG	GTACTGGCAA	GGCGATCGAT	ATAGACGAGT	TCGACACCAT	GCCCGGGAGC	240
TACAAACAGC	TGATCGTATG	GGATCCGCAA	AACAAGGCTA	TACTCGGAGG	CTACCGCTTT	300
ATCTATGGGC	GGGACGTTGC	TTTCGATACC	GATGGCAAGC	CTTTGCTGGC	AACGGCAGAG	360
ATGTTTCGCT	TCAGTGATGC	TTTTTTGCAC	GATTATCTCC	CCTACACAGT	CGAATTGGGA	420
CGTTTCGTTG	TGTCGCTCCA	GTACCAATCG	ACACGGATGG	GCACAAAGGC	CATTTTGTG	480
CTGGACAATC	TTTGGGACGG	TATCGGAGCA	CTCACTGTAG	TCAATCCAGA	GGCACTCTAT	540
TTCTATGGCA	AGGTGACCAT	GTACAAAGAC	TATGATCGGC	GAGCTCGCAA	TCTGATCCTG	600
TATTTTCTTC	GCAAGCACTT	CTCCGATCCG	GAAGGCTTGG	TCAAGCCTAT	TCATCCCCTA	660
CCGATAGAGA	TCAGTGCGGA	GGACGAAGCC	TTGTTCTCCT	CATCCGACTT	TGACACCAAT	720
TACAAGACTC	TCAATATAGA	AGTGCGCAAG	CTGGGTATCA	ATATCCCTCC	TCTCGTGAGT	780
GCATATATAG	CTTTGTCTCC	GGAGATGCGT	GTTTTCGGCA	CTGCAGTGAA	TGAGTCTTTC	840
GGAGAGGTGG	AGGAAACCGG	CATATTCAAT	GCTGTGGGTA	AGATCCTGGA	AGAGAAAAAA	900
CAACGGCACA	TAGAGAGCTT	CATCCTCAGC	CGGAACGAAA	AAAAAGGTCT	CGACAGTAGC	960
AATGGCCGAT	CA					972

(2) INFORMATION FOR SEQ ID NO:212

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1641 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1641
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

ATGAAAACCA	TTGTAAGATA	CAGCCGCCTT	CCGGTCGCTC	TCTTCTTTTG	CCTTTTGGGA	60
GCTGTGCACT	TGTCTGTGCA	GGCGCAGATG	CTCAATACTC	CTTTCGAGCT	GTCGGATCAG	120
ATCGTCTCGT	CTCCCACCGA	AAGGCAATAC	AGGGAGATTT	GTGTGCAAAC	GAAAGAAAAA	180
AGGGGGGCCG	ATCTTTTCCC	GTTGAGCGAT	AAGCTGCGCG	ATTCGGCCTA	TGTTCTGTTT	240
GGCTCGGCCT	ATGGCGATAT	TGCGGGCGAC	TATCTTCCGT	ACAACGGCAA	TAATACTCC	300
TCGCTCTCGC	TCGAATCGGG	TGGTCGCATC	AGTGTCCGTA	ACTATGGCAC	ATTGCAGGGC	360
AGTGCTTCTC	ACTCACGTGG	CATGCACAAA	CGCATCGGCT	GGAATGCTCT	GCGCAACGCC	420
GAGCCCTACT	ATCCTTATTT	GCTGTCCGAT	TCGACCGCG	GAGACTATCA	TTTCGAAGAC	480
TATCGGCTTG	CCGGCTACTA	TTCTTTTCGC	GCCGGCCGCT	TGCCCCCTCG	TATAGGCTTC	540
TCATACAGGG	GCGAAGTTGC	TTATCGGCTG	ACCGATCCGC	GTACGACCAA	TACGACCGGT	600
GCATTGGAGC	TTTCTTGTGC	TACCTCTTTG	ACGCTGCCTC	GAGAGAACAG	GCTATCGCTT	660
TCGGCTGCGT	ATCTCTATCA	TAGACAAAC	CTCACACAGT	ACAACCTGGC	TCCCGGGCAG	720
CAGGACAAAT	TCTTCGTCAG	CTACGGTTTC	GGTCAGGTGG	ATGTCAGCAA	CAGCCCTATC	780
TGGTTCGTA	TCTCCAGAAT	GAACTACGTC	AACGGATGGA	AGCTTAGCTC	CCGTCTGGAT	840
ACCCGTAGGG	GCGATGCCAT	CGGTCTCGAC	TACAGCGGCT	ACTTCTCTGA	TACCGAaGAG	900
AGGTGCTCCA	TCAATCTCTT	TGCTTTGCTT	TACAATCGCC	TGCGACTCTA	TGGTAGCTGG	960
CATCTGTGCG	ACTTCGATTT	TTCATTTTCA	GCCGACTATG	CTCTGCGCCA	AGGGATAGAG	1020
CGGATATACG	AAGACTACAA	GCCGGATGAT	AATTATCATA	TCTACGACCT	CCGTATCTTG	1080
GCCATTGCC	GCTGGTATAT	GCTCAATGAG	TTTTCTGCCC	AAGCCCAAGC	CTCCTACCGT	1140
ATTGCGACGG	ATAGAGGTGG	TGCCCTGAGA	GTGAGTGCCG	GTAGTGATTT	CTACGGCTAT	1200
GATGAGACGT	ATCGCAAGCA	TGGACATCAT	ACCATGAGCG	GAATGCTACG	TCCTTTTGCC	1260
GGTATAGCCT	ATGACCATGC	CGGATCCAAA	TTGGATTTTG	GACTTTCGCT	TTCGGCTGCT	1320
TATCGAATGG	TGCTGACGCA	TTTCGTATAAG	ATTCGTACCA	TCCAGAAAGA	GCAGCTCGAC	1380
TATCAGCTGG	CCTATTTGCC	CTATGCCTAT	CGTAATAGAG	AAGGCGTGGA	GGTGCGTTCC	1440
TCTCTGTACG	TCTCGATTCC	GATGCAGAAT	ACCCACCGCC	TGATGACAGA	GCTGCGGTTG	1500
TATGGCGACC	TGATGAAAAG	AAAGGACGGT	ATAGCCTATG	GCAAAACGCC	CGGTGTCATC	1560
TCACATATCC	TGTCCGATCC	GCAAGCCGAA	CGAACGTCCG	GCCATACCAT	CGGGGCTATC	1620
TGCAATATCT	CCTACCTCTT	C				1641

(2) INFORMATION FOR SEQ ID NO:213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

ATGAAAAAAC	TTACATGAT	TGCCGCCTTA	GCCGTCCTGC	CTTCTGCT	GACGGCACAA	60
GCACCCGTCT	CCAACAGCGA	GATAGATAGT	CTTAGCAATG	TGCAGCTCCA	GACCGTACAG	120
GTCTGTAGCTA	CTCGCGCCAC	GGCGAAAAAC	CCTGTGCTT	ACACCAACGT	TCGCAAGGCC	180
GAACTTTCCA	AGTCCAATTA	TGGTCGTGAC	ATCCCTATC	TGCTGATGCT	GACTCCCTCC	240
GTGGTAGCCA	CCAGCGATGC	CGGTACGGGT	ATCGGATATT	CCGGCTTTTG	CGTGCGTGCC	300
ACCGATGCCA	ATCGCATCAA	CATAACTACC	AATGGAGTAC	CCCTCAACGA	CTCCGAATCT	360
CAGTCCGTCT	TTTGGGTGAA	TATGCCCGAC	TTCCCTCTT	CCATCGAAGA	CCTTCAGGTG	420
CAGCGAGGTG	TGGGTACTTC	CACCAATGGT	GCCGGAGCTT	TTGGGGCAAG	TGTCAATATG	480
CGTACGGATA	ATTTGGGACT	GGCTCCTTAT	GGCCGTGTCG	ATTTGAGCGG	AGGTTCGTTT	540
GGCACATTC	GCCGATCGGT	CAAACTCGGT	AGCGGACGCA	TCGGTCGCCA	TTGGGCAGTG	600
GATGCCCGCC	TGTCCAAAAT	CGGTTCCGAC	GGCTACGTGG	ATAGAGGAAG	CGTGGATCTG	660
AAATCCTATT	TCGCACAGGT	GGGCTATTTC	GGTAGCAACA	CGGCTCTCAG	GTTTCATCACT	720
TTCCGAGGAA	AAGAGTTTAC	GGGTATCGCA	TGGAACGGTC	TTTCCAAGGA	GGATGAAGCC	780
AAATATGGCC	GCCGATACAA	CAGTGCCGGT	CTTATGTACG	TGGACGCGCA	AGGAGTACCG	840
CACCTACTACC	ACCAATACCGA	CAATTACGAG	CAGCGTCACT	ACCATGCCAT	CATGACGCAC	900
AGCTTCTCTC	CTTCCGTTAT	CCTCAACCTC	ACGGCACACT	ACACGGCCGG	ATATGGCTAT	960
ACGACGAAT	ATCGTACCGG	ACGTAAACTA	AAGGAATATG	CACTGCAGCC	CTATGTGGAA	1020
AACAGTGTGA	CCGTGAAGAA	AACGGATCTC	ATCCGTGAGA	AGTATCTGGA	CAATGACTTC	1080
GGAGGACTCA	TGCGTTTCGT	TAACTGGCAC	ACCGGTGCAT	GGGATTTGCA	GTTCCGGGCC	1140
TCGGGCAATA	TCTATAAAGG	AGACCACTTC	GGCCGTATCA	CTTACATCAA	AAAGTACAAT	1200
CAGCCCTTAG	CTCCCGACTT	CGAATATTAT	CGGAACAGGG	CAGACAAAAG	AGAAGGTGCA	1260
GCCTTTGCCA	AAGCCAACCTG	GCAGATCACT	CCGGAACCTGA	ACATGTATGC	CGACCTCCAG	1320
TATCGTACCA	TCCGCTACAC	GATAAACGGC	ATCACGGACG	AATATGATGA	GGTACAGGGA	1380
AGTATGCAGC	ACATCGATTT	GGACAAGACC	TTCCGCTTCC	TCAATCCGAA	GGCCGGTCTT	1440

ACCTATAGTT	TCGACGATGC	TCATACTGCC	TATGCTTCTG	TTGCGGTAGC	ACACCGCGAG	1500
CCTAACAGAA	CCAATTACAC	CGAAGCCGGA	ATAGGACAGT	ATCCTACGCC	TGAGCGACTG	1560
ATCGACTATG	AGCTGGGCTA	CCGCTATGCT	TCGCCCCTCT	TGTCGGCCCG	AGTAGGTCTC	1620
TATTATATGC	AATACAAGGA	CCAACTCGTG	CTGGATGGCC	GTTTGAGCGA	TGTGGGACAG	1680
ATGCTCACAA	GCAACGTCCC	CGACAGCTAC	CGTATGGGAC	TGGAGCTGAC	TCTCGGTTGG	1740
CAGATCCTTC	CTCGTTTGCT	GCGTTGGGAT	GCTTCTTTCA	CTATGAGTCG	CAACAAAATC	1800
GACCGCTACG	TACAATATAC	ATCCGTATAT	GATGCGGACT	ACAACTGGCT	CGAACTCAAG	1860
GAGGAGACCC	TCGAAAGCAC	GGATATAGCC	TACTCGCCCA	ATGTCATTGC	CGGCAGCATG	1920
CTTACCCCTCT	CTCATGCCGG	TTTCGAAATG	GCTTGGACGA	GCCGCTTCGT	CAGCAAGCAA	1980
TATCTGGACA	ATACACAGCG	CAGCGATCGC	ATGCTTTCCT	CCTATTGGGT	GAACGACCTC	2040
CGCCTCGGCT	ATGTGCTGCC	GGTTCAC TTC	GTTAAGAGAG	TGGCACTGGG	CGTACAGCTC	2100
AATAATCTCT	TCAACCTCAT	GTATGCGTCC	AATGCCTACA	TCTACGATGC	CGGTTACGTA	2160
CAGGCATCCG	GAGAACTAAG	TGCATATGCC	GATCTGCGTT	ATTATCCTCA	GGCCGGATT T	2220
AATGCACTGG	GTAGTCTGAC	AATCGATTTC				2250

(2) INFORMATION FOR SEQ ID NO:214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

ATGAAAAGAA	GGTTTCTATC	GCTGTTACTG	CTGTACATAC	TCTCTTCCAT	CAGCCTTTCT	60
GCTCAGCGGT	TTCCGATGGT	GCAGGGAATC	GAGTTGGATA	CCGATTTCGT	TTTCTCTCTG	120
CCCAAGCGTC	CTTGGCGCGC	CATCGGTAAT	ACGATAGGCG	TCAATCTGGC	CGTATGGGGC	180
TTCGATCATT	TCATCATGAA	CGAGGACTTT	GCAGACATCA	GTTGGCAGAC	TATCAAGAGC	240
AATTTCCAAA	CAGGCTTTGG	CTGGGACAAT	GACAAGTTTG	TCACCAACCT	CTTCGCACAT	300
CCTTATCACG	GATCGCTCTA	TTTCAATGCA	GCGAGGTCGA	ACGGTTTGAG	CTTCAGGCAC	360
TCTGCTCCGT	TTGCCTTCTT	TGGCAGTCTC	ATGTGGGAGC	TGCTTATGGA	AAACGAGCCA	420
CCGAGTATCA	ACGACCTCTG	TGCCACCACC	ATAGGCGGTA	TAGCTTTGGG	GGAGATGGGG	480
CACAGGCTGT	CGGACCTGCT	CATCGACAAT	CGTACCACAG	GGTGGGAACG	TATGGGGCGC	540
GAGGTGGCTA	TCGCTCTGAT	CAATCCGATG	CGCTTTCTCA	ACCGTCTGAC	AGCAGGAGAG	600
GTGACTTCTG	TCGGGAGTCG	CAGCGGACAG	ATATTTTCAGT	CTGTCCCCAT	AAACATAGTC	660
GTCGATGCCG	GTTCTTCGTT	TTTGGCAGAC	AAGCGGCATG	CCCGAACC GG	TGCCACGGCT	720
CTGACCCTGA	ATCTGAGATT	CGACTACGGC	GATCCATTCC	GAAGCGAGAC	TTTCTCTCCA	780
TACGATTCTT	TCCAATTCAA	AGCCGGATTG	AGTTTCTCCG	AATCGCAACC	TCTGCTGAGC	840
CAGATCAATC	TGATCGGAAT	CCTAAGCGGA	TGCCAACTGC	TCGCACACGA	ACGAACGGTT	900
TTGGTGGGAG	GTTCTTTTCA	GCACCTTCGAC	TACTACAATT	CGGAAAAACG	AATAAGCAAA	960
AATTCGGAGG	AGGTACTCGT	CACCCCATAC	CGTATCTCGC	AAGTGGCAGC	TCTGGGAGGC	1020
GGTCTTATCT	TCCAGCACCA	CGGAAAAATT	CGACGACGTC	CTCTGGAGCT	ATATGCCGAG	1080
ACCTACCTGA	ATGTCGTCCC	GATGGGAGCC	AGTCTGTCCG	ATCACTACAA	CGTGGACAAT	1140
CGGGACTATA	ACCTCGGCAG	CGGATTGAGC	GGCAAGCTAT	ACCTTGGTGC	TACGTACAAT	1200
GATCTGTGGA	GCTGGCTCTT	GGGAGTCGAA	AGCTATCGGC	TCTACACATG	GATCGGGTAT	1260
GAAGAGCCGC	ACCAGAAAAA	TACCGATGTC	AGCTCTTTTA	TGGTGCAGGG	GGACGAAAAGC	1320
AAGGCGCGCC	TACTGGTGAC	GAGTTCGGAG	TTCGCATTTC	ATCCTGGCCC	CTGGCATGTA	1380
GCCATCGTCG	CTCGCCGTTT	CATCCGCAAA	ACAGCCTATC	AATTCTACCC	TAACGTATCA	1440
TTCGATACCG	GCGACATACA	GCTGCGTGTC	GGATTTCACT	TC		1482

(2) INFORMATION FOR SEQ ID NO:215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

```
ATGAAACGAC TGATTGTTTT TCTGGCAATG GGTGGCTTGC TGTTCACCTT TGCGAACGCA      60
CAAGAAGCAA ACGTGCATC TGACACTCCC AAAAAGGACT GGACTATAAA AGGTGTGACC      120
GGACTAAATG CCTCTCAGAC TTCTCTGACC AACTGGGCTG CCGGTGGAGA AAACACGGTG      180
GCAGGTAACC TCTATTGAA CATAGATGCC AACTACCTGA AAGATAAATG GAGTTGGGAC      240
AACGGTTTGC GTACAGACTT CCGTCTGACC TACACAACAG CCAACAAGTG GAACAAAAGT      300
GTAGACAAGA TCGAACTCTT CACGAAGGCC GGCTATGAGA TCGGCAAACA TTGGTACGGA      360
AGTGCCTTTT TCACCTTCCT CTCACAGTAT GCCAAAGGAT ATGAGAAGCC CTCGGATCAC      420
TTGACAGGAG TCAAGCATAT CTCTAATTTT TTCGCTCCTG CATATCTCAC TCTCGGTATT      480
GGTGCAGGACT ATAAGCCCAA TGAGAAGTTC TCTCTCTACC TCTCTCTAC AACGGGCAAG      540
CTGACTGTAG TAGCAGACGA CTACCTCTCA AGTTTGGGAG CCTTCGGGGT GAAAGTTGGT      600
GAAAAGACAA TGTTTGAATC TGGTGCTTTG GTAGTGGGTT CGGCCAATAT AAATCTGATG      660
GAGAATGTCA ATTTGATAAC CAAGGCTTCA TTCTTCTCGG CTTATACGCA CGACTTTGGC      720
AACATTGACA TCAATTGGGA GGCTATGCTG GCCATGAAGA TCAACAAGTT CTCACGGCT      780
ACGATAGCCA CCAATCTTAT CTACGACGAT GATGTGAAGA TCAACGATGG CCCGAAAATC      840
CAGTTCAAAG AAGTTGTGGG CGTGGGTGTT GCGTACACTT TC                        882
```

(2) INFORMATION FOR SEQ ID NO:216

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 612 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

```
ATGAAGAAAA TGATTTTGGC AGCTACTATG CTGCTCGCAA CAATCGGTTT TGCAAATGCT      60
CAGAGTCGTC CTGCTCTTAG ACTGGATGCT AACTTTGTGC GTAGTAACTT AATGCAAAAA      120
GTCGCAAAACA CGAGCGTGAA CAATAAGATG ATCGTAGGCT TACGTGTTGG TGCTGCTGCT      180
GAGTTCGCTC TTAGCAATGA TGGATTCTAT CTCGCCCCCG GATTGGCCTA TACGATGAGA      240
GGTGCTAAGA TGGAATCACT AAGTGAAACG ACAACTCGCT TGCATTATCT GCAAATACCG      300
GTGAATGCCG GTATGAGATT TAGCTTTGCT GACAACATGG CTATTTTATT GGAAGCAGGT      360
CCCTATTTTC CATATGGTGT CGCCGGAACG ATTAAGACTA AAGTTGCAGG CGTTACGGCT      420
TCTGTAGATG CCTTTGGTGA TAACGGATAT AACCGTTTCG ACTTGGGCTT GGGCTTGTCT      480
GCTGCCTTGA GCTACGACCG TTATTACGTA CAAATTGGAT ATGAGCATGG ATTGCTTAAT      540
ATGTTGAAGG ATGCTCCGGA TAAGACTTCT TTGCGTAATC ATGACTTCTT TGTGGGTCTC      600
GGTGTTCGCT TC                        612
```

(2) INFORMATION FOR SEQ ID NO:217

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

```
ATGAAAAGGA TTTTACTGT AGCCCTTGTG CTAATTGCTT CGGTCACTAT GGCCATCGGA      60
CAAAGCCGCC CGGCACCTCG CGTAGATGCC AACTTCGTAG GCAGCAATCA GAGCATGAAA      120
AGAGACCGAT ATGTGTGGGA CACCAAAATG AATGTCGGCC TCGGGTTCGG TGCCGCTGCC      180
GAATTCATGA TCGGATCAAG AGGATTCTAC TTGGCTCCGG GTCTGAACTA TACGATGAAG      240
GGCTCCAAAA CCGAATGGGA TATACCCGAA ATGGTTCCTG GTACCTATAT TACGATGGTT      300
TCCACTCGCT TGCATATCT GCAACTGCCG ATCAATGCCG GCATGCGGTT CGACCTGATG      360
AATGACATGG CGGTTTCGAT CGAAGCGGGT CCTTTCCTTG CATACGGTAT ATATGGTACA      420
TATCGGCAGA AGTTGGAAGG ATGGAAGCCG AACAACTACA GCACAGAGTT TTTTGGCCCA      480
ACGCTTGGTG GCCCAACAAA TATCCGCTGG GACATCGGGG CAAACATAAT AGCCGCATTC      540
CACTATAAGC GTTATTATAT ACAGATAGGC TATGAACATG GATTTGTGGA TATTGTGTCA      600
GGTGGAGGTT CTGATATTC CCGACTGAAC GACAATAGGC AATCCTCTTC GACGACCGCT      660
CTAAGAGAAA AGGGAAATAA CGAATACGCT TATAATCGTG ACTTCTTCGT GGGCATAGGT      720
TACCGCTTT
```

(2) INFORMATION FOR SEQ ID NO:218

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

```
ATGAAAAGAA TGCTGCTGCT TCTCGTTGTA TTATTATATG GAATTGCAGG CCGATTGGCT      60
GCACAAGACG TTATCAGACC ATGGTCATTG CAGGTCGGAG CGGGATACTC CGATACGGAG      120
AACATCCCGG GAGGATTAC CTATGGTTTC TATTTGGGAA AGCGTATGGG GAGCTTTCTG      180
GAAGTGGGGC TGTCCATGTA CAACTCCACA CGTCAAACAG CCAACAATGC AGACTCCTTT      240
GCATCGAAGC AAGGAGACGG ATCTTTTCAG GTAAATATGT CTTCTCCGAA TGAGAAGTGG      300
TCATTCTTCG ATGCAGGCAG TGCCAACATG TATATGATCG TCGTCGGAGT CAATCCTCTC      360
CATCTGTTT GGCAGAATAG CCGGCACAAT TTGTTTCTGG CAGTACAAGC CGGCCTGTCC      420
AATAAGCACA ATATTCATTT CATCTATGGA GACAAGGGAG CCAAAGTCAG TATCTACACC      480
AATTCGAATA CCTACATCGG TTACGGAGCA CGGTAGCCT ACGAATATCA AATTCATAAA      540
AACGTGGGGG CGGGTGCCGC TGTAAATGTAC GACCACGGCA ATAAGATGCT TACGGCCATG      600
GCCACGCTCT CCACTCATTT T
```

(2) INFORMATION FOR SEQ ID NO:219

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2853 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

```
ATGAGAGTAT CCGATCTCTG TTCCAGACTT TCATGGTTAT TACCCGTAAT CCTGTGTCGGA      60
TTGCTCTGTG CTACTTTGGT CGCTGCGGAA CGTCCTATGG CCGGAGCAGT CGGATTGCAC      120
CACCGTCGGC ATGCTGCGCT GTCTGATTCT ACAGCGAAAG ACACGGTGCC TCTCGCAAAA      180
CCTATTCTCTG ACAGTGCTTT TCGAGATTCC CTTCCTGCCG ATTCCACCGG ATCGATGCGG      240
CAAGATAGCG TGTATGACGA TGAATTCGAA TTGGAAGATA TAGTGAGATA CGAAGCTGCC      300
GATTCCATCG TTTTGCTCGG ACAGAATCGT GCCTATCTTT TCGGCAAGAG CTATGTGAGC      360
TATCAAAAGA GTCGCTTGGA GGCAAATCTT ATGTATCTCA ATACCGACAG CAGTACGGTT      420
TATACTCGCT ATGTCTCTGA TACGGCCGGT TATCCGATGG CCTTTCCTGT TTTCAAGGAT      480
GGAGAGCAGT CGTTCGAAGC CAAGAATCTT ACCTACAAC TCCGCACGGA GAAGGGGATT      540
ATCAGCGGAG TGATCACGCA GCGAGGCGAA GGCTATCTGA CTGCCGGTAA GACCAAGAAG      600
ATGCCCGACA AGTATCATGT TATGCAAGGA GGGCGTTATA CGACCTGCGA CAATCACGAT      660
CATCCTCACT TCTATATCAA TCTTTCCAAG GCAAAGGTGC ATCCGGAGAA AGACATCGTC      720
ACAGGTCGGG TCAATCTGGT TATCGCCGAT ATGCCGCTGC CGATAGGTCT TCCTTTCGGC      780
TATTTTCCCT TTTCCAACAA ATACTCTTCC GGTATATTGA TGCCACGTA CGGAGAGGAC      840
AATCGCTATG GATTTTATTT GAGGAATGGT GGATATTATT TTGCTTTCAG CGACTATATC      900
GATTTGGCAT TGCCTGGGGA GATCTTTTCC AAAGGGTCAT GGGGCATTTC AGCCCAATCG      960
AAATATAAGA AGAGGTATAA GTACAACGGC TCGTTCGAAG CCAATTATCT GGATCGAAG     1020
TCCGGCGACA AATACGTGCC CGGAGACTAC AGCAAGACCA CCAAGTCTGAA TATCCGATGG     1080
ACACACAGTC AGGATCCGAA GGCCAATCCT TTGCAACGCT TGTGCGCCAA TGTCAATTTT     1140
GCCACCGGGA GCTATTTCCA GAATTCGCTG AATACCACCT ATGATGTCAA TGCCCGTACT     1200
GCTACGACAC GAAGTTCGGC CGTGAGCTAT TCGCGCAAGT TTCCGGGTAC TCCTTTTTCG     1260
ATTACGGGTA GCATGGATAT CAGCCAGAAC ATGCGCGATA CGACGGTGAG CCTTACCTTG     1320
CCGAATCTTT CGATTAATAT GTCCACGCGT TATCCTTTCA AGCGGAAGAC CCGTGTAGGA     1380
CCGGAGCGAT GGTACGAGAA GTTGAGTGTG GGCTATTCCG GTCAGCTTCG CAATAGTATC     1440
TTGACAAAAG AGAAAGATTT GCTCCAGAGC AATCTCGTGC GCGATTGGAA GAATGGTATG     1500
CGTCATFCCG TACCGATCAG TTTGACTGTC CCTTTGTTGG ATTATATCAA TCTGACTATG     1560
GGGGTTAACT ACAAATGAGT GTGGTACACG AAAGGCATAC GGAAGTCGTG GAATGAGGAT     1620
AAGAAAACAT TCCTGCCTTC GGACACGACC TATAAATTCC GCAGACTGTA CGATTACAGT     1680
CTGTCCGCAG GCTTATCTAC CACATTGTAC GGTATGTTC AAGCCTTGGAA ACCTTTTTC     1740
TTCGGAGGCA ATCTCATTAT GATCCGTGAT CGCTTCAACG CCACTGTGAG TTTCTCCTAT     1800
ATGCCGAGT TACCGAAACG CGGATATGGC TTTTGGGAGC TTCTTGAGCA TACGGATCAG     1860
AACGGCAAGC TGCATACGCT GCTCTACTCT CTTATTTCG AGCAGATATT CGGTGCTCCC     1920
TCCATGGGCA ATGCAGGATC TGTCAATTTT TCTTTTGACA ACAACTTAGA GGCCAAGATC     1980
AAATCCAAAT CGGATTGCAG AGGGATCAAG AAGATCAGCC TGATAGATCA GTTCACATGG     2040
TCTACATCCT ATAATATGTT TGCCGATTCT ATCCGATGGA GCAATATCTC GGCTTCGCTG     2100
GCACTTCGCC TCTCCAAGAG CTTTACCTTG CGCTTGTCGG GTCTGTTCGA TCCCTATTTG     2160
ACGAAGTATT ATGAGGGAGA AGATGGGAAG ATCATTCCCT ATAAGAGCAA CGACCTGCGC     2220
ATTTTAAACG GCAAGGGATT GGCACGCCTG ATCAGTACGG GTACTTCTTT CAGCTATACG     2280
CTCAACAAAG AGTCGCTCAG CGGATTGATA GCTCTTTTCA GTGGCAAAAA GGAGCGGAGA     2340
GATGAAAAGA AAAACACAGG GGCTACTCCT CATGAAGGAG ACGATGCTGC CGATATACTT     2400
GAGGGAGGAA GACCGCAAAA TGAAAGTGGG GGGTCGCTCC TCGAGCGCAA CCGTCAGGGC     2460
GGAGCAGTGG ATCAGGATGG TTACTTCGCA TATTCGATCC CATGGAGCCT GTCCTTCGAC     2520
TATAGTTGGA ATATTGCTAC CGACTACAAT AGGTACAATG TCAATAAGAT GGAGCACTAC     2580
TACCGGGTAA CGCAGAATCT GAGCTTTCGC GGCAATATCC AGCCTACACC GAACTGGAGC     2640
TTCGATTCA ATGCGAATA CAATTCGAC TTGAAGAAAA TAACATCGCT TACCTGCAAC     2700
GTCACGCGC ACATGCACTG CTGGGCTATC TCGGCCAGTT TCATCCCTAT AGGAGCATAC     2760
AAGTCTTATA ATTTCTGCTAT ATCGGTGAAG AGTTCACCTT TGCAGGATCT GAAGTATCAG     2820
CAGAGCAATC GTCCCATCAC GAATACTTGG TAT                                     2853
```

(2) INFORMATION FOR SEQ ID NO:220

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

```

ATGATGAAAC GATATACAAT AATTCTTGCA GTTTTCTTT TATTCTGCAC GGTATTTACC      60
TTTCAAATAA AAGCTCGCCC TTATGAAAGA TTTCAGATG TAGAGAAGCC TTGGATTACG      120
AAACATTCAA TGGATTCTAA ATTGGTGCC TTAAGTAAGG GTAACCTAAT TCAAGCTGAA      180
ATTGTATACC AATCTGTTTC TGAACATAGT GACTTAGTTA TTTCACCTGT GAACGAAATA      240
AGGCCTGCAA ATCGTTTCCC TTCGCATAGG AAGTCTTTT TTGCAGAAAA TCTACGGGCA      300
TCTCCCCCG TAGTTCCCGT TGCCGTCGAC AAGTATGCGG TACCGGTTGC CAATCCAATG      360
GATCCTGAAA ATCCCAATGC CTGGGATGTG ACGCTAAAA TCACTACTAA AGCGGTAACA      420
GTACCTGTGC ATGTGGTGAT GGTATCGAC CAGTCTTCGT CAATGGGAGG GCAAAACATT      480
GCCAGATTAA AGTCTGCCAT TGCATCGGGA CAGCGTTTGT TGAaaaaaaAT GTTGCCTAAG      540
GGGACGGCTA CAGAAGGGGT GCGTATCGCT CTGTGTAGTT ATGACCATGA GCCTCATCGC      600
TTATCTGATT TTACCAAGA CACTGCTTTT CTCTGTCAAA AAATCCGGGC TTTGACTCCT      660
ATTGCGGGA AATCTAACCA GGGGGGGCTT AAAATGGCGA GAAACATTAT GGCCACTTCT      720
ACTGCTGTGG ATAAGCATAT CATATTGATG TCTGACGGGT TAGCGACGGA GCAGTATCCT      780
GTTAAAAATG TAACTACTGC AGACTTCATT GGCAAACTG GAAATGCGAA TGATCCCATT      840
GATTTGGTTA TACAAGGAGC AATTAATTTC CCTACAAAT ATGTTTCCAA CAATCCATCT      900
ACACCTCTTA CCCCATAAT TCCAATCAT TCTTCTAAAG TTGGACGGAG AAATCTGCCG      960
GAATCCAAAT TCGATTATAG TAATCTGAGT GCAAGGATTA CTTTGTATGG TGTGCTGGC      1020
GCAATTGTCT ATGAACCGAG GTTTCCTCAT CCTATTATT ATTATTTCCC TTGTAACGCT      1080
GCTATCAATG AGGCTCAGT TGCGAAAAAC TCTGGTTATA CAATCCATAC TATTGGCTAT      1140
GACCTGGGAG ATTTTGCCTT TCGTCAACAT TCGTTGAAAC TAACCGCTAC AGACGAGAAT      1200
CACTTCTTTA CGGCGACACC GGCCAATTTA GCTGCAGCGT TTGATAATAT TGCCCAAACT      1260
ATTAATATAG GTATACAGAG GGGGGAGGTG ACGGACTTTG TAGCTCCTGG TTTCATCGTT      1320
AAAAATCTGA CGCAATCGGG AGATGTTACT CATTGCTAA ATGTTTCAAA TGGAACGGTG      1380
CACTATGATG TCTCTACTAA AAAACTGACA TGGACTACTG GTACTATCCT GAGCTCATCA      1440
GAAGCTACCA TAACTTATCG TATTTATGCC GATTTGGATT ATATACAGAA CAATGATATT      1500
CCGGTAAATA CTAATTCTGC TATCGGCCCG GATCTTGGTG GATTCGATAC CAATACCGAG      1560
GCAAAATTGA CCTATACCAA TTCCAATGGC GAACCGAATC AGCAGTTAAT TTTCCACGT      1620
CCGACGGTTA AGTTAGGTTA GGGTGTATT AAGCGGCACT ATGTATTGGT AAATAAGAC      1680
GGTCAACCCA TACAGGCAAA TGGAACAGTT GTCAGTTCCC TAAGCGAGGC TCATGTTCTA      1740
CAGTCACAAG ATTTCTTTT GCCTCAGGT GGAGGTCATA TTGTTCCCAA ATGGATAAAG      1800
TTGGACAAA CGACCGAAGC ATTACAGTAC TATTCGTAC CGCCGACTAA CACGGTCATC      1860
ACTACTGCCG ATGTAAACG TTAGCTTTT GTCGAAGTCC CAGGCTCCAC GCCGAATCCG      1920
GGCCAATCG GTATCAGTTG GAAAAAACCG GCAGGAAACG CTTACTTCGC TTACAAGCTC      1980
CTCAATTATT GGATGGGAGG AACACAGAGC CAACAGAGTG AATGGGATGT GACGTCCAAT      2040
TGGACAGGAG CCCAAGTACC GCTCAGAGGA GAAGATGTAG AGTTTGCAAC GACAGAAAT      2100
TTCCGTTCTC CGGCGGTAGC CGATTGTCAT GTCCCGACAA CCAACCCCAA AATTATCGGT      2160
AACCTTATCA ATAATTCCGA CAAGGATTTA GTTGTTACCA CAAGCAGTCA ATTGACGATC      2220
AACGGCGTGG TTGAGGATAA CAATCCGAAT GTCGGTACGA TCGTCGTGAA GTCGTGAAA      2280
GACAATCCTA CGGGGACATT GCTTTTGCC AATCCGGGCT ATAATCAAAA TGTAGGGGG      2340
ACCGTCGAGT TTACAAATCA GGGATATGAT TGTGCCGATT GTGGTATGTA TCGCAGGAGC      2400
TGGCAGTATT TCGGTATCCC TGTCATGAA TCAGGTTTT CAATTAATGA TGTGGGCGGA      2460
AACGAGACCG TCAACCAATG GGTGAGCCT TTCAATGGCG ATAAGTGGCG GCCAGCACCT      2520
TATGCACCTG ATACAGAGCT TCAAAAATTC AAGGGCTACC AGATCACGAA TGACGTGCAG      2580
GCACAGCCTA CGGGAGTTT CAGCTTCAAG GGTATGATT GTGTGTGCGA TGCCTTCCTG      2640
AATCTGACAC GCACGTCCGG TGTCAACTAC TCGGGCGCCA ACTTGATCGG CAACTCATAC      2700
ACTGGAGCCA TCACATCAA GCAGGGTATT GTCTTCCCGC CGGAAGTCGA GCAGACGGTG      2760
TATCTGTTCA ACACGGGAAC ACGCGACCAG TGGCGTAAGC TTAATGGAAG CACGGTTTCA      2820
GGCTATCGAG CCGGTAGTGA CCTCTGTGA CCAAGGATCA CAGCGGGTCA GGACAATCTT      2880
CCGGATCGTA TTCCATCGAT GCATTCTTC TTGGTGAAGA TGCAGAACGG AGCGTCTTGT      2940
ACGTGTCANA TCTGTACGA TAAGCTGCTC AAGAACACGA CTGTAAACAA CGGTAATGGT      3000
ACGCAGATCA CATGGCGATC CGGCAACTCC GGATCGGCGA ATATGCCGTC ACTTGTGATG      3060
GATGTTCTTG GTAACGAGTC GGCCGACCGT TTGTGGATCT TTACCGATGG GGGTCTTTCT      3120
TTCGGATTTC ACAACGGCTG GGATGGTCGC AAGCTGACTG AAAAAGGTTT GTCACAACTT      3180
TATGCGATGT CTGACATCGG TAATGATAAA TTCCAGGTTG CAGGGGTTCC GGAGTTGAAT      3240
AACCTGCTGA TCGGCTTCGA TGCGGATAAG GATGGTCAAT ACACGTTGGA GTTTGCTCTT      3300
TCGGATCATT TTGCGAAAGG GGCTGTTTAC CTGCACGATC TTCAGTCAGG AGCCAAACAC      3360
CGTATTACGA ATTCTACGTC GTATTCTTC GATGCCAAGC GGGGAGATTC CGGGGCTCGT      3420
TTCCGCTTGT CATATGGATG TGATGAGAAC GTAGATGATT CGCATGTCGT GAGTACAAAT      3480
GGCCGTGAAA TTATAATTCT GAATCAAGAT GCTCTTGAAT GCACTGTAAC CTTATTACAA      3540
ATAGAAGGTA AGCTTCTTCG GCGCTTGAAA GTATTAGCTG GTCATAGAGA AGTCATGAAA      3600
GTGCAGACCG GAGGGGCCCTA TATTGTGCAT CTTCAAAATG CTTTCACTAA TGATGTGCAT      3660
AAGTGCTTGG TTGAGTAT

```

(2) INFORMATION FOR SEQ ID NO:221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

ATGAAACGAT	ATACAATAAT	TCTTGCAGTT	TTTCTTTTAT	TCTGCACGGT	ATTTACCTTT	60
CAAATAAAAG	CTCGCCCTTA	TGAAAGATTT	GCAGATGTAG	AGAAGCCTTG	GATTCAGAAA	120
CATTCAATGG	ATTCTAAATT	GGTGCCTGCA	AATAAGGGTA	ACTTAATTCA	AGCTGAAATT	180
GTATACCAAT	CTGTTTCTGA	ACATAGTGAC	TTAGTTATTT	CACCTGTGAA	CGAAATAAGG	240
CCTGCAAATC	GTTTCCCTTC	GCATAGGAAG	TCTTTTTTTG	CAGAAAATCT	ACGGGCATCT	300
CCCCCCGTAG	TTCCCGTTGC	CGTCGACAAG	TATGCGGTAC	CGGTTGCCAA	TCCAATGGAT	360
CCTGAAAATC	CCAATGCCTG	GGATGTGACG	CTAAAAATCA	CTACTAAAGC	GGTAACAGTA	420
CCTGTTCGATG	TGGTGATGGT	TATCGACCAG	TCTTCGTCAA	TGGGAGGGCA	AAACATTGCC	480
AGATTAAAGT	CTGCCATTGC	ATCGGGACAG	CGTTTTGTGA	AAAAAATGTT	GCCTAAGGGG	540
ACGGCTACAG	AAGGGGTGCG	TATCGCTCTT	GTGAGTTATG	ACCATGAGCC	TCATCGCTTA	600
TCTGATTTTA	CCAAAGACAC	TGCTTTTCTC	TGTCAAAAAA	TCCGGGCTTT	GACTCCTATT	660
TGGGGAAACAC	ATACCCAGGG	GGGGCTTAAA	ATGGCGAGAA	ACATTATGGC	CACTTCTACT	720
GCTGTGGATA	AGCATATCAT	ATTGATGTCT	GACGGGTTAG	CGACGGAGCA	GTATCCTGTT	780
AAAAATGTAA	CTACTGCAGA	CTTCATTGGC	AAAACCTGGAA	ATGCGAATGA	TCCCATTGAT	840
TTGGTTATAC	AAGGAGCAAT	TAATTTCCCT	ACAAATTATG	TTTCCAACAA	TCCATCTACA	900
CCCTCTTACCC	CAAATTATCC	AACCTATTCT	TCTAAAGTTG	GACGGAGAAA	TCTGCCGGAA	960
TCCAAATTCG	ATTATAGTAA	TCTGAGTGCA	AGGATTACTT	TTGATGGTGT	TGCTGGCGCA	1020
TTGGTCTATG	AACCGAGGTT	TCCTCATCCC	TATTATTATT	ATTTCCTTGG	TAACGCTGCT	1080
ATCAATGAGG	CTCAGTTTGC	GAAAACTCT	GGTTATACAA	TCCATACTAT	TGGCTATGAC	1140
CTGGGAGATT	TTGCCTTGGC	CAACAATTCG	TTGAAACTAA	CCGCTACAGA	CGAGAATCAC	1200
TTCTTTACGG	CGACACCGGC	CAATTTAGCT	GCAGCGTTTG	ATAATATTGC	CCAAACTATT	1260
AATATAGGTA	TACAGAGGGG	GGAGGTGACG	GACTTTGTAG	CTCCTGGTTT	CATCGTTAAA	1320
AATCTGACGC	AATCGGGAGA	TGTTACTCAT	TTGCTAAATG	TTTCAAATGG	AACGGTGCAC	1380
TATGATGTCT	CTACTAAAAA	ACTGACATGG	ACTACTGGTA	CTATCCTGAG	CTCATCAGAA	1440
GCTACCATAA	CTTATCGTAT	TTATCCGAT	TTGGATTATA	TACAGAACAA	TGATATTCCG	1500
GTAATACTA	CTTCTGCTAT	CGGCCCGGAT	CTTGGTGGAT	TCGATACCAA	TACCGAGGCA	1560
AAATTGACCT	ATACCAATTC	CAATGGCGAA	CCGAATCAGC	AGTTAATTTT	CCCACGTCCG	1620
ACGGTTAAGT	TAGGTTATGG	TGTTATTAAG	CGGCACTATG	TATTGGTAAA	TAAAGACGGT	1680
CAACCCATAC	AGGCAAATGG	AACAGTTGTC	AGTTCCCTAA	GCGAGGCTCA	TGTTCTACAG	1740
TCACAAGATT	TCTTTTGGCC	CTCAGGTGGA	GGTCATATTG	TTCCCAAATG	GATAAAGTTG	1800
GACAAAACGA	CCGAAGCATT	ACAGTACTAT	TCCGTACCGC	CGACTAACAC	GGTCATCACT	1860
ACTGCCGATG	GTAACCGTTA	TCGTTTTGTC	GAAGTCCCAG	GCTCCACGCC	GAATCCGGGC	1920
CAAATCGGTA	TCAGTTGGAA	AAAACCGGCA	GGAACGCTT	ACTTCGCTTA	CAAGCTCCTC	1980
AATTATTGGA	TGGGAGGAAC	AACAGACCAA	CAGAGTGAAT	GGGATGTGAC	GTCCAATTGG	2040
ACAGGAGCCC	AAGTACCGCT	CACAGGAGAA	GATGTAGAGT	TTGCAACGAC	AGAAAATTTT	2100
GGTTCTCCGG	CGGTAGCCGA	TTTGCATGTC	CCGACAACCA	ACCCCAAAT	TATCGGTAAC	2160
CTTATCAATA	ATTCCGACAA	GGATTTAGTT	GTTACCACAA	GCAGTCAATT	GACGATCAAC	2220
GGCGTGGTTG	AGGATAACAA	TCCGAATGTC	GGTACGATCG	TCGTGAAGTC	GTCGAAAGAC	2280
AATCTACGG	GGACATTGCT	TTTTGCCAAT	CCGGGCTATA	ATCAAAATGT	AGGGGGGACC	2340
GTCGAGTTTT	ACAATCAGGG	ATATGATTGT	GCCGATTGTG	GTATGTATCG	CAGGAGCTGG	2400
CAGTATTTCG	GTATCCCTGT	CAATGAATCA	GGTTTTCCAA	TTAATGATGT	GGGCGGAAAC	2460
GAGACCGTCA	ACCAATGGGT	TGAGCCTTTC	AATGGCGATA	AGTGGCGGCC	AGCACCTTAT	2520
GCACCTGATA	CAGAGCTTCA	AAAATTCAAG	GGCTACCAGA	TCACGAATGA	CGTGCAGGCA	2580
CAGCCTACGG	GAGTTTACAG	CTTCAAGGGT	ATGATTTGTG	TGTGCGATGC	CTTCCTGAAT	2640
CTGACACGCA	CGTCCGGTGT	CACTACTCG	GGCGCCAACT	TGATCGGCAA	CTCATACACT	2700
GGAGCCATCG	ACATCAAGCA	GGGTATTGTC	TTCCCGCCGG	AAGTCGAGCA	GACGGTGTAT	2760
CTGTTCAACA	CGGGAACACG	CGACCAGTGG	CGTAAGCTTA	ATGGAAGCAC	GGTTTCAGGC	2820
TATCGAGCCG	GTCAGTACCT	CTCTGTACCT	AAGAATACAG	CGGGTCAGGA	CAATCTTCCG	2880
GATCGTATTC	CATCGATGCA	TTCTTCTTGG	GTGAAGATGC	AGAACGGAGC	GTCTGTACG	2940
TTGCANATCT	TGTACGATAA	GCTGCTCAAG	AACACGACTG	TAAACAACGG	TAATGGTACG	3000
CAGATCACAT	GGCGATCCGG	CAACTCCGGA	TCGGCGAATA	TGCCGTCACT	TGTGATGGAT	3060
GTTCTTGGTA	ACGAGTCGGC	CGACCGTTTG	TGGATCTTTA	CCGATGGGGG	TCTTTCTTTC	3120
GGATTTCGACA	ACGGCTGGGA	TGGTCGCAAG	CTGACTGAAA	AAGGTTTGTG	ACAACTTTAT	3180
GCGATGTCTG	ACATCGGTAA	TGATAAATTC	CAGGTTCGAG	GGGTTCCGGA	GTTGAATAAC	3240
CTGCTGATCG	GCTTCGATGC	GGATAAGGAT	GGTCAATACA	CGTTGGAGTT	TGCTCTTTCG	3300
GATCATTTTG	CGAAAGGGGC	TGTTTACCTG	CACGATCTTC	AGTCAGGAGC	CAACACCCGT	3360
ATTACGAATT	CTACGTCGTA	TTCAATTCGAT	GCCAAGCGGG	GAGATTCCGG	GGCTCGTTTT	3420
CGCTTGTCAT	ATGGATGTGA	TGAGAACGTA	GATGATTTCG	ATGTCGTGAG	TACAAATGGC	3480
CGTGAAATTA	TAATCTGAA	TCAAGATGCT	CTTGACTGCA	CTGTAACCTT	ATTGACAATA	3540
GAAGGTAAGC	TTCTTCGCCG	CTTGAAAGTA	TTAGCTGGTC	ATAGAGAAGT	CATGAAAGTG	3600
CAGACCGGAG	GGGCCTATAT	TGTGCATCTT	CAAAATGCTT	TCATAATGA	TGTGCATAAG	3660
GTGCTGTTG	AGTAT					3675

(2) INFORMATION FOR SEQ ID NO:222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

```
ATGGAAGTGA AGAAAAACAC AGTGGTGCTA CGCCTTCTGA TTGGTTTCGT GGCCATTCTT      60
CTCTTCCACT CCTCACGGCT GTGGGGACAG GAAGGGGAGG GGAGTGCCCG ATACAGATTG      120
AAAGGATTTCG TGGATACCTA CCATGCCGTA CGCAGCTCTT CTCCTTTTGA TTTCATGAGC      180
TCGCGTACGA GAGTGAGAGG TGAGCTGGAG AGGTCGTTCG GTAATTCGAA AGTAGCCGTA      240
TCGGTCAATG CCACCTACAA TGCTCTACTG AAAGACGAGA CCGGCTTACG TTACGTGAA      300
GCCTTCTTCG AGCATCAGGA AGAGCATTGG GGGTTGCGCC TCGGACGACA GATTGTCTATT      360
TGGGGGGCTG CCGACGGTGT GCGCATCACG GATCTGATCT CCCCAGTGA TATGACCGAG      420
TTTCTGGCAC AGGATTACGA TGATATTCTG ATGCCGGTCA ATGCATTGCG TTTCTCTGTC      480
TTCAACGAAT CGATGAAAGT GGAAGTCGTG GTACTGCCTG TATTCGAGGG GTACCGTCTG      540
CCTGTGGATC CTCGCAATCC TTGGAATATC TTCTCCCTTT CGCCCATTCG TCAGGGGATG      600
AATATCGTCT GGAAAGAAGA AGCCGGCAAA CCGGCCTTCA AGGTTGCCAA TATCGAGTAC      660
GGTGCGCGAT GGAGCACTAC GCTCTCCGGT ATCGACTTCG CTTTGGCTGC ATTGCATACA      720
TGGAACAAGA TGCCCGTCAT CGAAGTACAG GGCATTGTGC CGACGGAAAT CATCGTTAGC      780
CCTCGCTATT ATCGTATGGG ATTTGTCTGC GCGACCTCT CCGTACCCGT CGGACAGTTT      840
GTTTTTCAGG GAGAGGCTGC GTTCAATATC GACAAACACT TCACCTATAA GAGTCATGCC      900
GAGCAAGAGG GTTTCCAAAC AATCAATTGG TTGGCCGGAG CCGATTGGTA TGCTCCCGGT      960
GAATGGATGA TCTCAGGACA ATTCTCAATG GAAAGCATAT TCAGGTATAG GGATTTTCATC     1020
TCCCAAAGAC AACATTCTAC CCTGATTACT CTCAATGTTT CCAAGAAATT CTTCGGCAGT     1080
ACACTCCAAC TTTCGGACTT CACCTACTAC GACCTTACGG GCAAAGGATG GTTCAGTCGC     1140
TTTGCAAGCTG ACTATGCCTT GAACGATCAG ATACATCTGA TGGCCGGATA TGACTGGTTC     1200
AGTAGTAAGG GCAGCGGTAT ATTCGATCGC TACAAAGACA ATTCCGAAGT CTGGTTCAAA     1260
GCCCGCTACA GCTTC                                         1275
```

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

```
ATGTCCTCCT GTGAGGTGGC TTATTTTTCA CTAAAGCCGA TCGATCTGCA GAACATCCGC      60
GAACGGAATC ACTCTTCCGA CATCGCGCTT TCCAATTTAT TAGACAATTC GAATCAGCTA      120
TTAGCTACTA TTCTGATCGG GAATAATGTG ATTAATGTAG CCATCGTTAT CCTTCCAAT      180
TATGCCATCG AGCAGACATT CGTTTCTCTT TCTCCGATCA TTGGATTTCG GATCCAGACG      240
ATACTCCTGA CCACTGTTCT TTTGCTGTTT GGAGAGATTC TGCCGAAAGT GTATGCGCGG      300
AAGAATCCGC TGCAATACTC GCGCTTTTCT GCTGCAGCTA TGTCCGTTAT CTATAAGATA      360
```

TTGTCACCGT	TTTCAAAATT	GCTGGTCAAA	AGTACCGCA	TCGTTACCAG	AGGTATCAGC	420
AAGAAGAAAT	ACGATATGTC	CGTGGATGAG	CTCTCGAAAG	CGGTAGCCCT	CACCACTACG	480
GAGGGAGAG	CGGAGGAGAA	AGAAATGATT	AACGAAATCA	TCAAATCTTA	TAATAAGACA	540
GCCTGCGAAA	TCATGGTTCC	GCGTATCGAT	ATTGTGGATG	TGGATCTGAG	CTGGCCATTT	600
CGTAAGATGC	TTGACTTCGT	TGTTTCGTCG	GGTTATTCCA	GACTTCCCGT	TTCAGAGGGG	660
TCAGAAGACA	ATATCAAAGG	GGTGATTTAC	ATCAAAGATC	TAATCCCACA	CATGGATAAA	720
GGCGATGAAT	TCGACTGGCA	TCTCTGTGAT	CGTAAAGCAT	ATTTTGTCCC	CGAAAACAAG	780
CGCATAGATG	ATTTGCTCGA	GGAGTTCAGA	GCCAATAAGG	TGCATGTCTC	CATCGTTGTG	840
GATGAGTTTC	GTGGCACTTG	CGGACTGATC	ACAATGGAGG	ACATATTGGA	AGAGATCGTC	900
GGCGAGATTA	CGGACGAGTA	CGATGAGGAA	GAATCCCGCT	TTAAGGTTTT	GGGGGATGGC	960
AGTTATCTTT	TCGAAGGAAA	AACGTCTCTC	TCCGATGTTC	GACACTATCT	TGACCTTCCG	1020
GAAAATGCTT	TCGGTGAATT	GGGGGACGAG	GATAGATACG	TAAGTGGGCT	CTTCTTGGA	1080
ATCAAGCAGG	AACTCCCCCA	TGTGGGCGAT	ACAGCAGTGT	ACGAGCCATT	CCGCTTTCAA	1140
GTGACCCAAA	TGGACAAGCG	CCGAATCATC	GAAATCAAGA	TTTTCCCTTT	CGAGCGCACT	1200
TGGGAGGTCG	AA					1212

(2) INFORMATION FOR SEQ ID NO:224

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 780 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...780
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

ATGAAACTAT	TACTTTATCT	CCTATTGGTC	TTGTCGACTC	TATCCCCGAT	GTATTCGCAA	60
ATGCTCTTCT	CAGAGAATCT	CACAAATGAAT	ATAGACAGCA	CCAAAACCAT	ACAAGGAACG	120
ATATTGCCCG	TACTGGATTT	CAAAACCGAA	AAGGAAAATG	TGTTACCTT	CAAAAATACT	180
GCCAATCTCA	ATCTGCTGAT	AAAGCACGGT	CAAGTAATCA	ACTTAATTAA	TAAGCTTGAG	240
TTTTCTACCT	ATGGCAATAA	AGTAACCGTA	AGTGGAGGAT	ATGTACACAC	CGAATACCGC	300
TATTTGTTGC	ATCATGTTTT	TGAGGTTTAT	CCTTATGTGC	AGTCGCAATG	GGCAGAAAGT	360
AGAGGAATGA	AATATAAGGT	TTTACGGGA	TTACAGTCGC	GTTATCGGCT	GGTAAATAGT	420
GATAACTGTC	TCATGTTTGC	AACATTGGGG	GTATTTTTCG	AATTTCGAAA	GTGGGAACAG	480
CCAGCCACTA	GCCTCTTTGC	AGGAACGTAT	GCATACAGCC	GAAGTATCAA	AAGCCACCTG	540
TCTATCAGTT	TCAGACATCG	GTTGGGTGAA	CATTGGGAAT	TTACAACCTAC	GGCTATTCAC	600
CAGGGAAGC	CTGACAGTTA	TTTTAAGAAG	GCACGTTTTC	GAGGAGCTAT	CGACCTCAAA	660
TACCATATCA	CACCTACGAT	AGGAATACGC	GGGCCTATC	GGATCATCTA	CGATACTGCC	720
CCTATTGTAC	CTGTGCGGAA	AGATTACAAC	ACCGTTGATG	TTGGTATCGA	TATTCGTTT	780

(2) INFORMATION FOR SEQ ID NO:225

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2502
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

ATGAAACGAA	TCGTTTTATC	ATCTTTCCTG	TTCGTTCTGT	CCATACTTTC	TTTGATGGCA	60
CAGAACAAATA	CCCTCGATGT	ACACATATCC	GGTACGATCA	AGGATGCCTC	CTCCGGCGAA	120
CCAGTGCCCT	ATGCCACTGT	AAGCATCCGG	CTGACAGGAG	CAGATACCAC	ACAGGTGTTC	180
CGACAAAGTGA	CTGACGGCAA	CGGCTACTTC	GTCTAGGCC	TGCCGGCAGC	TCCCTCCTAT	240
CACCTGACAG	CTTCGTTTGT	AGGTATGAAA	ACCCATACCA	TGCAGATTAG	TCGGGGAAAT	300
GGACAGCACG	ACATCAAATC	CATCGACATT	TCTCTCGAAT	CCGAGGACAA	ACAACTCTCC	360
ACCGTCACCG	TATCGGCAGC	ACGACCACTG	GTGAAGATGG	AGATAGACCG	CCTGTCCTAT	420
AAATATGAAAG	ATGACCCCCG	AGCCAAGACG	AACAACCTGC	TCGAAATGCT	GCGCAACGTT	480
CCTTTGGTAA	CGGTGGATGG	TCAGGGCAAT	ATCCAGGTGA	AAGGATCTTC	CAACTTCAAA	540
ATCCACCTCA	ATGGCAGGCC	ATCGACCATG	GTGAGCAGCA	ACCCGAAGGA	GGTCTTTCGC	600
TCCATTCTCTG	CCCATACGAT	CAAACGGGTG	GAGGTTCATCA	CCGATCCGGG	TGTAAAGTAC	660
GATGCGGAAG	GCACAAGTGC	CATCCTGGAC	ATCGTCACGG	AAGAAGGTAA	GAAGCTGGAA	720
GGATATTTCAG	GTTCATCAC	GGCCAGTGTG	AGCAACAATC	CCACAGCCAA	CGGTAGTATC	780
TTTCTGACAG	CAAAGTCCGG	CAAAGTCGGG	CTGACTACCA	ACTATAACTA	CTACGGTGGC	840
AAAAACAAGG	GCTCTCGCTA	CTTTACCGAA	CGTACTACAT	CCATGCTCCA	AACGATAGAA	900
GAAGGCAAAG	GGCAAGAAAC	CTTTGGCGGA	CACTTCGGCA	ATGCCCTCCT	CTCATTCGAG	960
ATAGATTTCGC	TCAATCTCTT	TACGGTGGGC	GGCAATGTAC	GCCTTTGGGA	GATGACCACC	1020
ATCCGGAACA	CCGGTACAAA	AAGCTTTGCC	GGCAGCAACC	TCATGTCTTA	CATAGACAGA	1080
AAACTCAAAA	CACAGATGGA	TGCCGGATCA	TACGAGCTCA	ATGCCGACTA	TCAGCACAGC	1140
ACTCGCCTGC	CGGGCGAATT	GCTCACCGTT	TCCTACCGCT	TCACTCACAA	TCCTAATAAT	1200
AGCGAGACCT	TCATTGACCA	ATGGAAGCGC	GATCCGCTCA	ACACAGCTAA	TACGATCCAG	1260
TACGCCGGCC	AGCACTCCAA	ATCCGATGCG	GGCATGGACG	AACATACGGC	ACAAGTGGAC	1320
TATACACGTC	CCTTAGGACA	AGCACATTCT	TTGGAAGCAG	GGCTGAAGTA	CATCTATCGT	1380
CATGCCACGA	GCATCCTCT	CTATGAGATA	CGACCATCCG	AAGATGCTCC	GTGGCAGCCC	1440
GGCTCTCTAT	ATGCACAGAA	TCCGTCGAAC	GGAAAGTTCC	GCCACGATCA	ATACATCGGA	1500
GCAGCCTATG	CCAGCTACAA	CTATCGTAAG	GATCAGTATT	CTTTGCAAAAC	CGGCCTCCGA	1560
GTGGAAGCA	GCAGGCTGAA	AGCACTCTTT	CCCGAAAACG	CAGCAGCAGA	TTTCTCCAC	1620
AACTCGTTTCG	ACTGGGTGCC	ACAGCTCAGC	CTCGGCTATA	CCCCCTCGCC	CATGAAGCAG	1680
CTTAAGCTGG	CCTATAACTT	CCGAATCCAA	CGTCCTGCAA	TCGGCCAAC	GAATCCCTAC	1740
CGGCTACAGA	CCAACGATTA	TCAGGTACAG	TATGGTAATC	CCGACCTAAA	GTCGGAGAAG	1800
CGTCAACCAG	TCGGTCTCTC	CTATAATCAA	TACGGAGCCA	AGGTCATGCT	TACAGCATCG	1860
CTCGACTACG	ACTTCTGCAA	CAACGCCATC	CAGAATTACA	CCTTCTCCGA	CCCGGCCAAT	1920
CCCAATCTGT	TCCACCAGAC	CTATGGCAAT	ATCGGACGAG	AGCATTCTTT	CAGCTTGAAT	1980
ACCTATGCCA	TGTACACGCC	GGCCGTATGG	GTGAGGATTA	TGCTCAACGG	AAATATCGAT	2040
CGCACATTCC	AAAAGAGCGA	AGCACTCGGC	ATTGATGTCA	ATTGATGGTC	CGGCATGGTA	2100
TACTCAGGCC	TGATGTTTAC	CCTGCCGAAG	GATTGGACTG	TGAATCTCTT	CGGAGGTTAT	2160
TATCATGGGG	GAAGAAGCTA	CCAGACGAAG	TATGATGGCA	ATGTATTCAA	CAATATCGGT	2220
ATAGCCAAAC	AGCTTTTTCGA	CAAAAAATTG	AGAGTCTCGC	TGAGCGCAAA	CAACATTCAT	2280
GCGAAGTATT	CGACATGGAA	GAGCCGGACC	ATCGGCAATG	GATTTACTAT	TTATTTCGGAA	2340
AATGCCGGTA	TACAACGGAG	TGTTTCCCTC	AGCCTCACCT	ACAGCTTCGG	TAAGATGAAT	2400
ACACAAGTGC	GCAAGGTAGA	GCGTACGATC	GTCAACGACG	ACCTCAAGCA	AACCTCATCC	2460
CAAGGACAGC	AGGGTGGCGG	ACAAGGAAAT	CCTACCGGCA	AT		2502

(2) INFORMATION FOR SEQ ID NO:226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

ATGAGACTCT	CTGCCATTCT	TATCGCTTTG	ATTGTGATGC	TGCCTGCTGT	GCTTAGCGGG	60
CAGCATTATT	ATTCCATGGC	GGGAGAGCGA	CTGGAGACGG	ACAGCATTCG	TCCGAACGAA	120
CTCTCGGCAT	CGATCCGAAG	TGCGCTTTTC	TTTCGGAACA	ATGAATACAA	TGCACGTTTC	180
GTCAAAGGTT	ATACGTTGCC	GGGTGCACGG	GTTTCCGCTT	TTGCCTCTTA	CTCGCTGCCG	240
GCAGCACATG	GTGTGAAGCT	TTGCTCCGGA	GTATCTACCC	TGAACACTAG	GGGGGCAAGT	300
CGCTATCCGG	CCGGTATCGC	TTATTCCGAT	TTACCTTATT	GGACGGACTA	TAACGACTAT	360
GTACGCTTGC	GTATCCTGCC	TTATGTACAG	GCCATGCTGA	AGCCGACGGC	CACGACTGCT	420
CTCATGCTGG	GCAATATAGC	CGGTGGTACG	GCTCACGGAC	TGATCGAACC	GATCTACAAT	480
CCTGAGTTGG	ATTTGACGGC	TGATCCTGAA	GCCGGTGTGC	AATTTCGGGG	TGATTGGACA	540

CGTTTCCGAA	TGGATGTTTG	GGTCAATTGG	ATGAGCATGA	TTTTCAAAA	TGACAATCAT	600
CAGGAGTCGT	TTGTCTTTGG	CTTGTCCACT	ACTTCGAAAT	TGTTATCGGG	TGAAGGCAAA	660
TGGCGACTCG	AACTGCCCTT	GCAGGCTATT	GCCACGCATC	GCGGCGGGGA	ATACAACTGG	720
GCGCAGCAGG	ATACCGTGCA	TACATGGGTC	AATGGAGCTG	TCGGACTTAA	GCTTTCGTAT	780
CGCCCTCGTA	CCGACAAACC	CATGCAGATT	TGGGGATCTG	CTTATGGTGT	GGCAGCCTTG	840
TCAAGCGGAG	GATACTTCCC	TTACGAAAGA	GGGTGGGGCG	GTTATCTTTC	TCTCGGAATG	900
GACTTGGAGC	ACTTCGCTTT	TCGTACCGAC	TATTGGTACG	GCAGGCATTA	CGTTTCTCCC	960
TTTGCTGCAC	CTTTCGCCAA	TTCCTGACG	TATGACAAAC	AGCCTCTTAC	GAACGGTTGG	1020
GGCGATTATA	TTCGTCTCTA	TGCCGACTAT	TCGTGGCGGA	TGGCACGAAG	TGTTTCGTTG	1080
GCGGCTGTTG	CTCGGTATG	GTTCCAGCCT	TCGGATCGTT	TTGCGATGAG	CCACGCCTTG	1140
GAACTGACGA	TGCGTATCGA	TCCCAAATTC	CCAATAGCTT	TTCTGAAAGG	CAATCAT	1197

(2) INFORMATION FOR SEQ ID NO:227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

ATGAACAAAT	CGCTATTATC	ATTGGCATGC	CTCATCTGT	GCGGTATGCC	GGCCATCGCC	60
CAACAGACAG	GACCGGCCGA	ACGCAGCGGC	GAGCCTTCTC	TGGCCGAACG	TGTATTTCGGT	120
CTGGAGCAGA	AGCAGAAAAA	GCTGAAGGTG	TACTTAGGCA	TACAGTCGTT	CTACGACCAG	180
CCGCTTGTCG	ATGACGAATC	CCATATCGGA	CACTTCAAGG	TACAGGAGCT	GCGGATGTCT	240
GCTCATGGCG	AACTGAACCG	CCACCTCAGC	TTCGACTGGC	GACAACGTCT	CAACCGTGCC	300
GCCGACGGCA	CTTCGTTTGC	CGACAATCTC	TCCAATGCCA	TCGACATCGC	AGGTGTGGAC	360
TGGCACCCGA	ACGACAAGGT	GTCTTTCTTC	TTCGGACGTC	AGTACGCGCG	TTTCGGAGGG	420
ATAGAATACG	ACATGAACCC	CGTAGAGATC	TACCAGTACA	GCGACCTTGT	GGATTACATG	480
ACCTGCTATA	CTTCGGGCGT	GAACCTCGCA	TGGAAC TTCC	ACCCCGAACA	GCAGCTGCAG	540
CTACAGGTAC	TCAATGCTTA	CAACAACCGC	TTCGCCGACC	GCTACCACTG	GACACCCGAT	600
GTCGCTACCG	CCACGAGCTA	CCCGCTCCTC	TACTCGGCAC	AGTGAACCG	TACCCTCCTC	660
GGAGGAGCAC	TGCATATGCG	TTACGCCGTG	TCGATGGCTC	ATCAGGCCCA	AGAGCGTAAT	720
ATGTGGTACT	TCACTGCGGG	CAACCTGTTC	AATCCGGGCA	AACGGATCAA	CGGATACCTC	780
GACCTCACCT	ACTCGATCGA	GGGATTGGAC	GACAAAGGCA	TTATGACTGC	TCGCTACGGC	840
AAGGGCAAGA	CCCTCACGGA	CGTCAAGTAC	TATGCTCTGG	TATCGAAGTG	GAAC TTCCGC	900
ATTTTCGATC	AGTCGAATCT	CTTCCTCAAA	GGCATGTACG	AGAACGGCTA	TGCGCCTGCC	960
CAATACGGCG	AGAGCAGCCA	CACGCGCCAC	TCCTACGGCT	ATATGGGAGG	GGTGGAATAT	1020
TACCCTACGG	AGACCAACTT	CCGTCTGTTC	GTCACTTACA	TAGGACGGCA	TTACCGGTAC	1080
AGTGCGACCG	AGACGGAAAG	CACCAATGCT	CTTCGCGCCG	GTCTGATCTA	TCAGATACCT	1140
TTCTTA						1146

(2) INFORMATION FOR SEQ ID NO:228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

```
ATGAAACATT TGTTTAAGTC GACATTAGTA CTTCTTTGTG CTCTTTCTTT TTCCGGTACC      60
TATACCTTTG CACAAGAAAA TAATACAGAA AAGTCACGAT TTGATTTTTC TGTTAGGCTG      120
GGACAGGGAT ATATTGCAGG TTCAACTACC AACCTGATGT ATGGGTATAC ATCTGCTAAC      180
GATAGACTTT TGTCTGGTGC AATTTATCTG GGCTTGACAC CAAGTAAGAA AGAAAATGCA      240
ACCGGCGTAG CATTCGTTT CTTATCNCCC TCTCCGGGTT ATTATGTCGA TATATCCGGC      300
AAAGAAAATA CTTGAATTA TGCCTTTTAC GTTGTGCGAG CATATAATAG AATAGCCATT      360
CCTATACGCC CTATCAAAAA TTTTAATTTT ATCTTCTCTA CAGAAGTCGG AATGGCTTGG      420
ATGAGTCGTC ATGAGCAAAT TTACAATTCT ACTTCGCAGA CTTGGGATAA GCAGCGCAAG      480
TCGAGGTCGG GACTGGATTT TGGTCTCGGG ATGCATCTGC AATNCCACAT TAATAAGACC      540
GTTACTTTTA TGGCAGGAAC CGATCTTACG TCTTGCAATG TCGGAAAAAG GATCAATGAC      600
TACCAGCAAA AGGATCGAAC CTTCAATGCA CTTATCGACA ACAGTATTGG CATAGGATTA      660
AACCTC
```

(2) INFORMATION FOR SEQ ID NO:229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

```
ATGATTATCA AGAAAATGCT GAAAAATAAA TTGGCCCCCT TGGCCATACT GTTCCTTTTT      60
GCTCCAAAGG CTATGAAGGC TCAGGAGCAA CTGAATGTGG TACACACCTC TGTGCCATCG      120
CTGAATATCA GTCCGGATGC ACGTGC GGATATAGGTGT GGCAACGACG      180
CCGGATGCGT ATTACAGTA TTGAATCCG AGTAAATATG CTTTCATGGA TACGAAAGCC      240
GGTATTAGCT TCTCATATAC ACCTGGCTG TCCAAGCTGG TCAATGATAT TGCCCTGATG      300
CAGATGACCG GTTCTACAA ATTGGGAACA GACGAGAATC AGGCTATTAG TGCTTCTCTG      360
CGTTATTTCA CATTAGGAAA GTTGGAGACT TTCGACGAAT TGGGCGAATC CATGGGAGAG      420
GCCCCATCCCA ATGAATTTGC TGTCGATTG GGCTATAGCC GCCAGTTGTC GGAGAACTTC      480
TCCATGGCTG TTGCACTGCG TTACATCCGC TCAGACCAA GCACCTACAA CACCGGAGAG      540
AATCAGGCCG GAAATGCCTT TGGCGCGGAT ATAGCCGGTT ATTTGCAGAA GTATGTGCTA      600
CTGGGTAATG CCGGAGAGCT GTGTCGTTG GGTTCACAG TAAAGAATAT CGGAACGAAG      660
ATCTCCTATG ACGGAGGTGT CACGAGTTT TTCATCCCTA CTTGTTGAA TCTCGGGACG      720
GGGCTGTTGT ATCCGATCGA TGACTATAAC AGCATCAAT TCAACCTTGA ACTTAGCAAG      780
CTGCTGTGAC CCACTCCTCC TATCATGGAT CAAAACGATC AGGCCGGGTA TGAGGCTGCA      840
CTCAAGAAAT ATCAGGAAAC TTCTTCGATC AGCGGTATAT TCTCTTCTTT CGGTGATGCG      900
CCGGGAGGAC TCAAGGAAGA ATTCCGTGAG ATTACATGGG GACTTGGGGC TGAATATAGC      960
TATGACGATA AATTTTTTGT TCGTGCCGGA TATTCATACC TGCACCCAC CAAAGGCAAT      1020
TTGCAGTACT TCACGGCCGG TGCCGGCTTC AAAATGAACA TATTCCGTAT CGATGCTTCC      1080
TACCTGTTGT CTACGATCCA GAGTAATCCG TTGGATCAGA CTCTGCGGTT TACGCTTGCT      1140
TTCGATATGG ATGGATTGCG CAATTTGTTC CAC
```

(2) INFORMATION FOR SEQ ID NO:230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

```
ATGAAAACAA CAGTTCAACA AATTATTCTG TGCCTGGCTT TAATGATGTC AGGTGTATTG      60
GGCGGAAACG CACAGAGCTT TTGGGAAGAA ATAGCTCCTC CTTTATCAG TAATGAGCCT      120
AACGTCAAGT ATATAATTCC CAATATGGGG ATTGATTCAA AGGGAACAAT CTATGTAACC      180
GTGACAAAAA GGATTACGCA GGGAGCAAAT TATACTTCTG AGCAATTGGG TATGTACTAT      240
CGACCATTAG GTGATAATGA ACAGTGGTGG AAACATGATC CGTATTTTGA TGACAAGATA      300
GTTGCGGATA TTCAGACAGA TGCATATGGC AGAGTTTATG TATGTACGAC TTCTTCTCGA      360
GATCAAGAGT ATCAACTTTA TATAAACGAG CAGAACGAAT GGAGGTGTAT ATTCAAAACT      420
TCTGTGTCTA CATATGAGCA TGGTATGGCT GTTTTTCGCT CTTCGACAGG GGTGACTTAT      480
ATAGGTACCA GGCATCACAT CTTCGCATCA GGTGTAAATG ATTTTCGAGT CAACACTATC      540
TATGAAGACT CTACACCTAT GAGCTGTCGC TTTGCAGAGG CTACGAATAG TGGCACCATC      600
TATCTGGCAT TGATGCATGA AACCACAATG TCTACGACTA TCCTTACTTA TCAAAACGGT      660
GAGTTCGTCG ATATCTCGGA AAGTGAATTG AGTAACTCGA TTATTGCATC CATGTGCTCT      720
AATAAAGAAG GTGATATAAT AGCTCTTGTT ACTTCATATA CAGGATTATG GAGTGGAACC      780
CTTGCGATCA GAAAAGCAGA TGAAGGCAAA TGGCAACTTG TTGGCGGAGA TATACAGAAT      840
GCGATCGTTC AAAATATATG CATGATGGAC GACAACAAGA TTGCTTGTGA AGTCTTCGGG      900
ACTCCTAACG GAGTAGATGG TCGGACAAGG GTTTGTGTTT CTGACGCATC TGTCTTTGAT      960
TTTGAGTGGT ATGAAGATGA AATATACGGA GGCCTGATAT TTGACACTTT CTCTATAGC     1020
CCTTGAGACA AACTTCTTTA TCGGAAATTT GGTGGGATTA TGCTCAGGAG TAAAGAGTCT     1080
TTTATAACCT CTTTCAATTTC TCCGACAGTT GTACAAGGAG TGGATGTCTA TACTTTGGCC     1140
GGGAAGATAA GGATCGAAAG TGAAACTCCG GTGTCTGAGG TGTGCTTTT CGACCTGGCT     1200
GGCAGGATGG TACTTCGGCA AACCATTGAT AATAAAATCT ATTCGGACAT AGATACTAAC     1260
GGACTAAAGC GAAGCGGTAT TTACGTAGTC TCGGTGCGGC TCTCTTCCGG ACAGGTATTG     1320
AGTCATAAGG TGCAGGTA                                     1338
```

(2) INFORMATION FOR SEQ ID NO:231

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

```
ATGATAATCC GGTGTCTTAT CCGTCGTCG AGAACCGTCC TGTTCCGGTT GATATTCGTG      60
GTAGGTCTTT TCTCTGCGAT GGC CGCAAGAG AAAAAGGATA GTCTCTCTAC GGTT CAGCCA      120
GTGCCGAATA GCAGCATGGT GGAGCAGACC CCTCTTCTCT CCATTGATCA CCCCCTCCTG      180
CCCCGTTCTT TTCAGAATAC CCGTACACTG AAAAGGTTTA GAGACAAACA TCTTTCCGAT      240
GCTTTGCTCA ATGGATTGAA GCCTCATCGC TCATCTTTGC AATTGAATGA GGAAC TCAAC      300
TTCGCGGCAG AGCGTCGGGA TTTCTGTTCT CCCCTCTTGC AAAC TCGCCA CGTGCCGGT      360
GTCCTTTTCA TGGCGACCGAC CGATAGGATG CATTTTTATA CATCGGGCAA TATCGGTCTT      420
GGCCATGATT TATTGACCGG TGTGCGCAAG GACTTCGGAT GGAATGCTGG TGCCGACTTC      480
TTGCTGAGTC AAAATCTTAC GGCACATGTC CAAGGCGGTT GGCAGCAGAA TTTCGGCTTT      540
ATACCTATGA CGGCTGTCAA TGGCCAATG CGTTGGCAAG CCACCGAGAG ATTGAGTTT      600
ACCACCGGTA TCATTATCG ACAGGTACAG TGGAAATGCTT TCGATAATAG AACGTTCTCG      660
CTTAAAGGAA GTGCTCGATA CGAAGTGATG GACAATGTCT TTGTCAATGG ATTTGGCAGC      720
TATCCTCTCT ACAGCAGTAC GCGCTCAGGA CTCAATATGG CTGTTCCGAT GCATGGATT      780
GGCCCTCAGT ACGGTGGATC GCTTGAGCTG AAAGTCTCCG AGCGATTCCG CTTTGCCGTC      840
GGTATGGAGC GCGAATACAA TATCTGGACT CGTCGGTGGG AAACGCATTA CTTTGCTTAT      900
CCTGTATTCT ATGGCGATAA GAAG                                     924
```

(2) INFORMATION FOR SEQ ID NO:232

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

```
ATGAAACGA ATAGACGATA CGCATTTGTT TTGCCGCTTC TGCTACTCAC CGGATTGTTG      60
GCATGGGGGC AGGATTCTTC CCACGGTAGC AATACAGCGT TTGCAACTGA TTCTTCGAGT      120
AGAGAGTTGC CCACGGAGCA GTCCGCCTAC CGCATTCATT CTGCCTATAT GGTCCGTGGT      180
GGCGGAAGCA TAACGCGCGA CACCTATTG TCACCCCTTC GTTATGGAGG ATGGACACTG      240
AATTTGTTGG GAGAGAAGAC GTTCCCTCTC AAAGCCTCCG ATTCCCGTTG GATGATCCGT      300
ACCGGGCATG AGCTGGATT TGCCTTGATG GACAATCCGG CCAATAATGC TCATTTCTAT      360
TCCTTGCTGT ATAACGGTTC CGCTGCGGCT CTTTACCGCC TTGGCGCTAA GCATCTGCGA      420
GCCGCGTGGA TGGACAATCT GCGCTTGGA TTCCGCCCGG GCTTGGAAT CGGGCTTGGA      480
GGAATTTATA GTACACGCAA CGCAATAAT CCTGCGACAT TGAAGCTCTA CACCAATGCC      540
ATCGCCCAAG CCTCGATAGG ATACTACGTC CCCTCCGAAA CTTTCCCT GTATTTTCGG      600
TTGCTCTCCC AGATCAATCT CTTCCGTATA GCCTATGGAA ATGGTTTTGG TGAGAGCTAT      660
TACGAGAATT TTTGCTCAA TAACGGCATT GCAGGCTCCC TGCATTTAC TTATCCGGGC      720
AAGTTTACTC GGTTCACGAC ACTCATAACG GCGGATATTC CCATTCGGAA CTCTGTACG      780
CTTCGTGTCG GTTATCGCTA TTCCCATTTG GGCTCTTCGC TTAACGCATT GGATACTCGA      840
ATCCACAGTC ATACGGCTTT TATCGGTTT GTACGGAGT TTTACCGATT CCGTGGGCGC      900
AAAGCCATGA ATACCGGTCG GAGAACCACT CTTTACTATC ATGAT                      945
```

(2) INFORMATION FOR SEQ ID NO:233

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 855 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

```
ATGGTAGTGA CGTGCTCGT AATTGTGCGT ATTGTGGTAG TAGTGCGGTA CTCCTTGCGC      60
GTCCACGTAC ATAAGACCGG CACTGTTGTA TCGGCGGCCA TATTGGCTT CATCCTCCTT      120
GGAAAGACCG TTCCATGCGA TACCCGTAAC TTCTTTTCCT CCGAAAGTGA TGAACCTGAG      180
AGCCGTGTTG CTACCGAAAT AGCCACCTG TGCGAAATAG GATTTCAGAT CCACGCTTCC      240
TCTATCCACG TAGCCGTCCG AACCGATTTT GGACAGGCGG GCATCCACTG CCCAATGGCG      300
ACCGATGCGT CCGCTACCGA GTTTGACCGA TCGCGGAAT GTGCCGAACG AACCTCCGCT      360
CAAATCGACA CGGCCATAAG GAGCCAGTCC CAAATTATCC GTACGCATAT TGACACTTGC      420
CCCCAAAGCT CCGGCACCAT TGGTGGAAGT ACCCACACCT CGCTGCACCT GAAGGTCTTC      480
GATGGAAGAG GCGAAGTCGG GCATATTCAC CAAAAGACG GACTGAGATT CGGAGTCGTT      540
GAGGGGTACT CCATTGGTAG TTATGTTGAT GCGATTGGCA TCGGTGCCAC GCACGCGAAA      600
GCCGGAATAT CCGATACCGG TACCGGCATC GCTGGTGGCT ACCACGGAGG GAGTCAGCAT      660
CAGCAGATAG GGGATGTCAC GACCATAATT GGACTTGGAA AGTTCGGCCT TGCGAACGTT      720
GGTGTAAAGC ACAGGGGTTT TCGCCGTGGC GCGAGTAGCT ACGACCTGTA CGGTCTGGAG      780
CTGCACATTG CTAAGACTAT CTATCTCGCT GTTGAGACG GGTGCTTGTA CCGTCAGGCA      840
GAAAGGCAGG ACGGC                      855
```

(2) INFORMATION FOR SEQ ID NO:234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1797 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

```
ATGGAAAAC TAAAGAACAT TCAGCCCAGA GAGGATTTC ACTGGAAGA GTTTGAGGCC      60
GGTGGCGTCC ATGCTGCCGT GAGTCGTCAG GAGCAGGAAG CTGCTTATGA CAAAACGCTC      120
AATACCATCA AGGAAAAGGA AGTGGTAATG GGTAGGGTAA CTGCTATCAA CAAGCGTGAA      180
GTGGTTATCA ATGTAGGGTA CAAATCGGAA GGTGTGGTAC CTGCAACAGA ATTCCGCTAC      240
AATCCCGAAC TCAAAGTGGG AGACGAAGTG GAAGTTTATA TCGAGAATCA GGAAGATAAG      300
AAGGGCCAGC TCGTCTTGTC TCACCGCAAG GGTGCTGCCG CTCGCTCTTG GGAGCGCGTG      360
AACGAGGCTC TCGAAAAAGA CGAAATCGTA AAGGGCTATG TGAAGTGTG TACCAAGGGT      420
GGTATGATCG TCGATGTATT CGGTATCGAG GCTTTCCTCC CGGGATCACA GATCGACGTG      480
CGCCCCATTC GCGACTACGA TGCATTCGTT GAGAAGACGA TGGAGTTCAA GATTGTGAAA      540
ATCAATCAAG AATATAAGAA TGTAGTTGTT TCCCACAAGG TGCTCATCGA AGCAGAGCTC      600
GAACAACAGA AGAAAGAAAT CATCGGCAAG CTCGAAAAAG GGCAGGTACT CGAAGGTATC      660
GTCAAGAATA TACTTCTTA CGGAGTATTT ATCGACCTCG GTGGAGTGGA TGGTCTTATC      720
CATATCACTG ACCTTTCATG GGGTCGTGTG GCTCATCCGG AAGAAATCGT ACAGCTGGAT      780
CAGAAGATCA ATGTCGTTAT CCTCGACTTT GATGAAGATC GCAAGCGTAT CGCTCTCGGA      840
CTCAAACAGC TGATGCCTCA TCCTTGGGAT GCTCTCGACA GCGAGCTTAA GGTAGGCGAT      900
AAGGTGAAGG GTAAAGTTGT GGTGATGGCA GATTACGGTG CTTTCGTTGA GATTGCACAG      960
GGCGTTGAGG GTCTTATCCA CGTAAGCGAA ATGTCATGGA CACAGCACTT GCGTCTTGCT     1020
CAGGACTTCC TGCATGTAGG CGACGAAGTG GAAGCCGTGA TCCTGACGCT CGACCGCGAA     1080
GAACGCAAAA TGTCGCTCGG TCTGAAGCAA CTCAAGCCGG ATCCTTGGGC TGATATCGAA     1140
ACTCGTTTCC CTGTAGGCTC TCGTCACCAT GCTCGTGTTC GCAACTTCAC CAATTTTCGGT     1200
GTATTCGTTG AGATCGAAGA GGGCGTAGAT GGCCTTATCC ATATTTCCGA CCTTTCTTGG     1260
ACGAAGAAGA TCAAACACCC CAGCGAGTTT ACGGAAGTAG GTGCTGATAT CGAAGTTCAG     1320
GTAATCGAGA TCGACAAGGA AAACCGTCGT CTCAGCTTGG GTCACAAACA GTTGGAAGAG     1380
AATCCTTGGG ATGTATTCGA GACGGTATTC ACTGTAGGAT CTATCCACGA AGGAACGGTA     1440
ATCGAAGTGA TGGACAAGGG TGCTGTGCTT TCTCTGCCTT ACGGTGTGGA AGGTTTTGCC     1500
ACTCCGAAGC ACATGGTGAA GGAAGATGGC TCACAGGCTG TACTCGAAGA GAAGTTACCT     1560
TTCAAGGTGA TTGAGTTCAA TAAGGATGCC AAGCGAATCA TTGTATCTCA TAGCCGTGTA     1620
TTCGAAGATG AGCAGAAAAT GGCTCAGCGT GAAGCCAATG CAGAGCGTAA GGCTGAAGCC     1680
AAAGCGGCTC AGAAAGAAGC TGCTGCCGAA GCTGCCAATC CTGCACAGGC TGAGAGAAA     1740
GCCACTCTCG GAGACCTCGG CGAGCTGGCC GCTTTGAAAG AAAAGCTTTC AGAAAAAC     1797
```

(2) INFORMATION FOR SEQ ID NO:235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

```
ATGGGTAGGG TAACTGCTAT CAACAAGCGT GAAGTGGTTA TCAATGTAGG GTACAAATCG      60
GAAGGTGTGG TACCTGCAAC AGAATTCGCG TACAATCCCG AACTCAAAGT GGGAGACGAA      120
GTGGAAGTTT ATATCGAGAA TCAGGAAGAT AAGAAGGGCC AGCTCGTCTT GTCTCACC GC      180
AAGGGTCGTG CCGCTCGCTC TTGGGAGCGC GTGAACGAGG CTCTCGAAAA AGACGAAATC      240
GTAAAGGGCT ATGTGAAGTG TCGTACCAAG GGTGGTATGA TCGTCGATGT ATTCCGTATC      300
GAGGCTTTCC TCCCGGGATC ACAGATCGAC GTGCGCCCCA TCGCGACTA CGATGCATTC      360
GTTGAGAAGA CGATGGAGTT CAAGATTGTG AAAATCAATC AAGAATATAA GAATGTAGTT      420
GTTTCCACCA AGGTGCTCAT CGAAGCAGAG CTCGAACAAC AGAAGAAAAG AATCATCGGC      480
AAGCTCGAAA AAGGGCAGGT ACTCGAAGGT ATCGTCAAGA ATATTACTTC TTACGGAGTA      540
TTTATCGACC TCGGTGGAGT GGATGGTCTT ATCCATATCA CTGACCTTTC ATGGGGTCGT      600
GTGGCTCATC CGGAAGAAAT CGTACAGCTG GATCAGAAGA TCAATGTGCT TATCCTCGAC      660
TTTGTATGAA ATCGCAAGCG TATCGTCTC GGACTCAAAC AGCTGATGCC TCATCCTTGG      720
GATGCTCTCG ACAGCGAGCT TAAGGTAGGC GATAAGGTGA AGGGTAAAGT TGTGGTGATG      780
GCAGATTACG GTGCTTTCTG TGAGATTGCA CAGGGCGTTG AGGGTCTTAT CCACGTAAGC      840
GAAATGTCAT GGACACAGCA CTTGCGTTCT GCTCAGGACT TCCTGCATGT AGGCGACGAA      900
GTGGAAGCCG TGATCCTGAC GCTCGACCGC GAAGAACGCA AAATGTCGCT CGGTCTGAAG      960
CAACTCAAGC CGGATCCTTG GGCTGATATC GAAACTCGTT TCCCTGTAGG CTCTCGTCAC     1020
CATGCTCGTG TTCGCAACTT CACCAATTTT GGTGTATTCG TTGAGATCGA AGAGGGCGTA     1080
GATGGCCTTA TCCATATTTT CGACCTTTCT TGGACGAAGA AGATCAAACA CCCCAGCGAG     1140
TTTACGGAAG TAGGTGCTGA TATCGAAGTT CAGGTAATCG AGATCGACAA GGAAAACCGT     1200
CGTCTCAGCT TGGGTCACAA ACAGTTGGAA GAGAATCCTT GGGATGTATT CGAGACGGTA     1260
TTCACGTAGT GATCTATCCA CGAAGGAACG GTAATCGAAG TGATGGACAA GGGTGCTGTC     1320
GTTTCTCTGC CTTACGTGTG GGAAGGTTTT GCCACTCCGA AGCACATGGT GAAGGAAGAT     1380
GGCTCACAGG CTGTACTCGA AGAGAAGTTA CCTTTCGAAG TTATTGAGTT CAATAAGGAT     1440
GCCAAGCGAA TCATTGTATC TCATAGCCGT GTATTGGAAG ATGAGCAGAA AATGGCTCAG     1500
CGTGAAGCCA ATGCAGAGCG TAAGGCTGAA GCCAAGCGG CTCAGAAAGA AGCTGCTGCC     1560
GAAGCTGCCA ATCCTGCACA GGCTGTAGAG AAAGCCACTC TCGGAGACCT CGGCGAGCTG     1620
GCCGCTTTGA AAGAAAAGCT TTCAGAAAAC
```

(2) INFORMATION FOR SEQ ID NO:236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

```
ATGATCGTCG ATGTATTCGG TATCGAGGCT TTCCTCCCGG GATCACAGAT CGACGTGCGC      60
CCCATTCCGC ACTACGATGC ATTCGTTGAG AAGACGATGG AGTTCAAGAT TGTGAAAATC      120
AATCAAGAAT ATAAGAATGT AGTTGTTTCC CACAAGGTGC TCATCGAAGC AGAGCTCGAA      180
CAACAGAAGA AAGAAATCAT CGGCAAGCTC GAAAAAGGGC AGGTACTCGA AGGTATCGTC      240
AAGAATATTA CTTCTTACGG AGTATTTATC GACCTCGGTG GAGTGGATGG TCTTATCCAT      300
ATCACTGACC TTTCATGGGG TCGTGTGGCT CATCCGGAAG AAATCGTACA GCTGGATCAG      360
AAGATCAATG TCGTTATCCT CGACTTTGAT GAAGATCGCA AGCGTATCGC TCTCGGACTC      420
AAACAGCTGA TGCTCATCC TGGGATGCT CTCGACAGCG AGCTTAAGGT AGGCGATAAG      480
GTGAAGGGTA AAGTTGTGGT GATGGCAGAT TACGGTGCTT TCGTTGAGAT TGACAGGGC      540
GTTGAGGGTC TTATCCACGT AAGCGAAATG TCATGGACAC AGCACTTGCG TTCTGCTCAG      600
GACTTCTGTC ATGTAGGCGA CGAAGTGGAA GCCGTGATCC TGACGCTCGA CCGCGAAGAA      660
CGCAAAATGT CGCTCGGTCT GAAGCAACTC AAGCCGGATC CTGGGGCTGA TATCGAAACT      720
CGTTTCCCTG TAGGCTCTCG TCACCATGCT CGTGTTTCGA ACTTCACCAA TTTCGGTGTA      780
TTCGTTGAGA TCGAAGAGGG CGTAGATGGC CTATCCATA TTTCCGACCT TTCTTGGACG      840
AAGAAGATCA AACACCCCGC CGAGTTTACG GAAGTAGGTG CTGATATCGA AGTTCAGGTA      900
ATCGAGATCG ACAAGGAAAA CGCTCGTCTC AGCTTGGGTC ACAAACAGTT GGAAGAGAAT      960
CCTTGGGATG TATTCGAGAC GGTATTCACT GTAGGATCTA TCCACGAAGG AACGGTAATC     1020
GAAGTGATGG ACAAGGGTGC GTGCTTTCT CTGCCTTACG GTGTGGAAGG TTTTGCCACT     1080
CCGAAGCACA TGGTGAAGGA AGATGGCTCA CAGGCTGTAC TCGAAGAGAA GTTACCTTTC     1140
AAGGTTATTG AGTTCAATAA GGATGCCAAG CGAATCATTG TATCTCATAG CCGTGTATTC     1200
GAAGATGAGC AGAAAATGGC TCAGCGTGAA GCCAATGCAG AGCGTAAGGC TGAAGCCAAA     1260
```

GCGGCTCAGA AAGAAGCTGC TGCCGAAGCT GCCAATCCTG CACAGGCTGT AGAGAAAGCC 1320
 ACTCTCGGAG ACCTCGGCGA GCTGGCCGCT TTGAAAGAAA AGCTTTCAGA AAAC 1374

(2) INFORMATION FOR SEQ ID NO:237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

ATGGAGTTCA	AGATTGTGAA	AATCAATCAA	GAATATAAGA	ATGTAGTTGT	TTCCCACAAG	60
GTGCTCATCG	AAGCAGAGCT	CGAACAACAG	AAGAAAGAAA	TCATCGGCAA	GCTCGAAAAA	120
GGGCAGGTAC	TCGAAGGTAT	CGTCAAGAAT	ATTACTTCTT	ACGGAGTATT	TATCGACCTC	180
GGTGGAGTGG	ATGGTCTTAT	CCATATCACT	GACCTTTCAT	GGGGTCGTGT	GGCTCATCCG	240
GAAGAAATCG	TACAGCTGGA	TCAGAAGATC	AATGTCGTTA	TCCTCGACTT	TGATGAAGAT	300
CGCAAGCGTA	TCGCTCTCGG	ACTCAAACAG	CTGATGCCTC	ATCCTTGGA	TGCTCTCGAC	360
AGCGAGCTTA	AGGTAGGCGA	TAAGGTGAAG	GGTAAAGTTG	TGGTGATGGC	AGATTACGGT	420
GCTTTCGTTG	AGATTGCACA	GGGCGTTGAG	GGTCTTATCC	ACGTAAGCGA	AATGTCATGG	480
ACACAGCACT	TGCGTTCTGC	TCAGGACTTC	CTGCATGTAG	GCGACGAAGT	GGAAGCCGTG	540
ATCCTGACGC	TCGACCGCGA	AGAACGCAAA	ATGTCGCTCG	GTCTGAAGCA	ACTCAAGCCG	600
GATCCTTGGG	CTGATATCGA	AACTCGTTTC	CCTGTAGGCT	CTCGTCACCA	TGCTCGTGTT	660
GCCAACTTCA	CCAATTTCCG	TGTATTCTGT	GAGATCGAAG	AGGGCGTAGA	TGGCCTTATC	720
CATATTTCCG	ACCTTTCTTG	GACGAAGAAG	ATCAAACACC	CCAGCGAGTT	TACGGAAGTA	780
GGTGCTGATA	TCGAAGTTCA	GGTAATCGAG	ATCGACAAGG	AAAACCGTCG	TCTCAGCTTG	840
GGTCACAAAC	AGTTGGAAGA	GAATCCTTGG	GATGTATTCT	AGACGGTATT	CACTGTAGGA	900
TTCTATCAGC	AAGGAACGGT	AATCGAAGTG	ATGGACAAGG	GTGCTGTCTG	TTCTCTGCCT	960
TACGGTGTGG	AAGGTTTTGC	CACTCCGAAG	CACATGGTGA	AGGAAGATGG	CTCACAGGCT	1020
GTA CTGAAG	AGAAGTTACC	TTTCAAGGTT	ATTGAGTTCA	ATAAGGATGC	CAAGCGAATC	1080
ATTGTATCTC	ATAGCCGTGT	ATTCGAAGAT	GAGCAGAAAA	TGGCTCAGCG	TGAAGCCAAAT	1140
GCAGAGCGTA	AGGCTGAAGC	CAAAGCGGCT	CAGAAAGAAG	CTGCTGCCGA	AGCTGCCAAT	1200
CCTGCACAGG	CTGTAGAGAA	AGCCACTCTC	GGAGACCTCG	GCGAGCTGGC	CGCTTTGAAA	1260
GAAAAGCTTT	CAGAAAAAC					1278

(2) INFORMATION FOR SEQ ID NO:238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

ATGAAAAAAG	CTATTCTTTC	CGGAGCGGCC	TTGCTCTCTG	GCCTATGTGC	CAACGCACAA	60
AACGTGCAGT	TGCACTACGA	TTTCGGTCAT	TCCATCTACG	ACGAACTAGA	TGGACGTCCC	120
AAACTGACTA	CCACAGTGGA	AAACTTCACA	CCCGACAAAT	GGGGAAGCAC	CTTCTTCTTC	180

ATCGACATGG	ATTACACGGG	CAAGGGTATC	CAGTCGGCCT	ATTGGGAGAT	TTCGCGCGAA	240
CTGAAGTTT	GGCAAGCTCC	CGTTTCCATT	CATTTGGAGT	ACAACGGAGG	CCTCTCCACA	300
AGCTTTACTT	TCGGACACGA	TGCTCTAATC	GGTGCCACCT	ACACCTACAA	CAACCCCTCC	360
TTTACACGTG	GATTTACGAT	CACGCCCATG	TACAAGCATC	TGGGTGCGCA	CGACTTCCAC	420
ACCTATCAGA	TCACCGGCAC	TTGGTACATG	CACTTTCTGG	ACGGTCTGCT	TACCTTCAAC	480
GGCTTCCTCG	ATCTTTGGGG	TTTCCCCCAA	GAGAACCCAA	TCGGGGGGCC	TGTGCTCAAA	540
GAAGGGGATA	AGTTTCGTATT	CCTGTCCGAA	CCGCAGTTCT	GGATCAACCT	CAATCGCATC	600
AAAGGCATCG	ACAAGGATTT	CAATCTCAGC	ATAGGGACAG	AGATGGAAAT	CAGCAGGAAC	660
TTCGCTCGCA	TGGACAAATT	CTCCTGCATC	CCTACTCTTG	CGGTCAAATG	GACTTTCAAC	720

(2) INFORMATION FOR SEQ ID NO:239

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1302
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

ATGTATAAAG	ACTATAAGGG	TTGTATGCG	TCGCTTCGGT	GGTATGCCCT	GATCATTGGG	60
TTGCTATTTG	CAGCAGACGG	TATACAGGCT	CAGAACAACA	ACTTTACCGA	GTCGCCTTAC	120
ACTCGCTTCG	GCCTTGCCCG	TCTCGGAGAA	CGGACGACTA	TTAGTGGGCA	TTCCATGGGA	180
GGACTCGGCG	TCGGTCTGCG	TCAGGGCACA	TACGTCAATG	CCGTCAATCC	TGCTTCATAC	240
TCGGCTGTGG	ATTCGATGAC	GTTTATCTTC	GATTTCCGGT	CATCTACCGG	AATTACGTGG	300
TATGCCGAGA	ACGGGAAAAA	GGACAATAGG	AAAATGGGAA	ACATTGAGTA	TTTCGCCATG	360
CTTTTTCTTA	TTTCCAAATC	CATTGCTATG	AGTGCGGGAG	TGCTTCCTTA	CTCCGCATCC	420
GGGTACCAAGT	TCGGATCCGT	TGATCAAGTG	GAAGGAGGCA	GCGTCCAGTA	CACCCGTAAA	480
TACTTGGGGA	CAGGCAATCT	GAACGATCTC	TATGTCGGTA	TAGGTGCAAC	CCCGTTCAAA	540
AACTTCTCAA	TAGGAGCCAA	TGCTTCATCC	CTTTTGGGCG	GATTACACAC	CAGCAGGCAG	600
GTAATCTTCT	CCACGGAGGC	TCCTTACAAT	CCCGTACATC	TCTCGACGCT	GTAATTGAAG	660
GCTGCCAAGT	TCGACTTCGG	TATGCAGTAT	CACCTTCTTC	TCAAATCAGA	TCGTTTCGCTC	720
GTTATCGGTG	CCGTCTATTC	TCCGCGGGTG	AAGATGCATA	GCGAGCTGAC	TCAGATAAAG	780
AATCAGGTTT	AGAACGGTGT	AGTAGTGGAG	AGCGAAACCC	AAGAATATAT	CAAGGGAATG	840
GAATATTATA	CCCTGCCTCA	TACATTGGGG	ATAGGTTTTT	CTTATGAAAA	GAAAGATAAA	900
CTTCTCTTAG	GAGCAGACGT	CCAATATAGT	AAATGGAAAG	GCGAGAAATT	TTATAAATCC	960
GATTGCAAA	TCCAGGACAG	AATACGGGTA	TCTCTCGGCG	GAGAGATCAT	ACCGGATATA	1020
AATGCCGTTG	GGATGTGGCC	TAAAGTTCGC	TATCGCTTCG	GTTTACATGG	TGAAAATTCT	1080
TACCTGAAAG	TGCCGACTAA	AGGCGGTGTA	TATCAAGGAT	ACCATATCGT	AGGTGCTGTA	1140
TTCGGTATAG	GAATCCCGCT	CAATGACAGA	CGTTCGTTTC	TAAATGTCTC	TCTTGAATAT	1200
GACCGATTGA	TCCCGAAGGA	GGGTATGATC	AAAGAAAAATG	CTCTGAAATT	GACCTTCGCG	1260
CTCACGTTCA	ACGAGTCATG	GTTTAAAAAG	CTGAAACTGA	AC		1302

(2) INFORMATION FOR SEQ ID NO:240

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2778 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...2778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

```
ATGCGATCGA TTTATCAATT ACTGTTGTCA ATACTCCTTG CTTCTCTTGG TTTCGTCGGG      60
CTGGAAGCCC AACAGCCCG AGTAGCAGGT AGAGTATTGG ACGAAGAAG CAACCCCATG      120
ATTCAAGCCA ACGTACAGCT TGTACAGAGT ACCGGCCAAG TAGCCGTTGC CGCAGGTGCC      180
ACTAATGAAA AAGGGTTGTT CAGCCTGAAA ACGTCACAGG AGGGTGACTA CATTCTGCGC      240
GTTTCATATG TAGGTTACAC TACCCACGAC GAAAAAATAT CTCTTAGAAA CGGGCAAACC      300
ATTACGCTCA AAGATATATC CATGAACGAA GATGCCCGTC TTCTACAGAG TGTGACGGTG      360
CAGGCTAAAG CGGCAGAGGT CGTGGTACGC AACGATACGC TCGAATTCAA TGCCGGATCC      420
TATACCGTAG CACAGGGAGC TTCTATCGAG GAACTGATCA AGAAGCTACC CGGAGCAGAG      480
ATCGGATCCG ATGGGAAGAT CACCATCAAC GGCAAGGACA TTAGCAAGAT CCTTGTCGAT      540
GGCAAGAGAT TTTTCTCCAA AGATCCACAG GTGGCAATAA AGAATCTTCC GGCCGATATG      600
GTCAATAAAG TACAGGTACT GAACAACTG AGCGAGCTGT CGCGGATGAG CGGTTTCGAT      660
ATGGAGAAAG AGGAGCTCGT AATCAACCTG ACGGTGAAGC CCGAAAAAAA GAAAGGCCTC      720
TTCGGAACGC TTCAGGCCGG CTACGGTACC GACCAACGCT ATATGGCCGG AGGGAACGTC      780
AATCGGTTTC ATGGAATAAA GCAATGGACA TTGATCGGTA GTGCGAACAA TACGAACAAT      840
ATGGGCTTTA GCGAGATGGA CAGCGAGATG GGATCCATGA CCTTCTTCTC TCCCCAAGGC      900
GGTGGTCGAG CCGGCTTCGG CAATAGTGGG GGTGTACGT CTTCTGTCGAT GCTGGGCGGC      960
AACTTCAGTG TCGAATTCTC CTCTGCCCTT AATACAGGAG GCGATGCACG CTACGGATAC      1020
AACGACAAGG CCATAGAGAG GACCAACGCG GTGGAAAATA TCCTCGCCGA AGGGAATACT      1080
TATATGGACG AAAATATATT GGAACGCTCT TTCTCTCACA ATGGTCAGGC GCGATTTAGG      1140
ATGCAATGGA AACCGTCCGA ACTTACCGAA GTGGTATTCC AGCCGATCTT TTCGATATCC      1200
AAGATCGATG GGTTCCTTAA CGACACATAC GAGACGAAAG ATGCCACCGG AATCTCTATC      1260
AACAAAGGTT CTATCCACCA AACTACACAA GGAACAACCT TCAGACTGAA CGGAGAATTG      1320
GATATCAGTG ACAAGCTCAA CGACGAAGGC CGTACGATCA GTGCCTCCGT CAGTGGCGGT      1380
CTGACCGAGC AAGACGGAGA TGGCATATAT CAGGCTGTGC TCCAAAGCGT GGAGACGAAT      1440
CAAAAGCAAT TCAACGACAA CTCCAACCTG CAATATCGGC TTCGCCTCTC GTATGTGGAA      1500
CCGTGCGGTA AAAACTACTT CGCACAAAGC ATTCTGAACA GACGTTTCTC CCGTCGCAAT      1560
TCGGATCGTG AGGTGTACCG ACTGGGCGAT GACGGGCAAT ACTCCATATT AGACAGTCAG      1620
TACGGACTCT CCTACAGTAA CGAGTTCACC CAGTATCGCA TCGGACTCAA CCTCAAGAAG      1680
ATTGCCAAAA CGTGGGACTA CACCGTAGGA TTCAATGTGG ATCCCAACAG AACTGTCAGC      1740
TATCGGAGCG TAGCCGAGT AGAGCAGGAC AAACCTGGCTT TCAATCGTGT CAATCTCTCC      1800
CCGATGCTCC GAATCAACTA CAAACCGAGC AGGACTACCA ACCTCCGAGT GGAATACCGA      1860
GGACGCACGA CACAACCATC CATCAATCAG ATCGCTCCCG TTCAGGACAT CACGAATCCG      1920
CTATTCGTGA CGGAAGGCAA TCCCGGTCTG AAGCCGAGCT ATTCCAACAA TGTGATGGCC      1980
ATGTTCTCGG ACTTCGATGC CAAAAGTCAG CGAGCTTTCA ACATTGTTTT CTTCGCAAC      2040
TATACATTCG AGACATCGT CCCCATAACG CACTACGATC CGTCTACAGG GATCCGTACC      2100
ACTCGTTAGC AAAACGCCCT CCGTACGTGG CAAGCGAATC TTCATGGGAC ACTATCGCTT      2160
CCACTCAAGA ACAGGCATT TTCTTTTCAG ATGTCTTGT TCAACAGGTT GGCCGAAGGA      2220
CAAAGCTTCA TCAATGACGA TAAGAACAAA GCTCTCTCTT TCCGAACGAG GGAACGCCTG      2280
ACGCTGACCT ATCGCAACAA TTGGATCGAT ACGAGTATCG GTGGCAATAT CGGATTCTAT      2340
ATGGCGAATA ATAGTCTGAG CGGACAGAAA GATTCTCGCA CATAAGATT TGGCGGCAAT      2400
TATCAAGTTG CCCTAACGCT TCCCTATGGA TTCCGTATCG ACACGATGT TGAATACAAT      2460
ACGAACCTCG GTTACAGCGG AGGATTCAGT CTGGACGAAT GGCTTTGGAA TGCTTCGCTT      2520
TCATACAGCT TCCTCCGTGA CAAGGCCGGT ACGTGCCTG TCAATGGCTA TGACATCCTC      2580
GGTCAGCGGT AACGATATC CCGTTCTGCT TCGGCCATCA ATATAGAAGA GAGCATGTCC      2640
AATACGATCG GACGCTACGT GATGGTGGAC TTTATCTACC GATTCAACGC CTTCAAGTGGT      2700
GGTGGATCTC GCAGCGATCA TCAGCGTGGC AATATGAATC GTCCGGGCCC ACCTTTCGGC      2760
GGTGGCAGAC GACCGTCC      2778
```

(2) INFORMATION FOR SEQ ID NO:241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

ATGGTTATGA AGCTGATTAA AAGAAGTTTG CTCTGCTTG GAGCGGTACT GCTGATTACG 60

CTTCCTGCGT	ACTCGCAGAA	TGATGACATC	TTCGAAGATG	ACATCTATAC	ATCGCGAAAA	120
GAAATACGTA	AACAAAACCA	AGTTAAAGAC	TGGCAAAACC	AAGAGGACGG	ATACGGCGAC	180
GATACGGAAT	ATACAGTGGC	TCCGATCGG	GACATTGACG	CCTACAATCG	TAGAGATGGC	240
CAGTCCTACG	ATGGGAAAAA	GTTGTCCAAA	GACAAGAAAA	GAGACTCCAC	TCGTTCTTCT	300
GTTCCTGGTC	GCTATAGTCG	CCGCTTGGCT	CGATTCTATA	AGCCGAATAC	GATCGTCATT	360
TCAGGTGCCG	ACAATGTATA	TGTAACGTAT	GATGGTGAGT	ATTTCTGCTA	TGGAGACGAA	420
TACTATGATG	ACGCGTCGTC	TGTAAACATT	TACATCAACA	GTCTTGGTG	CGATCCGTTC	480
CCTTATACGT	CATGGTATCC	ATCTTTCTCC	GGCTGGTACA	ACTATACGTG	GAATATCCA	540
TGGTTCTACT	ACGGTAGCCA	TATCGGATGG	GGCGGTTATT	ACCCCGGATA	TAATTGGTAT	600
TGGAGCTACT	ACTATGATCC	TTTCTACAAT	CCCTATGGAA	TCGGTATGGG	TTGGGGATAT	660
CCTTATGGCT	GGGCGAGCTA	TTACGGTTGG	GGTGGCTATC	CGGGAGTGAT	ACATCACTAC	720
CACCACTACC	CCAAGAAGAC	CTATTCCAAT	GGTCAGCATT	CCGGAGCTTA	CTATTCTTAT	780
GGCCGACCGA	ATCGTATCAA	AGGTGGAACG	TCCGGTGCCA	AACTTGGGAC	AGGACGCTAC	840
GATAGAATTC	AAAATTCGTC	TTCGCAAAAA	AATAAGTTCG	GATTGCAGTC	GAACAAACCC	900
AATAATAATC	TGCAAAATGT	CAAGTCGGGA	CGTACCGGCC	GAGCCAATAG	AGACCGAAAT	960
ATAGAAACGG	TAACTCCAAA	CAACGGGCAA	AAGCAGAATC	GTCCCGTATT	CCAGCAGAAT	1020
CAGTCCGGCA	ATGACCGACC	GACCGGACGG	AATATCCGCA	GCGAGAGACA	GGGGGAAAT	1080
AACGATAGGA	CATTTTCGAC	TCCTTCTCGT	AGCAATAGTA	ACGGTGGCTT	CTCCACGCCT	1140
TCTCGCTCTT	CTTCCGGCTC	TATGAGCGGA	GGTGGCGGAC	GTAGTGGCCG	GGGACGCAAT	1200

(2) INFORMATION FOR SEQ ID NO:242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGAAGCTGA	TTAAAAGAAG	TTTGCTCCTG	CTTGGAGCGG	TACTGCTGAT	TACGCTTCCT	60
GGGTACTCGC	AGAATGATGA	CATCTTCGAA	GATGACATCT	ATACATCGCG	AAAAGAAATA	120
CGTAAACAAA	ACCAAGTTAA	AGACTGGCAA	AACCAAGAGG	ACGGATACGG	CGACGATACG	180
GAATATACAG	TGGCTTCCGA	TCGGGACATT	GACGCCTACA	ATCGTAGAGA	TGGCCAGTCC	240
TACGATGGGA	AAAAGTTGTC	CAAAGACAAG	AAAAGAGACT	CCACTCGTTC	TTCTGTTCCC	300
GGTCGCTATA	GTCGCCGCTT	GGCTCGATTC	TATAAGCCGA	ATACGATCGT	CATTTACAGT	360
GCCGACAATG	TATATGTAAC	TGATGATGGT	GAGTATTTTC	TCTATGGAGA	CGAATACTAT	420
GATGACGCGT	CGTCTGTAAA	CATTTACATC	AACAGTCTTT	GGTGCGATCC	GTTCCCTTAT	480
ACGTCATGGT	ATCCATCTTT	CTCCGGCTGG	TACAACATA	CGTGGAACCT	TCCATGGTTC	540
TACTACGGTA	GCCATATCGG	ATGGGGCGGT	TATTACCCCG	GATATAATTG	GTATTGGAGC	600
TACTACTATG	ATCCTTTCTA	CAATCCCTAT	GGAATCGGTA	TGGGTTGGGG	ATATCCTTAT	660
GGCTGGGGCA	GCTATTACGG	TTGGGGTGGC	TATCCGGGAG	TGATACATCA	CTACCACCAC	720
TACCCCAAGA	AGACCTATTC	CAATGGTCAG	CATTCCGGAG	CTTACTATTC	TTATGGCCGA	780
CCGAATCGTA	TCAAAGGTGG	AACGTCCGGT	GCCAAACTTG	GGACAGGACG	CTACGATAGA	840
ATTCAAAATT	CGTCTTCGCA	AAAAAATAAG	TTCGGATTGC	AGTCGAACAA	ACCCAATAAT	900
AATCTGCAAA	ATGTCAAGTC	GGGACGTACC	GGCCGAGCCA	ATAGAGACCG	AAATATAGAA	960
ACGGTAACTC	CAAACAACGG	GCAAAAGCAG	AATCGTCCCG	TATTCCAGCA	GAATCAGTCC	1020
GGCAATGACC	GACCGACCGG	ACGGAATATC	CGCAGCGAGA	GACAGGGGGA	AAATAACGAT	1080
AGGACATTTT	CGACTCCTTC	TCGTAGCAAT	AGTAACGGTG	GCTTCTCCAC	GCCTTCTCGC	1140
TCTTCTTCCG	GCTCTATGAG	CGGAGGTGGC	GGACGTAGTG	GCCGGGGACG	CAAT	1194

(2) INFORMATION FOR SEQ ID NO:243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

```
ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG      60
GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC      120
TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT      180
CAGAGCGATA TGGTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC      240
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCCGTT CGAGGATCTC      300
TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGGGGCGTG GCGTTCCTCA CATGTATGTG      360
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC      420
GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC      480
GGACGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGGTATTGC AGGACAGCAG      540
CGTAACTACT TCACCCGAC GGGCAAGGTA TTCAATTCCG GCCGAGGCTA CCTACTGGGT      600
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGCGCGACAA TGAATATCAT      660
TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT      720
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC      780
ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT      840
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCTCA      900
TACTCCAAAA AAGGGATGAG TATCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTC      960
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC      1020
CAAGCTCACA CTTATACGCT GGGCGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA      1080
TGGGCTTTCC AAGGTGAACT GCGTTACAAC TTTGCTCGCC GGACAGCTCT CGGTGGACGC      1140
TACGGTACCG GCTTGCGTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAAGATGCTC      1200
AAAGAGAATC CCGACGAACT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG      1260
GGCGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC      1320
AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGTACTGCA CGGTGCAGCC      1380
GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG      1440
AGTAATAAGG TAGCCCTCCG TACCGAATG CAATATTTGC ACACGAAGCA GGATCAGGGT      1500
GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCTCTCG      1560
GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT      1620
CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG      1680
GGAGGTGTAT GTCGTGTGGT CCCTGAGACT CAGGGATTCT ACCTTTCTTA TAGACCAAT      1740
CTG                                     1743
```

(2) INFORMATION FOR SEQ ID NO:244

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

```
ATGCGTCTTT TATTTTGGAG CGCGTTGCGC AGCTCCTCTC TCCATGGTTC AGAGCGACGC      60
AGTCGGATAA GTTCTTCTGT AGTCATGTCA ATAAGGCAGA AAATAAGGTT ATTCCATCTC      120
TCGGTATGCG CCCAAACGCA TGATCATCTC ATCGAAATCC ACTTGGTGTG CATCGAATTC      180
GGGGCCATCG ACACAGACGA ATTTCTGCTG TCCTCCACAG CTTATACGAC AAGCCCCACA      240
CATACCGGTG CCATCCACCA TAATTGTATT GAGAGAAGCT ATGGTCGGTA TCTCGTAACG      300
TTTGGTCAGG AGAGAAACGA ACTTCATCAT CACAGCCGGC CCGATCGTAA CGCAGAGGTC      360
TACCGTTTCC CGTTTGATAA CGCTTCCAC TCCATCCGTT ACGAGGCCTT TCGTCCCAT      420
AGACCATCG TCTGTCATGA TGATCACTTC ATCGCTATTG GCTCGCATTT GTTCTTCAAG      480
GATAACCAGA TCTTTAGTTC TGGCAGCCAA TACGACAATT ACACGGTTGC CTGCTTTGTG      540
GAAAGCCTCC ACGATCGGGA GCAAAGGAGC CACACCCACA CCGCTCCGG CACAAACCAC      600
```

TGTGCCGACC TTTTCGATAT GCGTACTCTG TCCCAGCGGA CCTACCACAT CCGTGATATA	660
GTCCGCGACT TCGAGTTCGG CCAATTTCTT GGAAGATTG CCCACGGCCT GAACCAC	717

(2) INFORMATION FOR SEQ ID NO:245

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...633
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

ATGTCAATAA GGCAGAAAAT AAGGTTATTC CATCTCTCGG TATGCGCCCA AACGCATGAT	60
CATCTCATCG AAATCCACTT GGTGTGCATC GAATTCGGGG CCATCGACAC AGACGAATTT	120
CGTCTGTCTT CCCACGCTTA TAGACAAGC CCCACACATA CCGGTGCCAT CCACCATAAT	180
TGTATTGAGA GAAGCTATGG TCGGTATCTC GTAACGTTTG GTCAGGAGAG AAACGAACTT	240
CATCATCACA GCCGGCCCCG TCGTAACGCA GAGGTCTACC GTTCCCGTT TGATAACGCT	300
TTCCACTCCA TCCGTTACGA GGCCTTTCGT CCCATAAGAC CCATCGTCTG TCATGATGAT	360
CACTTCATCG CTATTGGCTC GCATTTGTTC TTCAAGGATA ACCAGATCTT TAGTTCTGGC	420
AGCCAATACG ACAATTACAC GGTTCGCTGC TTTGTGGAAA GCCTCCACGA TCGGGAGCAA	480
AGGAGCCACA CCCACACCGC CTCGGGCACA AACCAGTGTG CCGACCTTTT CGATATGCGT	540
ACTCTGTCCC AGCGGACCTA CCACATCCGT GATATAGTCG CCGACTTCGA GTTCGGCCAA	600
TTTCTTGGA GATTTGCCA CGGCCTGAAC CAC	633

(2) INFORMATION FOR SEQ ID NO:246

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2343
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

ATGGATCGTC CTAAGCCTTC ATATATTGTT CGAATAGCAG CCATTCTCTG CTTGTTTGTC	60
GGCAGGCCTT TGTTTGCACA GAGCTATGTG GACTACGTCG ATCCGCTGAT CGGGACGCTA	120
AGTTCTTTTG AGCTGAGTGC GGGCAATACC TATCCGGTGA TCGGTTTACC GTGGGGAATG	180
AATAGCTGGA CACCGATGAC CCGGTGACCC GGTGACGGCT GGCAATATAC CTAATCGGCA	240
CACAAGATTG CCGGATTCAA ACAGACCCAC CAACCCAGTC CTTGGATCAA CGACTACGGC	300
CAATTCTCCC TTCTTCCCCT TACGGCACCG CAGAAGCCAT CATCGAACGA CTCCATAGCT	360
CTGACTAAAT GGTGCAAGCA ACTCTTTTCG GACGAACAGA CCTCGTGGTT CTCGCACAAA	420
GCGGAGACGG CGACGCCATA CTATTATAGT GTCTATTGTT CCGATTACGA CACACGCGTG	480
GAGATGGCTC CGACCGAGCG TGCAGCTATC TTTTCGCATC GTTATTCCGG CAATACCGAA	540
AGTGGCTCCG GTCGATGGCT TCGTCTTGAT GCCTTTACCG GTGGTTCGGA GATTAGCATC	600
GTGGATCCTC ACACCGTAGT GGGCATATCT CGCAAGAATA GCGGAGGTGT GCCGGCTAAC	660
TTGCGCTGTT ATTTTCATCT GCAGTCCGAT ACTCCTATGG CCGATGTCCT GCTTGAGACA	720
GATACCGGCA AGTCAGACGA AGCACAAGG GCATGGGCAG CCTGTCGCTT CGATTGCGAA	780
GAAGTTACCG TCCGGGTGGC ATCTTCTTTT ATCAGTGTG AGCAGGCCGA AAGAAATCTT	840

GCGGAAGTCA	AAGGGCAGAG	TTTCGACCGG	ATCAGACTTG	CCGGTCGCGA	AGCTTGAAT	900
AAGGTGCTCG	GACGCATACA	TGTGGAAGGA	GGAAACGAAGG	ATGAGCGCAC	TACATTCTAT	960
TCCGCACTCT	ATCGCTGTCT	GCTTTTTC	CGTCGCTTCT	ATGAGGAGGA	TGCTTCCGGC	1020
AATTTTGTGC	ATTACAGCCC	CTACAATGGA	GAGGTACTTC	CCGGTTATCT	CTATACCGAT	1080
ACCGGATTTT	GGGACACTTT	TCGAGCCCTT	TTCCCCCTGC	TCAATCTGCT	GTATCCCGAT	1140
GAAAACATTA	AAATTCAGGA	AGGTCTGCTG	AATGTATATC	GCGAGAGTGG	CTTTTCCCCC	1200
GAATGGGCCA	GTCCGGGCCA	TCGGGATTGT	ATGATAGGCA	ACAACTCTGC	TCTGTCTCTG	1260
GCGGATGCCT	ACCTCAAGGG	TGTTCCGGTA	GAAGATACCC	GTACACTGAT	GAACGGACTC	1320
TTGCATGCTA	CGAAAGCCGT	CCATCCGAAA	ATCTCCTCCA	CGGGTCGCAA	AGGTTGGGAG	1380
TGGTACAACT	CCTTAGGTTA	TGTTCCGGCT	GATGCAGGCA	TCGACGAAAG	TGCTGCCCGT	1440
ACGCTCGAAT	ATGCTTATAA	CGATTGGTGC	ATCCTCCGAC	TGGGGCGCAC	ATTGGGTGG	1500
GATAGAGCTG	CATTGGACAC	GTGGTCCAT	CGTTCGATGA	ACTATCGTCA	TCTGTTTCGAT	1560
CCGGAAACCA	AACCTCATGCG	CGGTAGAAAT	CAGGATGGTA	GTTTCCGGAC	ACCTTTTTC	1620
CCTTTCAAAT	GGGGAGATGT	ATTCACGGAG	GGCAATGCCT	GGCACTACAC	TTGGTCGGTC	1680
TTTCATGATG	TGCAGGGGCT	TATCGACCTG	ATGGGAGGAG	ATCGCCCGTT	CGTGTCTATG	1740
CTCGATTCCG	TATTCAATAC	TCCTCCTATG	TTCGATGAGA	GCTATTACGG	ATTTGTCATC	1800
CACGAAATCA	GAGAGATGCA	AATAGCGGAT	ATGGGCAATT	ATGCTCATGG	CAATCAACCC	1860
ATACAGCATA	TGATATATCT	GTATAATCAT	GCCGGTCATC	CATGGAAGC	TCAGGAGAGA	1920
CTACGCGAAG	TGATGGGGCG	GCTCTATCGT	CCTACTCCGG	ATGGGTATTG	CGGCGATGAA	1980
GACAACGGAC	AGACTTCGGC	TGGTACGTT	TTCTCTGCTT	TAGGCTTCTA	TCCTGTTACA	2040
CCCCTACGG	ATCAGTATGT	GCTCGGTTCT	CCGATTTTTT	CCAAGGTAAT	ACTCTCTTTT	2100
CCCGACGGAC	ACAAAACGGT	GTGTCATGCT	CCGGCCAACA	GTGCCGATAC	GCCTTACATC	2160
CGCTCGATCA	GCGTAGAAGG	AAAAGAATGG	AGCTGCAATT	ACCTGACTCA	CGAACAGCTT	2220
CGCTCTTCTG	CATCCATTCA	ATGGATGATG	GACACGAAAC	CCAATTATAA	TCGTGGGTATG	2280
AAGGAAAGTG	ACAGACCTTA	TTCCTTCTCC	ACGGAGCAAC	AGCGTCGCGC	TAATCACAGT	2340
AAT						2343

(2) INFORMATION FOR SEQ ID NO:247

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

ATGATGAAAT	CCATGCGCAG	CGTGCTGTG	CTACTCTTTC	CATTGTCTTT	GATCACTGCT	60
TTGGGCTGTA	GCAATAACAA	AGTGCCGAA	TCGAAGTCTG	TCTCTTTCGA	TTCGGCCTAT	120
CTCGAACGCT	ACATCCCTCT	GCGGGCAGAC	ATAGATACGC	CATCGCTGCA	TGTGATGATC	180
AGCTACGTCT	ATCCTTCGGG	AGATGATATG	CTCACAGAGA	TTTCAACGG	TTTGCTCTTC	240
GGCGACAGCC	TGATGGATTG	CTCTTCGGCG	GAGAATGCCA	TGGAAGGCTA	TGCACAGATG	300
CTGGGAGAAG	ACTATCGCTC	TAACAATGCC	GAAGCCAATC	TGCAAGGGCT	TCCTTCTGAC	360
CTTTTGGAAT	ATATCTACAA	GCAGGAAAAT	ACCATCGCTT	ATTGCGATAC	GGGATTGATC	420
TCCACGCGCA	TCAATACATA	TACTTACGAA	GGCGGTGCAC	ATACGGAGAA	TACAGTCCGG	480
TTTGCCAAACA	TCCTTCGCAC	CACCGGCAAG	GTGCTCGAAG	AGCGAGATAT	ATTCAAGATC	540
GACTATGCGG	AAAGGCTGTC	CGCACTCATC	ATAGGACAAT	TGGTGACGTA	TTTCGGCAAG	600
ACCACACCTG	CCGAATTGGA	TGCAATAGGT	TTCTTCAACG	CAGAAGAAAT	ACAGCCCAAT	660
GGCAATTTTA	TGATCGATGA	CAAAGGTCTC	ACATACTGTT	TCAATGAGTA	TCAGATAGCT	720
GCCTATGCCA	GAGGTGCTGT	CTATGTCCTG	CTCGGATATG	ACGTATTGGC	TCCTTTGCTA	780
AGGGATGATT	CCCCACTAAA	GCGTTACTTG	CCG			813

(2) INFORMATION FOR SEQ ID NO:248

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 810 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

ATGAAATCCA	TGCGCAGCGT	GCTGTTGCTA	CTCTTTCCAT	TGTCTTTGAT	CACTGCTTTG	60
GGCTGTAGCA	ATAACAAAGC	TGCCGAATCG	AAGTCTGTCT	CTTTCGATTC	GGCCTATCTC	120
GAACGCTACA	TCCCTCTGCG	GGCAGACATA	GATACGCCAT	CGCTGCATGT	GATGATCAGC	180
TACGTCTATC	CTTCGGGAGA	TGATATGCTC	ACAGAGATTT	TCAACGGTTT	GCTCTTCGGC	240
GACAGCCTGA	TGGATTCTCT	TTCGCCGGAG	AATGCCATGG	AAGGCTATGC	ACAGATGCTG	300
GGAGAAGACT	ATCGCTCTAA	CAATGCCGAA	GCCAATCTGC	AAGGGCTTCC	TTCTGACCTT	360
TTGGACTATA	TCTACAAGCA	GGAAAATACC	ATCGCTTATT	GCGATACGGG	ATTGATCTCC	420
ACGCGCATCA	ATACATATAC	TTACGAAGGC	GGTGACACATA	CGGAGAATAC	AGTCCGTTT	480
GCCAACATCC	TTCGCACCAC	CGGCAAGGTG	CTCGAAGAGC	GAGATATATT	CAAGATCGAC	540
TATGCGGAAA	GGCTGTCCCG	ACTCATCATA	GGACAATTGG	TGCACGATTT	CGGCAAGACC	600
ACACCTGCCG	AATTGGATGC	AATAGGTTTC	TTCAACGCAG	AAGAAATACA	GCCCAATGGC	660
AATTTTATGA	TCGATGACAA	AGGTCTCACA	TACTGTTTCA	ATGAGTATCA	GATAGCTGCT	720
TATGCCAGAG	GTGCTGTCTA	TGTCCGCTCT	GGATATGACG	TATTGGCTCC	TTTGCTAAGG	780
GATGATTCCC	CACTAAAGCG	TTACTTGCCG				810

(2) INFORMATION FOR SEQ ID NO:249

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

ATGCGCAGCG	TGCTGTTGCT	ACTCTTTCCA	TTGTCTTTGA	TCACTGCTTT	GGGCTGTAGC	60
AATAACAAAG	CTGCCGAATC	GAAGTCTGTC	TCTTTCGATT	CGGCCTATCT	CGAACGCTAC	120
ATCCCTCTGC	GGGCAGACAT	AGATACGCCA	TCGCTGCATG	TGATGATCAG	CTACGTCTAT	180
CCTTCGGGAG	ATGATATGCT	CACAGAGATT	TTCAACGGTT	TGCTCTTCGG	CGACAGCCTG	240
ATGGATTCTT	CTTCGCCGGA	GAATGCCATG	GAAGGCTATG	CACAGATGCT	GGGAGAAGAC	300
TATCGCTCTA	ACAATGCCGA	AGCCAATCTG	CAAGGGCTTC	CTTCTGACCT	TTTGGACTAT	360
ATCTACAAGC	AGGAAAATAC	CATCGCTTAT	TGCGATACGG	GATTGATCTC	CACGCGCATC	420
AATACATATA	CTTACGAAGG	CGGTGCACAT	ACGGAGAATA	CAGTCCGGTT	TGCCAACATC	480
CTTCGCACCA	CCGGCAAGGT	GCTCGAAGAG	CGAGATATAT	TCAAGATCGA	CTATGCGGAA	540
AGGCTGTCCG	CACTCATCAT	AGGACAATTG	GTGCACGATT	TCGGCAAGAC	CACACCTGCC	600
GAATTGGATG	CAATAGGTTT	CTTCAACGCA	GAAGAAATAC	AGCCCAATGG	CAATTTTATG	660
ATCGATGACA	AAGGTCTCAC	ATACTGTTTC	AATGAGTATC	AGATAGCTGC	TTATGCCAGA	720
GGTGCTGTCT	ATGTCCGTCT	CGGATATGAC	GTATTGGCTC	CTTTGCTAAG	GGATGATTCC	780
CCACTAAAGC	GTTACTTGCC	G				801

(2) INFORMATION FOR SEQ ID NO:250

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

ATGAAAAAAA	CTACTTTGAC	AGGATCGATA	TGTGCTTTAC	TCCTGTTTTT	GGGTCTCTCG	60
GCCAATGCCC	AATCGAAGTT	AAAGATCAAG	AGCATTGAGG	CAGCTACCAC	TTTCAGTTCG	120
GCCACGGCCG	GAAATGGTTT	TGGTGGCAAT	ATCTTCGGCA	TGGACATGAG	CATACGGATG	180
AGGGTACACC	ACAGCATCT	GCCCGAAGGG	TTGGATTTTT	CGGTAGGAAT	ACATGAAAGA	240
AGAGCACACT	GGGAAGAGGC	CGGAAGTCCG	AAGCTCATGT	ATACGAATGT	CCCAAGTATC	300
ATTGGTATTG	TTGAAAAGGT	AATAGTCTTC	GAAGACGCAG	AAGACTTTTT	TGACAAAAAA	360
GCTCTCGGCC	GCTTCTCAT	CAGTTTGGGG	ATATCCTATA	CCAAGCATCT	GGGAGCGTAT	420
TGGGGATGGA	CCAATGACGC	CCATATTCTT	TTCTCACCGA	TACCCAAGAG	CAAGGTCCAC	480
TATGACACCT	ACACAAGAGC	TGGCAGTGAC	CTTGACTTTC	AGTCCGAAGA	TGTTGCCACA	540
GTGAGCAATG	GCTTTTTCACC	GGGGATCGGA	CTCAAAAGTT	CTATTTGGTG	GAAAATGCCC	600
ATCAAGAGCA	AATATGATTT	TCGCCTCGGT	TTCAGCCTGG	GCTATGAGTA	TCTGAACCTG	660
CTATATCCGT	ATCGTAATTT	CAAGCTGGAT	GGAAATAAGC	CGCTTTCAGC	ACTATCTCCT	720
CGCATGAACC	ACATCGGCCA	TGTGGGCTTC	AACCTTACC	TGGGCTTTTG	GACTAAT	777

(2) INFORMATION FOR SEQ ID NO:251

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...3798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

ATGGGCAAGT	ATAAAAGAGC	TAAGTACCGC	TATTGGCTTT	TTCTTTCTG	TTCGGATTAT	60
TATACCTTTG	AGGGAGTTAC	TTTTTTATGC	GCATCTGACG	ATATGACAAC	CAAGAAACCC	120
CAAGCCATTT	TAGACTTAGA	GAAGGCCTAT	AACATTGAAA	TTCTGATCT	CTCCTCACAA	180
GAAGGGATAA	GCTGGTCGGT	AAATAGATAT	TTCAAGCAAG	ATTCTCCGG	TGCAGTCGTT	240
GAGCTTTGCT	TGCGAGAATG	TCAGATAGAA	AGCATGACTT	GGCTTATTGA	TTTTCTGCT	300
CTAAAAAAGC	TTGATCTATC	GTATAACCAA	ATCAGTAAGC	TAGAGGGTCT	AGAACGTCTT	360
ACTTCGTAA	CAAACTTCG	TCTAAGAAGT	AACCAAATCC	GTAAACTAGA	GGGCCTGGAT	420
AGTCTCACCT	CGCTAACAAA	ACTTTCTCTC	TCCGATAACC	AAATCAGTAA	GCTAGAGGGT	480
CTGGAACGTC	TCACCTCGTT	AGCGGAGCTT	TATCTTTTGG	ATAACCAAAT	CAGTAAACTA	540
GAGGGTCTGG	AACGTCTCAC	GTCTTAGCA	ACGCTTGAAC	TATCGGGTAA	CCAAATCCGT	600
AAGCTGGAGG	GTCTGGAACG	TCTCACGTCC	TTAGCAACGC	TTGAACTATC	GGGTAACCAA	660
ATCCGTAAAGC	TAGAGGGTCT	GGAAACGTCT	ACTTCGTTAA	CAAAGCTTCG	TCTAAGAAGT	720
AACCAAATCA	GTAAGCTAGA	GGGCTGGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACTA	780
TCGGGTAAAC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TCACGTCCTT	AGCAACGCTT	840
GAAGTGTCCG	GTAACCAAAT	CAGTAAGCTA	GAGGGTCTGG	AACGTCTCTC	TTCTGTTAACA	900
AAGCTTCGTC	TAAGAAGTAA	CCAGATCAGT	AAACTAGAGG	GCCTGGAACG	TCTCACCTCG	960
CTAACAAAAC	TTTCTCTCTC	CGATAACCAA	ATCAGTAAGC	TAGAGGGTCT	GGAACGTCTC	1020
ACCTCGTTAG	CGGAGCTTTA	TCTTTTGGAT	AACCAAATCC	GTAAGCTGGA	GGGCCTGGAA	1080
CGTCTCACCT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AAATCAGTAA	ACTAGAGGGC	1140
CTGGATAGTC	TACCTCGCT	AACAAAACCT	TCTCTCTCCG	ATAACCAAAT	CAGTAAACTA	1200
GAGGGCCTGG	AACGTCTCAC	GTCTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	1260
AAGCTGGAGG	GTCTTGATGG	TCTTGCTTCC	TTAACAAGGC	TTAGTCTAAG	GCACAACCAA	1320
ATCAGTAAGC	TGGAAGGACT	AGACAGACTA	AAGGTTTTGA	GAAAACCTGA	TGTTTCGGGC	1380
AATGATATT	GAATGATTGA	TGATATTAAG	CTATTGGCTC	CGATTCTGGA	GCAAACTTTA	1440
GAAAACTGA	GAATCCATGA	CAATCCATTT	GTTGCATCAT	CAGGCTTGAT	ACTCTCTCCT	1500

TATGATAATC	ATTGCCC	GGA	GATTAAAGCT	CTTCTTGAAA	AAGAAAAAGA	AAAACAGAAA	1560
AAGACTTCAG	TTGAATATCA	CCCATTTTGC	AAAGTAATGC	TATTGGGAAA	TCATTCTTCG		1620
GGTAAAAACAA	CATTTCTTAG	TCAATACGAT	ACAAATTATA	CGTATCAGAA	AAATACACAT		1680
GTGTTGTCTGA	TACATCGAAG	CAATAACCCCT	AATGCGATCT	TTTACGACTT	TGGGGGACAG		1740
GACTATTATC	ATGGGATTTA	CCAAGCCCTT	TTTACCACCC	AATCGTTATA	CCTTCTCTTT		1800
TGGGATGCTA	AGAAGGATCG	AAACTTTGTG	AGCGTAGATG	ATAAAGAATA	TCAGACTCTT		1860
AATTTCAATC	GCCCTTATTG	GTAGGACAG	ATAGCCTATG	CCTGCAATCG	TTGTATGTCC		1920
GTTGGAGGAA	ATCCTGATGG	CAAGGACACA	CCACAGACCA	CAGACGATAC	AATTATCATT		1980
CAGACTCATG	CCGATGAAAC	GGGCGCTAAG	CAGCAAACCT	TAGGCTGTGC	AGCCGAGAAT		2040
GGAGTATTGG	AAGAAATCTA	TGTATCCTTA	GAGCCCAAGG	CGAATAGTGC	CGTACATGCG		2100
CTCAACTATC	TGAATGAGCG	GGTGCAGAA	GTTGTCGCAA	GCAGGAGTAA	ATCAATTCAG		2160
ATCACAGAAA	AAGATAAGGG	ATTGTACGAA	GCTCTTCCCA	CAATCGCCGG	TGATAATAAA		2220
CACATCCCTA	TCTCTCTCGA	AGTCTTTGCG	GCTCAATTGA	ATAAGGGAAG	AGCTGAAAAAT		2280
GATCTTTTACA	CCATAGAGTA	TCTACAGACC	GAATTGAACC	AGCTTAGTCT	GCGAGGGGAG		2340
GTGCTTTACT	ATCGTGAGAA	TGAGAAGCTG	AACAATTATG	TCTGGTTAGA	TCCGGCAGCT		2400
TTTGTCCAAA	TGATTCATGG	AGAAATCCTC	CAAAAAGACA	ACATCAATAG	AGGAACAGTT		2460
CCTAAAGACA	TTTTTGAATG	CAAACGTCAT	AATCTAAGTT	CCGGAAGTAT	ATTTGAAGAA		2520
GATGGCCAAA	ATGGTAATAT	GATCTTGACG	CTATTATTGG	AAGAGCTGAT	CGTATATGAA		2580
GATAAGGACT	GCTATGTGAT	ACCGGGCTAT	CTCCCTTTGC	ATTCGGATGA	CGAAGCCTAT		2640
AAATGGCTTA	CTTTGGGATT	CGAGAGGCC	AATTTTGTCC	TCAAATTCGA	ACGTTTTATC		2700
CCCTTTGGCC	TGATCAACCA	GATTATAGCC	TACTATGGCC	GGGAAGAAGG	TGCTCTAAAG		2760
CGGTATTGGC	GAGATCAGGT	CATCTTCACA	GCAGGCCGTG	AGATGGATAG	GCAAACGCTT		2820
GAGCAAGAAG	AAGAGAAAG	GGGTTTGCCC	AAGACGAATG	CCGAGGATTA	TCAGATCTGG		2880
ATCAAGCTCG	ACTTTACCGA	CTTGGCCATA	TCCGTATTCA	TCAAAGAGCA	GAGAAAGACA		2940
TCAGCTAAGG	ATATGCAGCG	GAAAGAGGCT	ACTATCCTCA	GTGATATGTT	GGATATGTAT		3000
TGGAACAATA	TCCTCCGAG	GGAGCAAATA	GGAGATAAGG	ATACGGAGCA	AACGAGAAGC		3060
ACTATTCGTG	AAACAAACAG	AAAGAAGAGA	CCCATCCAGG	ATCTCTACCT	CTCCTGTGCC		3120
CAAGCGGATA	AAGATTTGAC	GGAGTCTCAT	TATATCCATT	TGGGCACGCT	GGACGATGAA		3180
AGCAAGACTA	CGGCGAGGAT	TGCAGCCTAT	CCGTTGAAGA	ACGGCGTTAT	CGATAAAGAG		3240
CGGGTGCGAG	AAGTATCGAC	TCGTCCCTAC	AAACATCTTT	CCGTCAATAA	AAATCTGGCT		3300
ACTGCAAAAC	AGATCTTTAT	TTCTTATTCC	AAAGAGGATC	AGACTGAACT	GGAGACCTGT		3360
CTGCAATTTT	TCAAACCCCT	GGAGAAGAAT	GGTCAGATCG	AGATCTACTA	TGATAAGTTG		3420
ACTAAGTTTG	AAACACCTAT	TCACCCTGAA	ATAAGAAAGC	GTATTGTCTGA	AGCCGACTGT		3480
ATAATCGCTT	TGATCAGCCA	ACGCTATCTG	GCCACGGATT	ACATCCTGGA	TCATGAGTTG		3540
CCTGTATTTC	GGGAGTATA	CAAGACCATA	GTGCCGATAT	TGATCAAGCC	TTGTACATTC		3600
GAAGACGATG	AGTTCTTTCG	GGAGAAATAT	TTTGCTCAGA	AAGCTCAAAT	AATCAATCTT		3660
GGAAAAGAGG	GAAAAACCAT	TAAAGCTTAT	GATAGTATTA	CGGCATCAGC	CCATCGTGAT		3720
GAAATTTGGG	TGGCAGTAGT	CAGAGAGTTC	AAAGAGAAGA	TATTAAGAAT	AACAAAACAG		3780
GAGGTAAATA	CAGATGAA						3798

(2) INFORMATION FOR SEQ ID NO:252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

ATGACAACCA	AGAAACCCCA	AGCCATTTTA	GACTTAGAGA	AGGCCTATAA	CATTGAAATT	60
CCTGATCTCT	CCTCACAAAG	AGGGATAAGC	TGGTCGGTAA	ATAGATATTT	CAAGCAAGAT	120
TCCTCCGGTG	CAGTCGTTGA	GCTTTGCTTG	CGAGAATGTC	AGATAGAAAG	CATGACTTGG	180
CTTATTGATT	TTCTTGCTCT	AAAAAAGCTT	GATCTATCGT	ATAACCAAAT	CAGTAAGCTA	240
GAGGGTCTAG	AACGTCTTAC	TTCGTTAACA	AACTTCGTC	TAAGAAGTAA	CCAAATCCGT	300
AAACTAGAGG	GCTTGGATAG	TCTCACCTCG	CTAACAAAC	TTTCTCTCTC	CGATAACCAA	360
ATCAGTAAGC	TAGAGGGTCT	GGAACGTCTC	ACCTCGTTAG	CGGAGCTTTA	TCTTTGGAT	420
AACCAAATCA	GTAAACTAGA	GGGTCTGGAA	CGTCTCACGT	CCTTAGCAAC	GCTTGAACCTA	480
TCGGGTAAAC	AAATCCGTAA	GCTGGAGGGT	CTGGAACGTC	TCACGTCCTT	AGCAACGCTT	540
GAACTATCGG	GTAAACCAAT	CCGTAAGCTA	GAGGGTCTGG	AACGTCTCAC	TTCGTTAACA	600
AAGCTTCGTC	TAAGAAGTAA	CCAAATCAGT	AAGCTAGAGG	GTCTGGAACG	TCTCACGTCC	660
TTAGCAACGC	TTGAACTATC	GGGTAACCAA	ATCCGTAAGC	TGGAGGGTCT	GGAACGTCTC	720
ACGTCCTTAG	CAACGCTTGA	ACTGTCGGGT	AACCAAATCA	GTAAGCTAGA	GGGTCTGGAA	780

CGTCTCTCTT	CGTTAACAAA	GCTTCGTCTA	AGAAGTAACC	AGATCAGTAA	ACTAGAGGGC	840
CTGGAACGTC	TCACCTCGCT	AACAAAACCT	TCTCTCTCCG	ATAACCAAAT	CAGTAAGCTA	900
GAGGGTCTGG	AACGTCTCAC	CTCGTTAGCG	GAGCTTTATC	TTTTGGATAA	CCAAATCCGT	960
AAGCTGGAGG	GCCTGGAAAG	TCTCACCTCG	TTAACAAAGC	TTCGTCTAAG	AAGTAACCAA	1020
ATCAGTAAAC	TAGAGGGCCT	GGATAGTCTC	ACCTCGCTAA	CAAAACTTTC	TCTCTCCGAT	1080
AACCAATCA	GTAAACTAGA	GGGCGCTGAA	CGTCTCACGT	CCTTAGCGGA	GCTTTATCTT	1140
TTGGATAACC	AAATCCGTAA	GCTGGAGGGT	CTTGATGGTC	TTGCTTCCTT	AACAAGGCTT	1200
AGTCTAAGGC	GCAACCAAAT	CAGTAAGCTG	GAAGGACTAG	ACAGACTAAA	GGTTTTGAGA	1260
AAACTTGATG	TTTCGGGCAA	TGATATTCAA	TCTATTGATG	ATATTAAAGCT	ATTGGCTCCG	1320
ATTCTGGAGC	AAACTTTAGA	AAAACCTGAGA	ATCCATGACA	ATCCATTGTG	TGCATCATCA	1380
GGCTTGATAC	TCTCTCCTTA	TGATAATCAT	TTGCCGGAGA	TTAAAGCTCT	TCTTGAAAAA	1440
GAAAAAGAAA	AACAGAAAAA	GACTTCAGTT	GAATATCACC	CATTTTGCAA	AGTAATGCTA	1500
TTGGGAAATC	ATTCTTCGGG	TAAACAACA	TTTCTTAGTC	AATACGATAC	AAATTATACG	1560
TATCAGAAAA	ATACACATGT	GTTGTGCGATA	CATCGAAGCA	ATAACCCATA	TGCGATCTTT	1620
TACGACTTTG	GGGGACAGGA	CTATTATCAT	GGGATTACC	AAGCCTTTT	TACCACCAA	1680
TCGTTATACC	TTCTCTTTTG	GGATGCTAAG	AAGGATCGAA	ACTTTGTGAG	CGTAGATGAT	1740
AAAGAATATC	AGACTCTTAA	TTTCAATCGC	CCCTATTGGT	TAGGACAGAT	AGCCTATGCC	1800
TGCAATCGTT	GTATGTCCTG	TGGAGGAAAT	CCTGATGGCA	AGGACACACC	ACAGACCACA	1860
GACGATACAA	TTATCATTC	GACTCATGCC	GATGAAACGG	GCGCTAAGCA	GCAAACCTTA	1920
GGCTGTGCAG	CCGAGAAATG	AGTATTGGAA	GAAATCTATG	TATCCTTAGA	GCCCAAGGCG	1980
AATAGTGCCG	TACATGCGCT	CAACTATCTG	AATGAGCGGG	TGCGAGAAGT	TGTCGCAAGC	2040
AGGAGTAAAT	CAATTAGAT	CACAGAAAAA	GATAAGGGAT	TGTACGAAGC	TCTTCCCACA	2100
ATCGCCGGTG	ATAATAAACA	CATCCCTATC	TCTCTCGAAG	CTCTTGCGGC	TCAATTGAAT	2160
AAGGGAAGAG	CTGAAAATGA	TCTTTACACC	ATAGAGTATC	TACAGACCGA	ATTGAACCAG	2220
CTTAGTCTGC	GAGGGGAGGT	GCTTTACTAT	CGTGAGAATG	AGAAGCTGAA	CAATTATGTC	2280
TGGTTAGATC	CGGCAGCTTT	TGTCCAAATG	ATTTCATGGAG	AAATCCTCCA	AAAAGACAAC	2340
ATCAATAGAG	GAACAGTTCC	TAAAGACATT	TTGAATGCA	AACTGCATAA	TCTAAGTTCC	2400
GGAGATATAT	TTGAAGAAGA	TGGCCAAAAT	GGTAATATGA	TCTTGCAGCT	ATTATTGGAA	2460
GAGCTGATCG	TATATGAAGA	TAAGGACTGC	TATGTGATAC	CGGGCTATCT	CCCTTTGCAT	2520
TCCGATGACG	AAGCCTATAA	ATGGCTTACT	TTGGGATTTCG	AGAGGCCCAA	TTTTGTCTCT	2580
AAATTCGAAC	GTTTTATCCC	CTTTGGCCTG	ATCAACCAGA	TTATAGCCTA	CTATGGCCGG	2640
GAAGAAGGTG	CTCTAAGCG	GTATTGGCGA	GATCAGGTCA	TCTTCACAGC	AGGCCGTGAG	2700
ATGGATAGGC	AAACGCTTGA	GCAAGAAGAA	GAGAAAGAGG	GTTTGCCCAA	GACGAATGCC	2760
GAGGATTATC	AGATCTGGAT	CAAGCTCGAC	TTTACCGACT	TGGCCATATC	CGTATTCATC	2820
AAAGAGCAGA	GAAAGACATC	AGCTAAGGAT	ATGCAGCGGA	AAGAGGCTAC	TATCCTCAGT	2880
GATATGTTGG	ATATGTATTG	GAACAATATC	CCTCCGAGGG	AGCAAATAGG	AGATAAGGAT	2940
ACGGAGCAAA	CGAGAAGCAC	TATTTCGTGAA	ACAAACAGAA	AGAAGAGACC	CATCCAGGAT	3000
CTCTACCTCT	CCTGTGCCCA	AGCGGATAAA	GATTTGACGG	AGTCTCATTA	TATCCATTTG	3060
GGCACGCTGG	ACGATGAAAG	CAAGACTACG	GCGAGGATTG	CAGCCTATCC	GTGAAGAAC	3120
GGCGTTATCG	ATAAAGAGCG	GGTGCAGAA	GTATCGACTC	GTCCCTACAA	ACATCTTTCC	3180
GTCAATAAAA	ATCTGGCTAC	TGCAAAACAG	ATCTTTATTT	CCTATTCCAA	AGAGGATCAG	3240
ACTGAACCTG	AGACCTGTCT	GCAATTTTTC	AAACCTTGG	AGAAGAATGG	TCAGATCGAG	3300
ATCTACTATG	ATAAGTTGAC	TAAGTTTGAA	ACACCTATTC	ACCCTGAAAT	AAGAAAGCGT	3360
ATTGTGGAAG	CCGACTGTAT	AATCGCTTTG	ATCAGCCAAC	GCTATCTGGC	CACGGATTAC	3420
ATCCTGGATC	ATGAGTTGCC	TGTATTTCCG	GAGTATAACA	AGACCATAGT	GCCGATATTG	3480
ATCAAGCCTT	GTACATTCGA	AGACGATGAG	TTCTTTCGGG	AGAAATATTT	TGCTCAGAAA	3540
GCTCAAATAA	TCAATCTTGG	AAAAGAGGGA	AAAACCATTA	AAGCTTATGA	TAGTATTACG	3600
GCATCAGCCC	ATCGTGATGA	AAATTGGGTG	GCAGTAGTCA	GAGAGTTCAA	AGAGAAGATA	3660
TTAAGAATAA	CAAAACAGGA	GGTAAATACA	GATGAA			3696

(2) INFORMATION FOR SEQ ID NO:253

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...3525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

ATGACTTGGC	TTATTGATTT	TCCTGCTCTA	AAAAGCTTG	ATCTATCGTA	TAACCAAATC	60
AGTAAGCTAG	AGGGTCTAGA	ACGTCTTACT	TCGTAAACAA	AACTTCGTCT	AAGAAAGTAA	120
CAAATCCGTA	AACTAGAGGG	CCTGGATAGT	CTCACCTCGC	TAACAAAAC	TTCTCTCTCC	180

GATAACCAAA	TCAGTAAGCT	AGAGGGTCTG	GAACGTCTCA	CCTCGTTAGC	GGAGCTTTAT	240
CTTTTGGATA	ACCAAATCAG	TAAACTAGAG	GGTCTGGAAC	GTCTCACGTC	CTTAGCAACG	300
CTTGAACATAT	CGGTAACCA	AATCCGTAAG	CTGGAGGGTC	TGGAACGCTC	CACGTCCTTA	360
GCAACGCTTG	AACTATCGGG	TAACCAAAATC	CGTAAGCTAG	AGGGTCTGGA	ACGTCCTCACT	420
TCGTTAACAA	AGCTTCGTCT	AAGAAGTAAC	CAAATCAGTA	AGCTAGAGGG	TCTGGAACGT	480
CTCACGTCCT	TAGCAACGCT	TGAACATATCG	GGTAACCAAA	TCCGTAAGCT	GGAGGGTCTG	540
GAACGTCTCA	CGTCCTTAGC	AACGCTTGAA	CTGTGCGGTA	ACCAAATCAG	TAAGCTAGAG	600
GGTCTGGAAC	GTCTCTCTTC	GTTAACAAAG	CTTCGTCTAA	GAAGTAACCA	GATCAGTAAA	660
CTAGAGGGCC	TGGAACGTCT	CACCTCGCTA	ACAAAACCTTT	CTCTCTCCGA	TAACCAAATC	720
AGTAAGCTAG	AGGGTCTGGA	ACGTCCTCACC	TCGTTAGCGG	AGCTTTATCT	TTTGGATAAC	780
CAAAATCCGTA	AGCTGGAGGG	CCTGGAACGT	CTCACCTCGT	TAACAAAGCT	TCGTCTAAGA	840
AGTAACCAAA	TCAGTAAACT	AGAGGGCCTG	GATAGTCTCA	CCTCGCTAAC	AAAACCTTTCT	900
CTCTCCGATA	ACCAAATCAG	TAAACTAGAG	GGCCTGGAAC	GTCTCACGTC	CTTAGCGGAG	960
CTTTATCTTT	TGGATAACCA	AATCCGTAAG	CTGGAGGGTC	TTGATGGTCT	TGCTTCCTTA	1020
ACAAGGCTTA	GTCTAAGCGG	CAACCAAATC	AGTAAGCTGG	AAGGACTAGA	CAGACTAAAG	1080
GTTTTTGAGAA	AACTTGATGT	TTCGGGCAAT	GATATTCAAT	CTATTGATGA	TATTAAGCTA	1140
TTGGCTCCGA	TTCTGGAGCA	AACTTTAGAA	AAACTGAGAA	TCCATGACAA	TCCATTGTGT	1200
GCATCATCAG	GCTTGATACT	CTCTCCTTAT	GATAATCATT	TGCCGGAGAT	TAAAGCTCTT	1260
CTTGAAAAAG	AAAAAGAAAA	ACAGAAAAAG	ACTTCAGTTG	AATATCACCC	ATTTTGCAAA	1320
GTAATGCTAT	TGGGAAATCA	TTCTTCGGGT	AAAACAACAT	TTCTTAGTCA	ATACGATACA	1380
AATTATACGT	ATCAGAAAAA	TACACATGTG	TTGTCGATAC	ATCGAAGCAA	TAACCTAAT	1440
GCGATCTTTT	ACGACTTTGG	GGGACAGGAC	TATTATCATG	GGATTTACCA	AGCCTTTTTT	1500
ACCACCCAAT	CGTTATACCT	TCTCTTTTGG	GATGCTAAGA	AGGATCGAAA	CTTTGTGAGC	1560
GTAGATGATA	AAGAATATCA	GACTCTTAAT	TTCAATCGCC	CCTATTGGTT	AGGACAGATA	1620
GCCTATGCCT	GCAATCGTTG	TATGTCCGTT	GGAGGAAATC	CTGATGGCAA	GGACACACCA	1680
CAGACCACAG	ACGATACAAT	TATCATTCAG	ACTCATGCCG	ATGAAACGGG	CGCTAAGCAG	1740
CAAACTTAG	CTGTGTCAGC	CGAGAATGGA	GTATTGGAAG	AAATCTATGT	ATCCTTAGAG	1800
CCCAAGGCGA	ATAGTGCCTG	ACATGCGCTC	AACTATCTGA	ATGAGCGGGT	GCGAGAAGTT	1860
GTCGCAAGCA	GGAGTAAATC	AATTCAGATC	ACAGAAAAAG	ATAAGGGATT	GTACGAAGCT	1920
CTTCCACAA	TCGCCGGTGA	TAATAAACAC	ATCCCTATCT	CTCTCGAAGC	TCTTGCGGCT	1980
CAATTGAATA	AGGGAAGAGC	TGAAAATGAT	CTTTACACCA	TAGAGTATCT	ACAGACCGAA	2040
TTGAACAGC	TTAGTCTGCG	AGGGAGGTTG	CTTTACTATC	GTGAGAATGA	GAAGCTGAAC	2100
AATTATGTCT	GGTTAGATCC	GGCAGCTTTT	GTCCAAATGA	TTCATGGAGA	AATCCTCCAA	2160
AAAGACAACA	TCAATAGAGG	AACAGTTTCT	AAAGACATTT	TTGAATGCAA	ACTGCATAAT	2220
CTAAGTTCCG	GAAGTATATT	TGAAGAAGAT	GGCCAAAATG	GTAATATGAT	CTTGCAGCTA	2280
TTATTGGAAG	AGCTGATCGT	ATATGAAGAT	AAGGACTGCT	ATGTGATACC	GGGCTATCTC	2340
CCTTTGCATT	CCGATGACGA	AGCCTATAAA	TGGCTTACTT	TGGGATTCGA	GAGGCCCAAT	2400
TTTGTCTCTA	AATTCGAACG	TTTTATCCCC	TTTGGCCTGA	TCAACCAGAT	TATAGCCTAC	2460
TATGGCCGGG	AAGAAGGTGC	TCTAAAGCGG	TATTGGCGAG	ATCAGGTCAT	CTTCACAGCA	2520
GGCCGTGAGA	TGGATAGGCA	AACGCTTGAG	CAAGAAGAAG	AGAAAGAGGG	TTTGCCCAAG	2580
ACGAATGCCG	AGGATTATCA	GATCTGGATC	AAGCTCGACT	TTACCGACTT	GGCCATATCC	2640
GTATTATCAT	AAGAGCAGAG	AAAGACATCA	GCTAAGGATA	TGCAGCGGAA	AGAGGCTACT	2700
ATCCTCAGTG	ATATGTTGGA	TATGTATTGG	AACAATATCC	CTCCGAGGGA	GCAAAATAGGA	2760
GATAAGGATA	CGGAGCAAAAC	GAGAAGCACT	ATTCTGTGAA	CAAACAGAAA	GAAGAGACCC	2820
ATCCAGGATC	TCTACCTCTC	CTGTGCCCAA	GCGGATAAAG	ATTTGACGGA	GTCTCATTAT	2880
ATCCATTTGG	GCACGCTGGA	CGATGAAAGC	AAGACTACGG	CGAGGATTGC	AGCCTATCCG	2940
TTGAAGAACG	GCGTTATCGA	TAAAGAGCGG	GTGCGAGAAG	TATCGACTCG	TCCCTACAAA	3000
CATCTTTCCG	TCAATAAAAA	TCTGGCTACT	GCAAAACAGA	TCTTTATTTT	CTATTCCAAA	3060
GAGGATCAGA	CTGAACCTGGA	GACCTGTCTG	CAATTTTTC	AACCCTTGGA	GAAGAATGGT	3120
CAGATCGAGA	TCTACTATGA	TAAGTTGACT	AAGTTTGAAA	CACCTATTCA	CCCTGAAATA	3180
AGAAAGCGTA	TTGTCGAAGC	CGACTGTATA	ATCGCTTTGA	TCAGCCAACG	CTATCTGGCC	3240
ACGGATTACA	TCCTGGATCA	TGAGTTGCCT	GTATTTGCGG	AGTATAACAA	GACCATAGTG	3300
CCGATATTGA	TCAAGCCTTG	TACATTGCAA	GACGATGAGT	TCCTTCGGGA	GAAATATTTT	3360
GCTCAGAAAG	CTCAAATAAT	CAATCTTGGA	AAAGAGGGAA	AAACCATTAA	AGCTTATGAT	3420
AGTATTACGG	CATCAGCCCA	TCGTGATGAA	AATTGGGTGG	CAGTAGTCAG	AGAGTTCAAA	3480
GAGAAGATAT	TAAGAATAAC	AAAACAGGAG	GTAAATACAG	ATGAA		3525

(2) INFORMATION FOR SEQ ID NO:254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

```
ATGATGAAAA AAGCATTGTGTTTCGTACTA CTGGTTTGCC TATTCTCCTC GTTCAGCAGT      60
TCCGCCCAAA CAACGACGAA CAGTAGCCGG AGTTATTTTA CAGGACGAAT CGAGAAGGTG      120
AGTTTGAAC TAgGGGTCCC CCCCgTAAGC ACAGAGGTTT GGGGAATGAC CCATGATGCG      180
AACGGTCTCC CTTTCGAAAT ACCTATCTCT TTCAGTCGTT TCAACAGCCA GGGAGATATA      240
GTACCACCTT ATTACATAGC GAATAGCGAG GCAACTTTGA ATGAATGGTG CGACTATGCA      300
CACCCGGGCG GCATCGTGAG GGTAGAAGGT CGTTTTTGGA AAATGACTTA CAACATACCA      360
ACCTACAATG CAGTCTGCAC CCGGATTACA TTCGAAAATC AAGAAATAGA AGGAACGATC      420
GTCTTGATAC CCAAGCCCAA AGTCTCGCTG CCTCATGTGT CGGAATCGGT GCCTTGCAATC      480
CGAACCgAAG CCGGGAGGGA ATTTATCCTT TGCGAAGAAG ACGACACCTT TGTGTCTCAC      540
GATGGTAACG AAGTAACGAT AGGCGGTAAA CCTTTCTTGC TCAATACCAA CGTAAAGATT      600
GTGGGGGACG TATCTCAAAA GTATGCCGTG GGGGTAGGAG AAATTCGATT CCTGCAGATT      660
TGTGCCCAAA CAGTATCACA ACAAAAAA                                     687
```

(2) INFORMATION FOR SEQ ID NO:255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

```
ATGAAAAAAG CATTGTGTTT CGTACTACTG GTTGCCTAT TCTCCTCGTT CAGCAGTTCC      60
GCCCAAAACA CGACGAACAG TAGCCGGAGT TATTTTACAG GACGAATCGA GAAGGTGAGT      120
TTGAACCTAG GGGTCCCCCC CGTAAGCACA GAGGTTTGGG GAATGACCCA TGATGCGAAC      180
GGTCTCCCTT TCgAAATACC TATCTCTTTC AGTCGTTTCA ACAGCCAGGG AGATATAGCT      240
ACCACTTATT ACATAGCGAA TAGCGAGGCA ACTTTGAATG AATGGTGCGA CTATGCACAC      300
CCGGGCGGCA TCGTGAGGgT AGAAGGTCGT TTTTGAAAA TGACTTACAA CATACCAACC      360
TACAATGCAG TCTGCACCCG GATTACATTC GAAAATCAAG AAATAGAAGG AACGATCGTC      420
TTGATACCCA AGCCCAAAGT CTCGCTGCCT CATGTGTCGG AATCGGTGCC TTGCATCCGA      480
ACCGAAGCCG GGAGGGAATT TATCCTTTGC GAAGAAGACG ACACCTTTGT GTCTCACGAT      540
GGTAACGAAG TAACGATAGG CGGTAAACCT TTCTTGCTCA ATACCAACGT AAAGATTGTG      600
GGGGACGTAT CTCAAAAGTA TGCCGTGGGG GTAGGAGAAA TTCGATTCTT GCAGATTTGT      660
GCCCAAACAG TATCACAACA AAAA                                     684
```

(2) INFORMATION FOR SEQ ID NO:256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

ATGAAGACAA	AAGTTTTACG	CAAATTCGTG	GTGGCGGCTT	TCGCCGTCGC	AACCCCTCTGT	60
CCTCTCGCCC	AAGCGCAGAC	GATGGGAGGA	GATGATGTCA	AGGTGGTCCA	GTACAATCAG	120
GAAAAACTGG	TACAAACGAG	GATGAGTGTG	GCGGACAACG	GATGGATCTA	TGTAATGACC	180
CACAGTGGAT	ACGACACCGG	CAATAGCAAT	GTGAAGATCT	TCCGCTCCAA	AGACCAAGGT	240
GCCACATACC	AAAAGTTGAG	GGATTGGGAT	CCATCGGATG	ATTATCAGTT	TCAAGACTTC	300
GATATCGTGG	TAACGGGTAA	GAATGAATCC	GACATCAAGA	TTTGGTCGGT	AGAGCTCATG	360
AATAAGCCCG	GAGGATATAA	GAGTAGAGTT	GCGGTCTTCA	GTGCGCATGC	CAACGCGCAG	420
AATGCGAAAC	TCGTGTATAA	GGAAGACTTC	TCCAATGTGC	AGTTGTACGA	TGTGGATATA	480
GCGTCCAACT	ATCGTTCGCC	TTCTTCTCTT	AACAATGGTG	GCAACCCTTT	TGCTTTGGCT	540
TTGCTTACA	CCGGCTTCAA	CAATACGCAC	AAAATAAGTT	TTGTGGACTA	TGTGTTCTCT	600
CTGAATGGAG	GGCAAAATTT	CAATAAAAAC	TTACTCTTCA	GTCAAGATGG	AGAGAAGAAA	660
ATTGACAAGG	TGGATCTCTC	ATTGGGTAGC	ACCTCTGAAT	CCATGGGTCA	CAATGCCTGG	720
CCGCTAATGG	GTGTGGTATT	CGAAATGAAT	AAACAAGGGG	GAAAAAGCGA	TATCGGTTTC	780
TTGTGCAACT	TTGTCGACAA	TGATCCCGAA	TTTCAGTGGT	CAGGCCCTAT	AAAAGTGAGT	840
GAAAGCGACA	TGTCGTTTCA	CCCCAAAATC	CAAATGTTGC	TGGACGAGGA	TAACAATACG	900
ATCAATGGGG	AGAGTTGCCA	CAACTTCATG	ATTACGTACA	GCGATTATGA	TTCTGAATAT	960
TCGGATTGGG	ACATTGCGTA	TGTATATCCC	AAGAAATCGT	TCAAGTATGA	AAAAGGAAAA	1020
ACTCCGACTA	TGGATGATCT	GGTGGAAGCT	TTCTTACAG	CTTCGTACCA	GAGTGAGACC	1080
AATCGGGGCG	TGCGGTATAG	TGATAACGCC	AATCACTACC	TGATTACATA	TGCCAAAAAA	1140
GAAGAGAACG	GTACGAACAC	GCTGAAATAC	CGCTGGGCCA	ATTATGACAA	GATTCATAAC	1200
AAAGATTTGT	GGAGCGACAC	ATTACGTAT	ACATCATCTG	CCAATGCTCT	CTACACACCT	1260
CAAGTAGACA	TCAATCCGAC	CAAGGGTCTC	GTGTGCTGGT	CATGGGTGGA	ATATCTGCCG	1320
GGCAAAACGGA	TGGTTTGGTC	TGATACGCAG	TGGACCCATG	CCAACGGTGT	AGAAGACATC	1380
GTAATGCAAG	AAGGCAGCAT	GAAGCTCTAC	CCGAATCCGG	CTCAAGAATA	TGCTGTGATT	1440
AGCCTGCCGA	CGGCAGCAAA	CTGCAAGGCT	GTGTTTTACG	ATATGCAGGG	CAGAGTAGTC	1500
GCTGAGGCTT	CTTTCTCCGG	CAACGAATAC	AGGCTGAACG	TGCAGCACTT	GGCTAAGGGT	1560
ACGTACATAC	TCAAGGTCGT	ATCCGATACG	GAGCGTTTCG	TAGAGAAGCT	CATCGTGGAA	1620

(2) INFORMATION FOR SEQ ID NO:257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

ATGCTGACGA	TCCGAAACTT	CCTCCTCTTT	TGTTGTCTGT	CGCTGATAGC	GTTTGCTGCC	60
GATGCACAAA	GCTCTGTCTC	TTGCGGTAGA	CGACTGACAG	AATATGTCAA	TCCCTTTATC	120
GGAACGGCCA	ATTACGGTAC	CACGAATCCG	GGAGCAGTAT	TGCCCAATGG	GTTGATGAGC	180
GTTACCCCTT	TCAATGTCAG	CGGATCGACA	GAGAATCGCT	TCGACAAAGA	TTGCGGTTGG	240
TGGAGTGCGC	CTTATTGCGC	CGACAATAGT	TACTGCATCG	GTTTCAGCCA	TGTGAATCTG	300
AGTGGAGTAG	GCTGTCCCAG	ACTGAGTGGA	ATACTGCTGA	TGGCCACTTC	CGGCACATTC	360
GATCCTGATT	ACTGCTGCTA	TGGCTCTTCG	CTCAGTCGAG	AATATGCGCG	CCCGGGAGAA	420
TACAAGGCTG	TATTGGACAA	ATACGGTATA	GATGCAGCCG	TGACCGTAAC	CGAGCGGACT	480
GCTTTGACCG	AATTGCTTTT	TCCCGAAGGA	GAAGGCCATA	TCCTGCTGAA	CCTGGGACAG	540
GCCCTAAGCA	ATGAATCGGG	AGCCTCTGTT	CGATTCTTAA	ACGACTCCAC	AGTCGTCGGC	600
AGCAGGCTGA	TGGGGACGTT	CTGCTACAAT	CCGCAAGCAG	TTTTTCGTCA	GTATTTTCGTA	660
CTTCAGGTGA	GTCGGCGACC	GATCTCTGCC	GGCTATTGGA	AGAAGCAGCC	TCCTATGACA	720
GTGAAGCCCC	AATGGGATTC	GACTGCAGGG	AAATATAAGC	AGTACGACGG	CTACAAGCGT	780
GAGATGAGCG	GTGATGACAT	CGGTGTCCGA	TTCTCGTTCA	ACTGCGATCA	GGGGGAAAAG	840
ATCTATGTAC	GATCGGCCGT	TTCATTTCGT	AGCGAAGCCA	ATGCGCTCTA	TAATCTGGAA	900
GCGGAGCAAG	AAGAGGTGTT	CAAAAGTGTC	GGAGGGAATC	CGGCCAAGGC	TTTCTCCGCT	960
ATACGCTCTC	GCGCTATAGA	GCGTTGGGAG	GAAGCCCTCG	GTACGGTGGA	AGTGAAGGA	1020
GGCACACCGG	ATGAAAAGAC	GATATTCTAT	ACCGCACTCT	ATCACCTGCT	GATACATCCG	1080
AATATCCTAC	AAGATGCCAA	TGGAGAATAT	CCTATGATGG	GCAGTGCCAA	AACGGGTAAT	1140
ACGGCTCACG	ACCGCTACAC	CGTGTCTCTC	CTTTGGGACA	CGTACCGCAA	TGTACACCCG	1200
CTGCTCTGCC	TCCTCTATCC	GGAGAAGCAG	TTGGATATGG	TACGGACACT	GATCGACATG	1260
TACCGAGAGA	CGGGGTGGCT	GCCGAGATGG	GAGCTGTACG	GACAGGAGAC	CCTGACGATG	1320
GAGGGCGACC	CCTCGCTTAT	GCTCATCAAT	GACACTTGCG	AAAGGGGCCT	TCGTGCTTTC	1380
GATACGGCAA	CGGCCTATGA	AGCCATGAAA	AAAAATGCTT	CTTCGGCAGG	AGCGACCCAT	1440

CCGATCCGTC	CTGACAACGA	CGACTATCTC	ACCCTCGGCT	TGCTACCGCT	TCGCGAACAG	1500
TACGACAATT	CCGTATCGCA	TGCGCTGGAA	TACTATCTGG	CCGACTGGAA	TCTGTCCCGG	1560
TTTGCCACG	CACCTTGGGA	TAAAGAAGAC	GCAGCTCTAT	TCGGAAAACG	CTCGTTGGGC	1620
TACAGACACT	ATTATAATAA	GGAGTATGGT	ATGCTGTGTC	CATTGCTGCC	GGATGGATCA	1680
TTCTCTACTC	CTTTCGATCC	CAAACAGGGT	GAAAACCTCG	AGCCTAATCC	CGGTTTCCAC	1740
GAGGGCAGTG	CTTATAACTA	TGCCTTTTTC	GTTCCCACG	ATATACAAGG	GCTTGCCCGG	1800
CTGATGGGAG	GAGCAAAGGT	TTTTTCGGAA	AGGTTGCAGA	AAGTCTTCGA	TGAAGGATAT	1860
TATGATCCGA	CCAACGAGCC	GGACATCGCC	TATCCTTACC	TCTTCTCCTA	TTTCCCAAG	1920
GAAGCATGGC	GAACGCAGAA	ATTGACCCGG	GAGTTGATAG	ACAAACATTT	TTGCAATGCT	1980
CCTAACGGCT	TGCCCCGTAA	TGACGATGCC	GGTACGATGA	GTGCTTGGCT	TGTCTATTCC	2040
ATGCTGGGAT	TCTACCCTGA	CTGTCCGGGC	AGCCCCACCT	ATACACTGAC	CTCGCCGGTA	2100
TTCCCCGAG	TTAGGATTCG	GCTCAATCCG	CAGTATTATC	CTCAGGGGGA	GTTGATCATT	2160
ACGACCAATA	CAGAGAATCA	ACCGACAGAT	TCCATTTACA	TCCATACGGT	TTCTCTTGGC	2220
AATAAACAC	TTCCGCATGG	AACAAGGCAT	ATCAGCCATG	CCGATTTGGT	GCGCTGCGGT	2280
CACCTCCGTT	ACGAACCTAG	CAATCGTCCT	CGA			2313

(2) INFORMATION FOR SEQ ID NO:258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ATGTGCAAAA	TAAGATTGAG	CCTCTTGAG	GCTCTTGTCG	TCTGCTTATT	GTTACCTCT	60
TTTTCTCTCC	AAGCTCAAGA	GGAAGGTATT	TGGAATACCC	TCTTGGCTAT	CCACAAGACG	120
GAAAAAGCCG	TAGAAAACGCC	CAAGAAAGTC	TTTGCCGTAG	CCAACGGAGT	ACTTTACTCG	180
GTGGGCAAAAG	AAGCTCCCCA	TGAGGCAAAAG	ATCTTCGACC	GTATCAGCGG	ACTCAGCGAT	240
ACATCGGTAA	GCAGCATAGC	CTACTCCGAG	CACTAAAAT	CCTTGGTCAT	ATACTATGCA	300
TCAGGCAATA	TCGACATCTT	GGACGAAGCA	GGCCGTGTGA	CCAACGTACC	TGCATTGAAA	360
GACAATATCG	ATCTGATAGA	CAAAACGCTC	AATCGCCTTT	TGATCGTAGG	CAACAGGGCT	420
TATTTGGCAG	GAGGATTCGG	CCTCTCCGTT	CTGGATGTG	CCGAAGCTCG	CATACCGGCT	480
ACCTACGCCA	AGGGAACATA	GGTGACCGAT	GTGGCTAAGT	TGGACAATGA	TCGCTTGCTG	540
ATGCTGAAAG	AAGGGCAGCT	CTTCATCGGA	AAAGAGACCG	ATAACCTGCA	AGATCCGGCC	600
GCATGGACAG	CCTTGTCTTT	GAATTTGCCG	ATGGGCTCGG	TCACCGGTCT	GGGCATTGTC	660
GGGGAAGACA	TCTGTTTCCT	GCTCGCCGAT	GGCCGTGTAT	ATGTCGCTGC	AAACCAATCG	720
TTTGAGCCGG	AGCTATTGCT	CTCTTCCTCC	GCCGATTAC	GACTGTATGT	GACGGATCGT	780
GGTCTGTTCA	TCTGTGCCGA	GAATCGAATT	TATTTATAG	AAAAAGGTCG	CAAAACGACA	840
CAATTTCCCTA	TAGCCGACGT	CCTTGGTGTC	GGTGCCATGA	ACGAAAGCAA	TACGGCATA	900
ATAGCATTGG	GAGAAGAAGG	TTTGGCTTCA	CTTCTTCTCG	CAGAGGGAAG	TACGGCCGAA	960
GCCATGCCTG	TAGCATTCGA	CGGACCGGGG	GACAATGATT	TCTACGAGAT	GCGGTTTAGT	1020
CACGGACGTC	TGTATGCAGC	CAGCGGACTC	TGGGGAACAA	ACCTGATGGG	ACATGCCGGT	1080
ATGGTGAAAG	TATACGACGG	CAACCGATGG	ACTAACTTCG	ACAAGAAGAC	CGTACAGGAA	1140
CAGTTGGGCG	GCGGATTCAG	TTTCAATGAT	GCTATCGATA	TAGCTGTTTC	CAACGGAGAC	1200
CCCGATCACT	TTTTTGTCGG	TACATGGGGA	AACGGTCTGT	TCGAATTCAA	GGATGGCAAA	1260
GCGATAGCTC	GCTATTCGGG	AAACGAAACT	GCTATCGCAG	AATGTAATCC	CGGAGATGCC	1320
CGTGTGAAAG	CGATTGCCTT	TACGAATAAG	GGCAACCTCT	GGGGGACGCT	CGGTGCCGTA	1380
GGCAAGAACA	TCTTCATGTA	CGATCCGAG	AGTAGCACAT	GGCATTCTTT	CAGCTATCCG	1440
GATGTAGCCA	ATCTGGCCTC	CTTCGGCAAT	ATGATTATCC	TACCAACCGG	AGACAAATGG	1500
GTAAATATCC	TTACCCGTAG	TGGCGGATCC	ACGCGCAAAAG	GTGTCTTGAT	CTTCAACGAT	1560
CGGGGTACAC	CGGAACGAC	TCTGGACGAC	AGCCATCTTT	ACGTCGAGCA	GTTGTCAAT	1620
CGCCTCGGGG	CAGCCATAGG	ACATAAGACT	ATCTATGCAA	TGGCCGTCGA	TCATAACGGC	1680
TCTGTCTGGA	TGGGATCGGA	TATAGGCATT	TTCCGGCTCT	ACAATGCAGC	CGGAGTATTG	1740
TCCTCGACTT	CTACCCCTAT	CGCTGTTCGG	CCGGTCGGAG	GAGAAGAACC	CAATTTGTAC	1800
TATGTGCTGG	ACAAGGTGAC	GGTGACAGAC	ATCGTCGTGG	ACAAACTCAA	TCACAAATGG	1860
GTTGCCACCC	AAGGGACAGG	ACTCTATCTC	CTTTCGGAAG	ATTGCAGTAA	GATCCTCGCG	1920
CAATTTACCG	TAGAAAACAG	CCCTTTGCTT	TCTAACACAA	TACTATCCCT	GGCCTTAAAT	1980
GACGATAACG	GACTGCTGTA	CATCGGTACG	GCGGACGGAC	TGATGACGTT	CCAAACGGGT	2040
ACGGGGAGTG	GATCAGCTTC	GGAACCTGAC	GGCGTCTATG	TATACCCCAA	TCCGCTAAGG	2100
CCGGAATATC	CCGATGGCGT	CACCATTGCC	GGACTGCAAG	CCGGCTGTAG	TGTCAAATC	2160
ACCGATACCA	CCGGCAGACT	GCTATACGAG	ACTGAGAGCG	TAACCACCGA	AGTCAAATGG	2220

AATGCTCGAG	GTGCCGATGG	CAATAGGGTA	GCTTCGGGCG	TATATGCCGT	TGCAGTGTAC	2280
GATCCGGTAT	CGAAAAAGTC	CAAAC TAATT	CGCTTCGCAG	TGATTTCGC		2328

(2) INFORMATION FOR SEQ ID NO:259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...3474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGAAACGAA	TACTTCCAAT	AGTCGCATTC	CTTTCTCTCT	TCCTTGCCCT	TGCTTTGCCT	60
GCGAAAGCGC	AACGAGCTAT	GGGGAAGACG	GCCGACCGTT	CGCTAATGGC	TTCGGGACAT	120
TGGGTCAAGA	TACGTGTCTGA	TGCAAGTGGA	GTGTATCGCC	TTACGGACGA	ACAGCTCCGT	180
GCCAATGGCT	TCTCCGATCC	GTCCAAGGTA	GGTGTGTTTC	GTATGGTGG	AGGGGTGCTT	240
CCCGAAGATC	TGAGCCGAT	CACGACAGAC	GATTTGCCTC	CGGTACCGGT	ACTCCGTCAG	300
GGCAATGCGC	TGTATTTCTA	TGCCGTGGGC	CCGGTGACAT	GGTCTACAA	TCCGGCCAAA	360
ACCACCATGG	AGCATACGGT	GAATACATAC	AGTACGCATG	GCTACTACTT	CCTGTCCGGAT	420
GCTGCCGAG	CACCTTTGCA	GATGTCCCAA	TATACGGGTG	GAGGTGCGTC	GGCCGAGGCT	480
TTGATCGACT	ACTACGATGA	GCTGATGCTC	CATGAACAGG	AATTGTATTC	GCCCAAAGAA	540
TCGGGACGAG	ATCTGTATGG	CGAGTCTTTC	AGTGCAGTCA	ATACGCGTAC	GGTCAAGTTC	600
CCTTTGAGGG	GCAACACCCG	CTCGTCTGGC	GAACTCGGTA	CCGTATTCTC	ATACATAGCC	660
AAGGCCAGAT	CGGCCGGTGG	CGGCCGTGAG	ATGTCGCTCT	CGGCGAATGG	CATTCTGATC	720
TTCAGCGATC	CTTTTTCAT	GACATCGAAT	GAAGTCTCCA	ATTCTATTT	GGCCGGCAAG	780
AAGCGTCGTC	TCTATCACAG	TACGCCGATG	AACAGCTTGG	TCAATGAGTT	GCGCTTGGAC	840
GCGAACTATA	GCATGACAGG	AGATGCGGTC	AATCTGGATT	TCATAGAGGT	GGCTACACAG	900
AACGACCTCC	GGTACGATGG	CGCACCCATG	CATATCAGGC	GGTTTTCCAA	TTTGCCCGTT	960
TTGGGGGGCG	AGTCTGCGG	GTTTCGTTATC	AGTGAGGTGC	CGGAGTCTCT	GGTGGTTTTG	1020
CAGGCCAATT	CTTCCCTGAC	AGCATCGCTT	GTTCCCGTTA	AGACTGTCCG	GGATAAGACC	1080
ATTGAGTTTC	TGGCTCCGCC	GAAGGGTCAG	GATCGTAGGA	CTATCAATAC	GTTTTATGCC	1140
GTGGACTTGT	CACAGGCTTC	TGCTCCGGAG	ATCCTCGGAG	CGGTACCCAA	TCAAAACCTG	1200
CATGGAGAGG	AAATCCCTGA	TCTGATCATT	GTCTTACTC	AGGCGCTCCT	CCTTGAGGCT	1260
GATCGACTGG	CCACCTATCG	TAGAGAGAAA	AACGGGCTGA	AGGTTTTGGT	CGTGTTCGAG	1320
GAACAGGTGT	TCAACGAGTT	TTCCGGGTGGA	ACTCCCGATG	CTACAGCATA	CCGCCTCTTT	1380
GCCAAATGT	TCTACGACAG	ATGGAAGGCA	AATGCACCTG	TGGGAGAGAC	CTTCCCGATG	1440
CAAATGCTTC	TCTTCGGTGA	TGGGGCTCAT	GACAACAGGA	AGGTCTCCGT	AGCTTGGCAG	1500
AAACCGTATC	TCCAACAAC	GGAGTTCTTG	CTGACATTCC	AAGCCGTCAA	TTGACGAAAC	1560
GTAAACAGTT	ATGTGACGGA	TGATTACTTC	GGCTTGCTGG	ATGATCAGCC	GGCCTCGGTC	1620
AATATCGGTT	GGCGCAATTA	TAATATGGCT	GTAGGGCGAT	TCCCGTACG	TACTCCGGCC	1680
GAAGCTCGCA	TCGCAGTGG	CAAGACCATC	CGATATGAGG	AGGATCGAGA	GAGTGGTGCC	1740
TGGCGTATTC	GTGCCTGTTT	TGCGGCAGAC	AACGGGGACA	AGCACGCAAC	CGAGACTTCC	1800
CGTTTGATCG	ATACCGTCAA	CGGTTATGCT	CCTGCCATCA	TGCCGGTACG	CGCCTTTCAG	1860
GACGTATATC	CGCATGTCAT	CGAGAACGGG	TTGCACAGCA	TTCCGGGTGC	AAAGAAAAAG	1920
ATGCTGGAAA	CCCTTCAGTC	GGGTATTATC	CTGCTTAATT	ATGCTGGTCA	TGGCGGTCTC	1980
GCCGGATGGT	CGGACGAGCA	TTTGCTGACG	CTCAACGATA	TACACAAATT	CAATTATAAG	2040
CATATGCCCA	TTTGGATTAC	TGCCACGTGC	GACTTTGCCA	ACTATGACAG	TCAGACGACC	2100
TCGGCAGGGG	AGGAGGTTTT	CTCCATGAG	AAGAGTGGCA	CTCCGATCAT	GTCTCTGACT	2160
ACGCGTGTGC	TTTACAATAC	GCAGAATGAG	AAGATCAATG	GTTTTATGCT	TCGGCGTATG	2220
TTTCGAGAAAG	CTAAGGATGG	GCGTTATCGT	ACGATGGGCG	AGATTATCCG	ATCGGCCAAA	2280
CAGGGGATGC	TCAGTACTGT	TTTCCCGGAT	TCGATCAACC	AGTTGAGTTT	CTTTCTGATG	2340
GGTGATCCGT	CCGTGCGTAT	GAATCTTCCT	ACCCACAAAG	TGCAATTGAC	CGCAATCAAC	2400
GGGCAAGATC	CCGAAGGCA	GTATGGAACT	ATTATGCTCA	AGTCTTTGGA	ACGGGTAGCT	2460
CTGAAGGGTA	AGGTAACCGA	TGAAAAGGGG	ACATTTCGACG	AGACATTTCAG	TGGCAAGGTT	2520
TTCTTGACCG	TTTTCGATGG	CAGAAAAGAAA	ATGACAGCTT	TGGAAGAGGA	GGGAAACGAT	2580
CTCTCTCTTG	TATATTATGA	CTATCCTAAC	GTGATGTATG	CCGGTATTGC	CGAGGTGAAA	2640
GACGGACTCT	TCGAAACTTC	GTTTATCGTA	CCCAAGGATG	TGAACTATTC	CGAGCACGAA	2700
GGCCGGATCA	ATCTTTATGC	TTATAACGAG	AGCACAAAGG	CGGAAGCCAT	GGGGGTAGAC	2760
TTCTCCATCA	GAGTCCAACC	GGGTATTCTT	GATGAGGTAA	CGGAAGATAA	TACACCGCCT	2820
AAAATCATAA	GCTGCTTCCT	CAATGACAGT	ACATTCCGAT	CGGGAGATGA	GGTTAATCCT	2880
ACTCTCTGT	TTATGGCCGA	AGTATTTCGAC	TTGAATGGAA	TCAATATCAC	GGGTAGCGGA	2940
GTAGGGCATG	ATATTACGCT	TTGTATCGAT	GGCCGTGCCG	ACCTGACCTA	CAACCTCAAT	3000

GCATATTTCA	CAAGTTCGGC	TACGGATGCA	GGTGTGGGCA	CTATTCTCTT	CATGATACCG	3060
GCTTTGGCCG	AAGGAGATCA	TACTGCCCGA	CTGACGGTTT	GGGACATTTT	CAATAATGCC	3120
GTCCATCATG	ACTTTTCATT	CAGAGTGGTA	GATGGCATTG	CTCCGGATGT	GGCTGATGTG	3180
ATTCTATTCC	CGAATCCGGT	ACGCGAGAGT	GCTACGTTCC	GAATCTTCCA	CAATCGCCCC	3240
GGAAGCGATT	TGAACGTGGC	CGTGGAGATC	TATGACTTCA	CCGGTCGTCT	TGTGAACAGT	3300
TTGCCAGTCA	AGACCTATTC	GTCTTCCTAC	GGAGAACCTA	TAGAGATCAA	GTGGGATCTG	3360
ACCTCCAAAT	ACGGAGTGAA	GATCGGAAAC	GGATTCTACC	TCTATCGTTG	TGTGGTGAAC	3420
TCTCCCGGAG	GACAGACGGC	CTCCATGGCC	AAGAAAATGA	TCGTGGTAGG	ACAA	3474

(2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGAAGAAAC	TTTTCCCAT	ATTATTACTC	ATATTGTCCA	TTTTGGTCGG	ATGTGGAAAA	60
AAAGAAAAAC	ACTCTGTAAC	TGAAATCGCC	CGAGAGAAAA	AGCGTATTAC	TGCATTGCTG	120
TACGAAAAAG	AACCTCCAC	TGATTCTGTT	AAACAGCTTT	ACGAGAACAG	CGTACAGAAC	180
AAGAACCCTT	TGGGACAAAT	GTTATTTCGG	ATCGAGGTCG	GCAAACGGAT	GCGTAATATG	240
TCCAATACA	CAGATGCGAT	GCTATATCAC	CAAAAAGGGT	TGAACGCTGC	ATTGAATCTA	300
AGGGACACCA	TCGTAGCCGC	ACAAGCATGG	AATCATCTCG	GAACGGATAG	CCGTCGTATC	360
GGTGCTTTGG	CAGAAGCTTC	GGATTATCAT	TACAAGGCTC	TTTCCTTGAT	AGAATCTTTT	420
AGCGGAAACC	AGAATAGGCC	TGCGATCAAA	GCCAGATCGG	CGGCCCTGAA	CGGCATCGGC	480
AACATCAATC	TTGAGTTAGG	ATACCATGAT	GAGGCCGAAA	AGAATTTCTT	GAAAGCACTG	540
CAAGGTGAGA	AAGAACTCGA	CAGTCCTCTC	GGGCAAGCTA	TCAACTATGC	GAACCTCGGA	600
CGTATCTATC	GACAACGCAA	AGAATACGAC	AAGGCTCGTA	CCTACTTCTT	CTTGCTCTCTG	660
GAGCAGAACA	ATATGGCAGA	GAATCTGATG	GGTATCGGAC	TCTGTAGCAT	CAATCTCGGA	720
GAAGTAGACG	AAGAAAAAGG	GGATTATCAA	AAGGCTTTGC	AAGAGTATGC	CACGGCATAAC	780
AACTGATGG	AACAGTTGTC	CGATCGATGG	CACTGGCTGA	ATTCTGTAT	CCCGATGGCA	840
CGTATCAATC	TCAAACAAGG	TAACGAAAGG	CTCTACCAGC	ATTTCAATTC	TTTGGCCGAA	900
GGGACTGCGA	AAGAAATTAA	TTCGACTTCA	CATCTGATAG	AAATATACAA	TCTTCAATAC	960
GAGAATCTCG	AGCGTAAAAA	AGAATACAAA	CAAGCCCTCG	AAGCATTCTG	TCTGAGCAAG	1020
ACGTTGAGCG	ACAGCATGTC	CATTGCGCAC	AAGGTCAGCA	GCATACAAGA	AACGCGATTG	1080
AACATCGAAC	GAAACAAGTC	CCAAAAAGAG	CTTGAAGAAA	TACAGCAAGT	AAGCAAGGCA	1140
AAACAAGAGA	AATCGAAGTT	TATCTCTCTG	AGCACTCTTT	TTGCCCTTTT	CATCTCGATT	1200
CTTTTGATT	CTGTTCTGAC	ATATGCATAC	CGTCAGGGCA	AGAAGCATAA	CAAGCTGATC	1260
AAAGAGACGG	ATAAACTTCG	CTCCGGCTTT	TTACCCGGTA	TTACACACGA	ATTTCGTACG	1320
CCATATCACG	TCATACAAGG	TTTGAATGAG	AAAATGAGTT	CAAGTCCTGA	TCTCCAAGCA	1380
TCGGACAGAA	CCGAGCTGCA	CAAGATAATA	GACAGACAGA	GTAGCCATAT	GCTGAATTTG	1440
GTGAACCAGC	TGTTGGATAT	TTGCAAGATC	AGAAGCGGAG	TATCCACGCC	CGAATGGCGC	1500
AATGGCGACA	TCGTCTCCTT	CGTACAGATT	CTCATCGATT	CGTTTGCAAC	ATACGCACAG	1560
GCTCAAGACA	TAACCTTGGA	GCTACAACCC	GAGAGCAAAC	CTATTGTCGT	GGACTTCGTC	1620
CCCTCCTACT	TGCAAAAAAT	CATATCCAAT	CTTTTGTTCA	ATGCCATCAA	GTATTCTTTA	1680
GCCGGAGGGA	GAGTGGTCAT	ATCTCTGGCA	AAAACCAAGA	ATGAAAAAAA	TCTGATCATA	1740
CGCGTTGCAG	ACAATGGCAT	AGGAATAGAT	AAAACGATC	AGGTCATAT	CTTCGACATC	1800
TTCTATCGAG	GACAGTCCGC	TACCGAAAG	CATGGATCAG	GCGTCGGACT	CTCGTTTACC	1860
AATATACTGG	TCGAAAACCT	TCGAGGTACG	ATCAAAGTGG	AAAGCCAGCC	GGGGAAAGGA	1920
AGTGCCCTCA	CCATCAGTAT	TCCTACACAA	AACCAGTCCT	CTTCGGCAGA	GATTCTTCCT	1980
TGGCTACCCT	CCTCCGATGA	CATTGTCCAC	CCTGTCCACA	TCGCGCCCGA	TGACTCACCG	2040
ACATCTCCGA	TGGTAGCAGC	TCTGAATCAT	CGCTTCGAGG	ACGAACGTCC	GACCATACTG	2100
CTCGTCGAGG	ACAATAAGGA	TATCAACCTG	CTCGTCAAAC	TACTCCTTTG	CGATCGCTAC	2160
AATGTGCTAT	CCGCCGCAAA	CGGAAAAGAG	GGTATAGCCC	TCGCTACCGA	GCATATTCCC	2220
GACATTATCA	TTACGGATAT	TATGATGCCG	ATAATGGATG	GGATAGAAAT	GACAATCCGG	2280
ATGAAGCAAT	CGCCTCTGCT	CTGTACACAT	CCCATTTGTC	CTTTGACGGC	CAAGAGTACC	2340
GAACAGGACA	GATTGGAAGG	AATCAAAAGC	GGTGTAGTCT	CTTATCTATG	CAAGCCATTC	2400
TCTCCGGAGG	AGCTTTTGAT	GCGGATCGAG	CAGCTTCTGA	AAGACCGTGA	GTTGCTCAAG	2460
AAGTTCTATA	TGCAAAAAC	CATGCTGGAT	CGGAAGCCGG	AGGAGGAGCC	TCAACCGATA	2520
GATGACAGCA	GTATGCAGTT	TCTCCTTGCT	GCCAAAGATG	CAGTGTCCGG	TGGAATCAAA	2580
CAAAATCCGG	ATTTTTCCTG	TCAAGACTTG	GCCGAAAAAA	TGTGCATGAG	TCCATCCCAA	2640

CTCAACAGAA	AGCTCACGAG	TGTCGTAGGT	TGCTCCACCA	TCGGCTACAT	ACAGCAGATC	2700
AAGATAAAAT	TGGCCTGCAA	GCTCCTTGCC	GATGAGAGCA	AAAACATCTC	CGACATTAGC	2760
ATTGAGGCAG	GCTTTTCGGA	TCCGGCTTAC	TTCTCTCGCA	CCTTCAAACG	CTACATGAAC	2820
TGCTCTCCCT	CCCAATATCG	GCAAAAATC	CTTGCCATGC	CGGGGAGCGA	CAAGGAGACA	2880
GTT						2883

(2) INFORMATION FOR SEQ ID NO:261

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1668 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1668
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

ATGAAAAAGC	TTTACAGGC	TAAAGCCTTG	ATTCTGGCAT	TGGGACTCTT	CCAACTGCCC	60
GCAATCGCCC	AAACGCAAAT	GCAAGCAGAC	CGAACAAACG	GTCAATTTCG	AACAGAAGAG	120
ATGCAACGAG	CATTCCAGGA	AACGAATCCC	CCTGCAGGTC	CTGTGCGTGC	TATCGCTGAG	180
TACGAACGCT	CTGCAGCCGT	TTTGGTACGC	TACCCGTTTCG	GTATCCCGAT	GGAATTGATC	240
AAAGAGCTGG	CCAAGAACGA	CAAGGTGATT	ACCATTGTGG	CGAGTGAAAG	CCAAAAAAGC	300
ACCGTTATAA	CCCAGTACAC	CCAAAGCGGT	GTGAATCTCT	CTAATTGCGA	TTTCATCATT	360
GCGAAAATCG	ACTCTTACTG	GACACGCGAC	TATACCGGTT	GGTTCGCAAT	GTACGATACG	420
AACAAAGTAG	GTCTCGTGGA	CTTTATTAT	AACCGCCCTC	GTCCCTAACG	TGATGAATTC	480
CCCAAATACG	AAGCACAAAT	TCTGGGCATC	GAGATGTTTCG	GGATGAAGCT	CAAGCAGACC	540
GGTGGCAACT	ACATGACGGA	CGGATATGGA	TCCGCTGTGC	AGTCACATAT	CGCATATACG	600
GAGAACTCCT	CTCTGTCTCA	AGCTCAAGTA	AATCAAAAGA	TGAAAGACTA	TCTCGGCATC	660
ACACATCATG	ATGTGGTACA	AGATCCGAAC	GGCGAATATA	TCAACCATGT	GGACTGTTGG	720
GGCAAGTATT	TGGCACCAGG	CAAAATCCTC	ATCAGGAAAG	TGCCTGACAA	TCACCCTCAG	780
CACCAAGCCC	TGGAAGATAT	GGCAGCCTAC	TTGCGAGCAC	AGACCTGCGC	ATGGGGAACG	840
AAGTACGAGG	TATATCGCGC	TTTGGCCACC	AATGAACAAC	CGTACACGAA	CTCTCTGATT	900
CTGAACAACA	GGGTATTGT	TCCTGTCAAT	GGCCCCGCCT	CCGTGGACAA	CGATGCTCTG	960
AACGTCTATA	AGACGGCAAT	GCCCCGTTAC	GAAATTATAG	GTGTCAAAGG	GGCTTCAGGA	1020
ACACCTTGGT	TAGGAACAGA	TGCCCTGCAT	TGTCGTACTC	ACGAGGTAGC	GGATAAGGGC	1080
TATCTCTATA	TCAAGCACTA	CCCGATACTG	GGCGAACAGG	CAGGCCCTGA	TTATAAGATC	1140
GAAGCAGATG	TCGTCTCATG	CGCCAATGCT	ACTATCTCGC	CGGTACAATG	TTACTATCGT	1200
ATCAATGGTT	CCGGTAGCTT	TAAGGCTGCT	GATATGACGA	TGGAATCAAC	AGGTCACAT	1260
ACTTATAGCT	TTACAGGTCT	TAACAAGAAT	GATAAGGTAG	AATACTATAT	CTCTGCCGCT	1320
GACAATAGTG	GTGCAAAAGA	GACTTATCCC	TTTATCGGCG	AACCTGATCC	TTTCAAGTTT	1380
ACGTGTATGA	ACGAAACCAA	TACATGTACT	GTGACCGGAG	CTGCCAAAGC	TCTTCGTGCA	1440
TGGTTCAACG	CCGGTCGTTC	AGAAGTGGCT	GTTTCGGTAA	GTTTGAATAT	TGCCGGCACA	1500
TATCGGATAA	AGCTTTATAA	CACCGCAGGA	GAAGAAGTCG	CTGCAATGAC	CAAGGAATTA	1560
GTAGCAGGGA	CGAGTGTCTT	CAGTATGGAT	GTGTATTCTC	AGGCTCCGGG	CACATATGTT	1620
CTGGTTGTTG	AAGGAAATGG	AATCCGTGAG	ACAATGAAAA	TTCTCAAA		1668

(2) INFORMATION FOR SEQ ID NO:262

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

ATGAAACTTT CATCTAAGAA AATCTTAGCA ATCATTGCAT TGCTGACGAT GGGACATGCT	60
GTGCAGGCAC AGTTTGTTC GGCTCCCACC ACAGGGATTC GCATGTCTGT CACTACAACC	120
AAGGCCGTAG GCGAAAAAAT CGAATTGTTG GTTCATTCCA TAGAGAAGAA AGGCATCTGG	180
ATCGATCTCA ATGGGGATGC CACTTACCAA CAAGGAGAGG AAATAACCGT ATTCGATGAG	240
GCATACCACG AATACACGAT CGGGACGCAA ACCCTCACTA TCTATGGTAA TACGACCCGA	300
TTGGGGTGTC GATCTACCGG TGCAACGGCT GTCGATGTAA CGAAAAACCC TAATCTGACC	360
TATCTCGCAT GCCCCAAAAA TAATCTGAAA TCATTGGACT TGACGCAAAA CCCAAAGCTG	420
CTGCGAGTTT GGTGCGACTC TAACGAAATA GAAAGTTTGG ACCTGAGTGG CAATCCGGCT	480
TTGATCATCT TCGGCTGTGA CAGGAATAAG CTGACTGAGC TGAAGACCGA TAACAACCCC	540
AAGTTGGCCT CTCTTTGGTG TTCTGATAAT AACCTGACGG AGTTGGAAC CAGTGCCAAT	600
CCTCGTCTCA ATGATCTTTG GTGCTTCGGT AATCGGATCA CGAAACTCGA TCTGAGTGCC	660
AATCCTCTAT TGGTAACACT TTGGTGCAGT GACAATGAGC TTTCGACCTT GGATCTTTCC	720
AAGAATTCCG ACGTTGTCTA CCGTTGGTGT TCATCGAACA AACTTACATC CTGAATCTG	780
TCGGGGGTGA AGGGACTGAG TGTTTTGGTT TGTCATTCCA ATCAGATCGC AGGTGAAGAA	840
ATGACGAAAG TGGTGAATGC TTTGCCCACA CTATCTCCCG GCGCAGGCGC TCAGAGCAAG	900
TTCTGCTGTT TAGACCTCAA GGACACTGAT GAGAAGAATA TCTGTACCGT AAAGGATGTG	960
GAAAAAGCTA AAAGTAAGAA CTGGCGAGTA TTGACTTCA ACGGTGATTC TGACAATATG	1020
CTTCCATACG AAGGAAGTCC GACATCGAAC TTGGCAGTAG ATGCTCCAC TGTCAGGATA	1080
TATCCCAATC CCGTAGGAAG ATATGCGCTC GTCGAGATCC CCGAGTCTCT TTAGGGCAG	1140
GAAGCTGCTT TATACGATAT GAATGGGGTA AAAGTCTATA GTTTCGCGGT AGAGTCTCTT	1200
CGTCAGAACA TTGACCTGAC ACATCTTCCC GACGGCACTT ATTTCTTCCG TCTCGATAAC	1260
TATACCACTA AGCTCATCAA ACAG	1284

(2) INFORMATION FOR SEQ ID NO:263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

ATGAGAAAAA CAATAATTTT CTGCTTGTG CTGCCCCTAT TTGGCTGTTC TTGGGCACAA	60
GAAAGAGTCG ATGAAAAAGT ATTCTCCGCA GGAACAAGTA TTTTtagggg CATCCTTGAA	120
AAGGTGAAAG CACCGCTTAT GTATGGAGAT CGTGAGGTAT GGGGTATGGC TCGTGCGAGC	180
GAGGATTCTT TTTTtataCT TCCGTTACG GATGACCTCA CTCCCGTGCT TTCTATAAC	240
CGTCTTACAA ACGAACCCTG CTTTGTGTCA GACCAAGGAA TAACTGAGTA TTTCaaattC	300
GCTCAAGAAG GTGATTACAT TGAAGTCGAA GGAAGCTCTG TATTcatggc GAATCTTTTG	360
TACTATCGTT TTTTCCCGAC AAGAATTACC TCCTATAATG CTCCCATTGA AGGTGTTGTG	420
AGCAAGACGG GAAATCCTGC TTTTACAATC CCGATGCTCC CGGGGGTTTC TGATTGCATA	480
GAAATCTCAA ACAACCGCAA AGTCTTTCTG ACCAATCAAT TAGGGGTGTG AAACATCACT	540
GACGGGATGG AACCTCCGAT TATTGCCGGA GTCTCTGCTT CCTATGGATC TTCCGTCCGG	600
GTGTATGGTC ATGTCTCACA GCGGTGGGAC ATCATAGGCC ATTGCTATTT GGATATCTAC	660
CCAACCAATT GCTATCCGCT CAGCACGAAA CCGTTGCAG GAGACGATGA GGTTTTTGTC	720
AAACAACAAG GCAGGCAAT AGAGATCGAT AGCAACAGCC CCATAGTCCA AGTGGTCGTA	780
TACGATCTTG AGGGGAAAG TGTTTTTCGC AAAAGAATGA CCGAAAACGC TTATACCCTA	840
TCCTTTAGAG CACCCATGCT CGGCTTTATG ACCATCATGA TCGAAACACA AAATTcGATT	900
ATCAATAAAA AACTTAATGT TACACAGCTA	930

(2) INFORMATION FOR SEQ ID NO:264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PORYPHYROMONAS GINGIVALIS

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

```
ATGAAAAAAA CAACCATTAT TTCTTTGATT GTCTTCGGTG CTTTCTTTGC AGCCGTGGGC      60
CAAACCAAGG ACAATTCTTC TTACAAACCT TTTTCGAAAG AAGATATTGC CGGAGGAGTT      120
TACTCTCTCC CGACTCAAAA TCGTGCGCAG AAGGACAATG CCGAGTGGCT TCTTACAGCG      180
ACCGTCTCCA CAAACCAGTC TGCAGATACT CACTTTATCT TCGATGAGAA CAACCGCTAT      240
ATCGCTCGTG ACATAAAAGC CAATGGGGTA AGAAAATCCA CGGACTCCAT TTACTACGAT      300
GCCAACGGGC GAATATCGCA TGTGGATCTT TATATCTCGT TCAGTGGCGG AGAGCCTGCA      360
CTCGACACCC GATTCAAGTA CACCTATGAT GACGAGGGAA AGATGACCGT GAGGGAAGTA      420
TTCATGTGGG TAATGGATCC GAATACACCT ATCTCACGCT TGGAATATCA TTATGATGCA      480
CAGGGCAGAC TGACCCACTG GATTTCTTTT GCTTTCGGGG CAGAATCCCA AAAGAATACG      540
TATCACTATA ATGAAAAAGG TCTGTTGGTC AGCGAAGTGC TGAGCAATGC AATGGGGACA      600
ACCTATTCAG ACACCGGCAA AACGGAATAC AGCTATGACG ATGCAGATAA TATGGTGAAG      660
GCCGAGTACT TCGTCGTCCA GCAAGGAAAG GCATGGCAAG TACTCAAAAG AGAGGAATAC      720
ACCTATGAGG ACAATATCTG CATACAATAT TTGGCTATTA ACGGTACCGA CACAAAGGTG      780
TACAAGCGAG ACATCGAGAG CGATAAGTCC ATCTCCGCAA ATGTCATTGA CATTCCGTCA      840
ATGCCGGAAC AGACCTGGCC TAATATGTAC GGATTCAACG CAAAGCGACT GAAAGAGACT      900
TATTCCTCCT ACGAAGGAGA TGTGGCTACT CCTATATTCG ACTATATCTA TACGTACAAG      960
GCTCTTACCT CAATGGCAAC ACCTTCGACA GAAGCTCAGG TAGCAGTCTA TCTCAATCCG     1020
TCAACGGGAG GGTTAGTGAT TCTGGCCAAC GGCATCACAC ATCTGAGCAT GTACGACTTG     1080
CAGGGTAAGC TTATCCGTGA TTGTGCCTTG AGCGGCGATA AGGTGGAAAT GGGTGTTCGGA     1140
TCTTTGACCA AAGGGACATA CCTGCTTAAA GTGAATACGG ATCAGGGAGC CTTTGTGAGA     1200
AAAGTCGTGA TTCGA                                     1215
```

(2) INFORMATION FOR SEQ ID NO:265

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 454 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

```
Phe Cys Val Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu
1          5          10          15
Asn Leu Lys Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln
20        25        30
Ser Pro Thr Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro
35        40        45
Lys Val Thr Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu
50        55        60
Met His His Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser
65        70        75        80
Gly Glu Val Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser
85        90        95
Ile Glu Val Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val
100       105       110
Gly Asp Pro Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu
115       120       125
Ser Ser Gly Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val
```

130	135	140
Ala Thr Pro Asp Ile	Ala Pro Arg Asp Ile Tyr	Ile Thr Ala Asn Phe
145	150	155
Thr Ala Pro Leu Ala	Pro Asp Phe Asp Phe Ile	Val Arg Gly Glu Glu
165	170	175
Arg Ala Leu Gln Thr	Ala Ile Asp Ala Leu Ala	Lys Leu Thr Thr Gly
180	185	190
Lys Val Tyr Val Gly	Leu Lys Pro Gly Ser Ser	Leu Gly Leu His Asn
195	200	205
Ala Glu Ile Val Glu	Val His Gly Pro His Pro	Ala Gly Asn Val Gly
210	215	220
Val Leu Ile Asn His	Thr Lys Pro Ile Asn Arg	Gly Glu Thr Val Trp
225	230	235
Thr Leu Lys Ala Thr	Asp Leu Ile Val Ile Gly	Arg Phe Leu Leu Thr
245	250	255
Gly Lys Ala Asp Phe	Thr Arg Met Ile Ala Met	Thr Gly Ser Asp Ala
260	265	270
Ala Ala His Gly Tyr	Val Arg Ile Met Pro Gly	Cys Asn Val Phe Ala
275	280	285
Ser Phe Pro Gly Arg	Leu Thr Ile Lys Glu Ser	His Glu Arg Val Ile
290	295	300
Asp Gly Asn Val Leu	Thr Gly Lys Lys Leu Cys	Glu Lys Glu Pro Phe
305	310	315
Leu Ser Ala Arg Cys	Asp Gln Ile Thr Val Ile	Pro Glu Gly Asp Asp
325	330	335
Val Asp Glu Leu Phe	Gly Trp Ala Ala Pro Arg	Leu Asp Gln Tyr Ser
340	345	350
Met Ser Arg Ala Tyr	Phe Ser Trp Leu Gln Gly	Lys Asn Lys Glu Tyr
355	360	365
Val Leu Asp Ala Arg	Ile Lys Gly Gly Glu Arg	Ala Met Ile Met Ser
370	375	380
Asn Glu Tyr Asp Arg	Val Phe Pro Met Asp Ile	Tyr Pro Glu Tyr Leu
385	390	395
Leu Lys Ala Ile Ile	Ala Phe Asp Ile Asp Lys	Met Glu Asp Leu Gly
405	410	415
Ile Tyr Glu Val Ala	Pro Glu Asp Phe Ala Thr	Cys Glu Phe Val Asp
420	425	430
Thr Ser Lys Ile Glu	Leu Gln Arg Ile Val Arg	Glu Gly Leu Asp Met
435	440	445
Leu Tyr Lys Glu Met	Asn	
450		

(2) INFORMATION FOR SEQ ID NO:266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

Glu	Leu	Ser	Lys	Cys	Tyr	Met	Asp	Lys	Val	Ser	Tyr	Ala	Leu	Gly	Leu
1			5						10					15	
Ser	Ile	Gly	Asn	Asn	Phe	Lys	Ser	Ser	Gly	Ile	Asp	Ser	Val	Val	Met
			20					25					30		
Asp	Asp	Phe	Met	Gln	Gly	Leu	Ser	Asp	Val	Leu	Glu	Glu	Lys	Ala	Pro
			35				40					45			
Gln	Leu	Ser	Tyr	Asp	Glu	Ala	Lys	Arg	Glu	Ile	Glu	Ala	Tyr	Phe	Met
			50				55				60				
Asp	Leu	Gln	Gln	Lys	Ala	Val	Lys	Leu	Asn	Lys	Glu	Ala	Gly	Glu	Glu
65				70					75					80	
Phe	Leu	Lys	Ile	Asn	Ala	His	Lys	Glu	Gly	Val	Thr	Thr	Leu	Pro	Ser
			85					90					95		
Gly	Leu	Gln	Tyr	Glu	Val	Ile	Lys	Met	Gly	Glu	Gly	Pro	Lys	Pro	Thr
			100				105						110		
Leu	Ser	Asp	Thr	Val	Thr	Cys	His	Tyr	His	Gly	Thr	Leu	Ile	Asn	Gly

(2) INFORMATION FOR SEQ ID NO:267

(2) INFORMATION FOR SEQ ID NO:268

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

```
Arg Unk Phe Leu Pro Glu Lys Ala Leu Tyr Ile Gly Cys Arg Val Glu
1      5      10      15
Thr Gln Glu Gly His Ala Val Gly Phe Gly Leu Asp Asp Gly Pro Ala
20      25      30
Met Lys Gly Lys Gly Asp Leu Val Gly Ser Tyr Leu Pro Gly Ala Ala
35      40      45
Pro Met Pro Phe Val Pro Leu Ser Asp Ile Pro Ala Arg Ser Met Asp
50      55      60
Ala Asn Phe Tyr Ile Tyr Ser Arg Ile Ser Leu Gly Ser Gly Thr Gln
65      70      75      80
Asp Val Leu Gln His Arg Met Lys Val Tyr Pro Asn Pro Ala Thr Thr
85      90      95
Glu Leu His Val Glu Ala Leu Ser Ala Trp Val Gly Glu Gln Ala Ala
100     105     110
Val Tyr Asp Met Arg Gly Arg Arg Val Ser Ala Arg Thr Val Asp Ser
115     120     125
Glu Lys Leu Cys Ile Asp Ile Ala Ser Leu Pro Val Gly Val Tyr Met
130     135     140
Leu Arg Ile Gly Ser Tyr Ser Ala Lys Phe Glu Lys Arg
145     150     155
```

(2) INFORMATION FOR SEQ ID NO:269

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

```
Thr Arg Asn Val Ser Leu Ile Lys Met Pro Arg Ile Met Lys Leu Lys
1      5      10      15
Ile Ala Leu Arg Leu Leu Leu Ala Thr Phe Ala Ile Val Leu Phe Ser
20      25      30
Pro Leu Ala Lys Ala Gln Met Asp Ile Gly Gly Asp Asp Val Leu Ile
35      40      45
Glu Thr Met Ser Thr Leu Ser Gly Tyr Ser Glu Asp Phe Tyr Tyr Lys
50      55      60
Met Ala Val Ala Asp Asn Gly Trp Ile Tyr Val Met Leu Asp Phe Ser
65      70      75      80
Arg Ile Tyr Phe Asp Asp Val Arg Leu Tyr Arg Ser Lys Asp Gly Gly
85      90      95
Ala Thr Tyr Gln Lys Leu Gly Ser Leu Gly Ser Leu Val Pro Tyr Asp
100     105     110
Phe Asp Val Ser His Cys Asp Phe Ile Val Thr Gly Lys Asp Glu Asp
115     120     125
Asp Ile Asn Val Trp Thr Val Met Thr Ala Phe Glu Tyr Val Gly Gly
130     135     140
Thr Ile Gly Asn Gly Val Leu Leu Met His Arg His Asp Ala Asp Ile
145     150     155     160
Asn Asn Thr Glu Cys Val Tyr Lys Lys Asp Phe Pro Asn Asn Arg Leu
165     170     175
Met Gly Val Ala Ile Ala Ser Asn Tyr Arg Ala Pro Ser Pro Tyr Gly
180     185     190
```


Leu Gly Gly Asp Pro Phe Ala Leu Ala Val Ala Val Ser Gly Ser Gly
 195 200 205
 Ser Asp His Ser Phe Leu Asp Tyr Ile Phe Ser Leu Asp Gly Gly Val
 210 215 220
 His Phe Glu Gln Lys Arg Ile Tyr Thr Arg Pro Gln Lys Leu Thr Ile
 225 230 235 240
 Asn Arg Val Asp Leu Ser Leu Gly Ser Thr Ser Pro Ser Leu Gly Phe
 245 250 255
 Asn Thr Trp Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Asn Leu
 260 265 270
 Asp Gly Phe Asp Ile Gly Phe Ile Ser Asn Phe Val Asp Tyr Asp Pro
 275 280 285
 Arg Tyr Ala Trp Ser Glu Pro Ile Ile Ile Glu Glu Asp Cys Gly Trp
 290 295 300
 Thr Asp Phe Asn Pro Leu Gly Ala Leu Ser Ile Glu Ile Gln Met Met
 305 310 315 320
 Leu Asp Asp Asn Ser Asp Asn Thr Val Gly Gly Glu Arg Ser His Asn
 325 330 335
 Phe Leu Ile Thr Tyr Pro Gly His Tyr Val Tyr Pro Lys Gln Ser Phe
 340 345 350
 Asn Tyr Ser Pro Gly His Thr Pro Thr Lys Lys Asp Leu Val Phe Lys
 355 360 365
 His Cys Ile Gly Ile Pro Ala Leu Ala Tyr Asp Lys Glu Gly Asp Arg
 370 375 380
 Tyr Leu Thr Thr Phe Gln Asp His Asn Leu Met Arg Tyr Arg Trp Ile
 385 390 395 400
 Lys Tyr Asp Asp Ile Asn Ser Phe Tyr Gly Trp Ser Trp Pro Tyr Val
 405 410 415
 Tyr Ala Lys Glu Ala Lys Asp Lys Lys Arg Arg Arg Pro Gln Val Ala
 420 425 430
 Leu Asn Pro Thr Asn Gly Lys Ala Cys Trp Val Trp His Thr Arg Lys
 435 440 445
 Ser Pro Tyr Asp Glu Thr Lys Pro His Pro Thr Pro Val Ile Ile Lys
 450 455 460
 His Phe Leu Trp Ser Asp Thr Glu Trp Val His Ala Leu Asp Val Gly
 465 470 475 480
 Asp Val Leu Gln Lys Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala
 485 490 495
 Lys Glu Tyr Val Leu Ile Asn Leu Pro Lys Glu Gly Gly His Glu Ala
 500 505 510
 Val Val Tyr Asp Met Gln Gly Arg Ile Val Glu Lys Val Ser Phe Ser
 515 520 525
 Gly Lys Glu Tyr Lys Leu Asn Val Gln Tyr Leu Ser Lys Gly Thr Tyr
 530 535 540
 Met Leu Lys Val Val Ala Asp Thr Glu Tyr Phe Val Glu Lys Ile Ile
 545 550 555 560
 Val Glu

(2) INFORMATION FOR SEQ ID NO:270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyrromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

Gln Met Lys Arg Leu Leu Pro Phe Leu Leu Ala Gly Leu Val Ala
 1 5 10 15
 Val Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val
 20 25 30
 His Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser
 35 40 45
 Val Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr
 50 55 60

```

Ile Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile
65      70      75      80
Asp Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe
      85      90      95
Asp Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly
      100      105      110
Ser Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr
      115      120      125
Pro Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro
      130      135      140
Phe Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr
      145      150      155      160
Leu Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln
      165      170      175
Gln Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu
      180      185      190
Phe Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu
      195      200      205
Pro Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr
      210      215      220
Asp Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr
      225      230      235      240
Leu Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser
      245      250      255
Ser Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro
      260      265      270
Asn Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser
      275      280      285
Gly Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp
      290      295      300
Met Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys
      305      310      315      320
Ile Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln
      325      330      335
Leu Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala
      340      345      350
Thr Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro
      355      360      365
Arg Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile
      370      375      380
Arg Ala Lys Val Ser Leu Arg
      385      390

```

(2) INFORMATION FOR SEQ ID NO:271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

```

Lys Arg Asn Pro Leu Pro Leu Thr Ala Ser Asn Arg Lys Ile Phe Ile
1      5      10      15
Lys Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu
      20      25      30
Leu Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys
      35      40      45
Gln Ser Glu Arg Tyr Val Val Leu Ser Leu Asp Gly Phe Arg Pro
      50      55      60
Asp Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln
      65      70      75      80
Glu Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe
      85      90      95
Pro Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly
      100      105      110

```

```

Ile Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile
115 120 125
Ser Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro
130 135 140
Val Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe
145 150 155 160
Trp Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp
165 170 175
Lys Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val
180 185 190
Ile Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met
195 200 205
Trp Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu
210 215 220
Ser Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly
225 230 235 240
Tyr Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp
245 250 255
Phe Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys
260 265 270
Cys Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met
275 280 285
Ala Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu
290 295 300
Arg Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg
305 310 315 320
Lys Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu
325 330 335
Gly Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala
340 345 350
Ile Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln
355 360 365
Ala Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg
370 375 380
Pro Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu
385 390 395 400
Ile Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu
405 410 415
Thr Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
420 425

```

(2) INFORMATION FOR SEQ ID NO:272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

```

Leu Ser Arg Gly Val Phe Pro Leu Met Tyr Gly Arg Arg Gly Ser Ile
1 5 10 15
Arg Ala Ser Ser Gly His Arg Asp Lys Ile Phe Lys Asn Thr Ile Ile
20 25 30
Arg Phe Ile Thr Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn
35 40 45
Ala Val Tyr Pro Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser
50 55 60
Leu Asp Ile Asp Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln
65 70 75 80
Pro Met Ala Asn Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu
85 90 95
Arg Phe Glu Glu Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser
100 105 110
Ala Ser Cys Val Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg
115 120 125

```

```

Pro Thr Gly His Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys
130      135      140
Glu Phe Leu His Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe
145      150      155      160
Ala His Lys Val Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu
165      170      175
His Leu Ser Thr Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val
180      185      190
Arg Arg Leu Leu Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys
195      200      205
Arg Ile Asp Glu Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu
210      215      220
Pro Glu Val Ser Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile
225      230      235      240
Ser Thr Gly Ala Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met
245      250      255
His Met Gln Gly Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile
260      265      270
His Ala Val Glu Ile Leu Ala Ala Asn Leu
275      280

```

(2) INFORMATION FOR SEQ ID NO:273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

```

Pro Leu Lys Lys Arg Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu
1      5      10      15
Val Val Glu Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile
20      25      30
Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu
35      40      45
Ile Gly Ser Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr
50      55      60
Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp
65      70      75      80
Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu
85      90      95
Gly Ile Val Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala
100      105      110
Glu Asn Leu Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala
115      120      125
Asp Arg Glu Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser
130      135      140
Arg Lys Ala Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln
145      150      155      160
Arg Val Gly Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu
165      170      175
Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile
180      185      190
Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met
195      200      205
Ser Thr His Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu
210      215      220
Ala Val Arg Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala
225      230      235      240
Asp Ala Val Ser Arg Lys Asn Thr Glu Ile Asp
245

```

(2) INFORMATION FOR SEQ ID NO:274

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

```
Thr Arg His Cys Pro Ala Cys Arg Ser Ser Phe His Leu Ile Lys Thr
1      5      10      15
Ser Lys Thr Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr
      20      25      30
Glu Glu Ile Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp
      35      40      45
Lys Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser
      50      55      60
Thr Leu Leu Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile
      65      70      75      80
Tyr Lys Leu Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg
      85      90      95
Thr Ala Val Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn
      100      105      110
Leu Ile Glu Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val
      115      120      125
Tyr Leu Gly Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala
      130      135      140
Leu Arg Lys Met Ser Ile Ser His Arg Ala Gly His Phe Pro Asn Gln
      145      150      155      160
Leu Ser Gly Gly Gln Gln Arg Val Ala Ile Ala Arg Ala Val Val
      165      170      175
Ala Asn Pro Lys Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp
      180      185      190
Ser Lys Asn Gly Ala Asp Val Met Glu Leu Leu Arg Gly Leu Asn Arg
      195      200      205
Glu Gly Ala Thr Ile Val Met Val Thr His Ser Glu His Asp Ala Arg
      210      215      220
Ser Ala Gly Arg Ile Ile Asn Leu Phe Asp Gly Lys Ile Arg
      225      230      235
```

(2) INFORMATION FOR SEQ ID NO:275

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 604 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

```
Ser Thr Glu Thr Asn Ser Lys Ser Glu Met Lys Glu Phe Phe Lys Met
1      5      10      15
Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu Phe
      20      25      30
Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala Ser
      35      40      45
Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile Leu
      50      55      60
His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro Trp
```

65					70					75					80
Ser	Met	Leu	Thr	Gly	Lys	Asp	Glu	Ser	Val	Ser	Leu	Ser	Gln	Ala	Val
				85					90					95	
Glu	Ala	Ile	Gly	Gln	Ala	Lys	Asn	Asn	Pro	Asn	Ile	Thr	Gly	Ile	Phe
			100					105					110		
Leu	Asp	Leu	Asp	Asn	Leu	Ser	Val	Gly	Met	Ala	Ser	Ala	Glu	Glu	Leu
		115					120				125				
Arg	Arg	Ala	Leu	Gln	Asp	Phe	Lys	Met	Ser	Gly	Lys	Phe	Val	Val	Ser
	130					135					140				
Tyr	Ala	Asp	Arg	Tyr	Thr	Gln	Lys	Gly	Tyr	Tyr	Leu	Ser	Ser	Ile	Ala
145					150				155					160	
Asp	Lys	Leu	Tyr	Leu	Asn	Pro	Lys	Gly	Met	Leu	Gly	Leu	Ile	Gly	Ile
			165					170						175	
Ala	Thr	Gln	Thr	Met	Phe	Tyr	Lys	Asp	Ala	Leu	Asp	Lys	Phe	Gly	Val
			180					185					190		
Lys	Met	Glu	Ile	Phe	Lys	Val	Gly	Thr	Tyr	Lys	Ala	Ala	Val	Glu	Pro
		195					200				205				
Phe	Met	Leu	Asn	Arg	Met	Ser	Asp	Ala	Asn	Arg	Glu	Gln	Ile	Thr	Thr
	210					215					220				
Tyr	Ile	Asn	Gly	Leu	Trp	Asp	Lys	Ile	Thr	Ser	Asp	Ile	Ala	Glu	Ser
225					230					235				240	
Arg	Lys	Thr	Ala	Met	Asp	Ser	Val	Lys	Met	Phe	Ala	Asp	Lys	Gly	Glu
			245					250						255	
Met	Phe	Gly	Leu	Ala	Glu	Lys	Ala	Val	Glu	Met	Lys	Leu	Val	Asp	Glu
		260					265						270		
Leu	Ala	Tyr	Arg	Thr	Asp	Val	Glu	Lys	Glu	Leu	Lys	Lys	Met	Ser	Gln
	275					280					285				
Arg	Gly	Glu	Lys	Asp	Glu	Leu	Arg	Phe	Val	Ser	Leu	Ser	Gln	Val	Leu
	290					295				300					
Ala	Asn	Gly	Pro	Met	Asn	Lys	Thr	Lys	Gly	Ser	Arg	Ile	Ala	Val	Leu
305					310					315				320	
Phe	Ala	Glu	Gly	Glu	Ile	Thr	Glu	Glu	Ile	Ile	Lys	Lys	Pro	Phe	Asp
			325					330						335	
Thr	Asp	Gly	Ser	Ser	Ile	Thr	Gln	Glu	Leu	Ala	Lys	Glu	Ile	Lys	Ala
		340					345					350			
Ala	Ala	Asp	Asp	Asp	Asp	Ile	Lys	Ala	Val	Val	Leu	Arg	Val	Asn	Ser
		355				360					365				
Pro	Gly	Gly	Ser	Ala	Phe	Thr	Ser	Glu	Gln	Ile	Trp	Lys	Gln	Val	Ala
	370					375					380				
Asp	Leu	Lys	Ala	Lys	Lys	Pro	Ile	Val	Val	Ser	Met	Gly	Asp	Val	Ala
385					390					395				400	
Ala	Ser	Gly	Gly	Tyr	Tyr	Ile	Ala	Cys	Ala	Ala	Asn	Ser	Ile	Val	Ala
			405					410						415	
Glu	His	Thr	Thr	Leu	Thr	Gly	Ser	Ile	Gly	Ile	Phe	Gly	Met	Phe	Pro
		420					425					430			
Asn	Phe	Ala	Gly	Val	Ala	Lys	Lys	Ile	Gly	Val	Asn	Met	Asp	Val	Val
	435					440					445				
Gln	Thr	Ser	Lys	Tyr	Ala	Asp	Leu	Gly	Asn	Thr	Phe	Ala	Pro	Met	Thr
	450				455					460					
Val	Glu	Asp	Arg	Ala	Leu	Ile	Gln	Arg	Tyr	Ile	Glu	Gln	Gly	Tyr	Asp
465					470					475				480	
Leu	Phe	Leu	Thr	Arg	Val	Ser	Glu	Gly	Arg	Asn	Arg	Thr	Lys	Ala	Gln
			485					490					495		
Ile	Asp	Ser	Ile	Ala	Gln	Gly	Arg	Val	Trp	Leu	Gly	Asp	Lys	Ala	Leu
		500					505					510			
Ala	Leu	Gly	Leu	Val	Asp	Glu	Leu	Gly	Gly	Leu	Asp	Thr	Ala	Ile	Lys
	515					520					525				
Arg	Ala	Ala	Lys	Leu	Ala	Gln	Leu	Gly	Gly	Asn	Tyr	Ser	Ile	Glu	Tyr
	530					535				540					
Gly	Lys	Thr	Lys	Arg	Asn	Phe	Phe	Glu	Glu	Leu	Leu	Ser	Ser	Ser	Ala
545					550					555				560	
Ala	Asp	Met	Lys	Ser	Ala	Ile	Leu	Ser	Thr	Ile	Leu	Ser	Asp	Pro	Glu
			565					570						575	
Ile	Glu	Val	Leu	Arg	Glu	Leu	Arg	Ser	Met	Pro	Pro	Arg	Pro	Ser	Gly
			580				585						590		
Ile	Gln	Ala	Arg	Leu	Pro	Tyr	Tyr	Phe	Met	Pro	Tyr				
	595					600									

(2) INFORMATION FOR SEQ ID NO:276

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

```
Leu Thr Leu Phe Cys Cys Asn Tyr Phe Lys Gln Met Arg Ala Asn Ile
1      5      10      15
Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe Phe Gly Thr Ala Ile
      20      25      30
Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu Ala Tyr Val Lys Gln
      35      40      45
Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg Tyr Asn Ile Pro Ala
      50      55      60
Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr Gly Ala Gly Ala Ser
      65      70      75      80
Thr Leu Ala Ser Val His Asn Asn His Phe Gly Ile Lys Cys His Lys
      85      90      95
Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp Asp Ala Pro Asn Glu
      100     105     110
Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser Tyr Glu Asp His Ser
      115     120     125
Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu Phe Lys Leu Asp Arg
      130     135     140
Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln Arg Cys Gly Tyr Ala
      145     150     155     160
Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys Met Val Glu Leu Tyr
      165     170     175
Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro Ser Trp Phe His Lys
      180     185     190
Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln Thr Thr Lys Gln Lys
      195     200     205
Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser Tyr Gly Leu Leu Tyr
      210     215     220
Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser Leu Ala Glu Glu Phe
      225     230     235     240
Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn Asp Ala Pro Val Asp
      245     250     255
Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu Glu Lys Lys His Ala
      260     265     270
Cys Ser Ile Ser Lys His Thr Gln His Val Val Arg Val Gly Asp Ser
      275     280     285
Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg Met Lys Asn Leu Tyr
      290     295     300
Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro Gln Glu Gly Asp Ile
      305     310     315     320
Leu Arg Leu Arg
```

(2) INFORMATION FOR SEQ ID NO:277

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

```
Arg Ile Pro Asp Glu Gln Thr Gly Arg Ile Met Asp Gly Arg Arg Tyr
1      5      10      15
Ser Asp Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Val
```


(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

```
Lys Ser Cys Arg Val Ile Gly Gln Thr Arg Arg Tyr Gly Cys Cys Pro
1      5      10      15
Val Gly Leu Arg Pro Cys His Gln Ser Leu Ser Gly Val Cys Arg Cys
20      25      30
Leu Phe Gln Ser Arg Pro Ala Val Ala Phe Ala Arg Lys Gly Gln Arg
35      40      45
Arg His Arg Arg Ser Glu Ser Gly Arg Arg Ile Arg Ala Leu Gln Gly
50      55      60
Val Gln His His Gln Thr Asn Glu His Glu Val Met Ile Ser Val Asn
65      70      75      80
Asn Leu Thr Val Asp Phe Gly Thr Arg Leu Leu Phe Asp Gln Val Ser
85      90      95
Phe Val Ile Asn Arg Arg Asp Arg Ile Ala Leu Val Gly Lys Asn Gly
100     105     110
Ala Gly Lys Ser Thr Leu Leu Lys Leu Ile Ala Gly Met Glu Glu Pro
115     120     125
Thr Ser Gly His Ile Ala Arg Pro Lys Gly Ile Arg Ile Gly Tyr Leu
130     135     140
Pro Gln Val Met Arg Leu Gln Asp Gly His Thr Val Tyr Glu Glu Val
145     150     155     160
Glu Gln Ala Phe Asn Asp Ile Arg Gln Ile Glu Glu Glu Ile Arg Arg
165     170     175
Leu Ser Asp Glu Met Ala Gly Arg Thr Asp Tyr Glu Ser Asp Asp Tyr
180     185     190
Ile Arg Leu Ile Glu His Tyr Thr Asn Met Ser Glu Thr Leu Ser Leu
195     200     205
Met Gln Gln Gly Asn Tyr His Ala Ala Ile Glu Gln Thr Leu Ile Gly
210     215     220
Leu Gly Phe Gly Arg Glu Asp Phe His Arg Pro Thr Ala Asp Phe Ser
225     230     235     240
Gly Gly Trp Arg Met Arg Ile Glu Leu Ala Lys Leu Leu Leu Gln Arg
245     250     255
Pro Glu Val Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ile Glu
260     265     270
Ser Ile Gly Trp Leu Glu Gln Phe Ile Ala Thr Asn Ala Gly Ala Val
275     280     285
Ile Leu Val Ser His Asp Arg Ala Phe Ile Asp Asn Thr Thr Thr Arg
290     295     300
Thr Ile Glu Ile Glu Leu Gly His Ile Tyr Asp Tyr Lys Thr Asn Tyr
305     310     315     320
Ser His Tyr Val Glu Leu Arg Glu Glu Arg Leu Arg Gln Gln Met Arg
325     330     335
Ala Tyr Glu Asn Gln Gln Lys Met Ile Arg Asp Thr Glu Asp Phe Ile
340     345     350
Glu Arg Phe Arg Tyr Lys Ala Thr Lys Ser Val Gln Val Gln Ser Arg
355     360     365
Ile Lys Gln Leu Glu Lys Val Glu Arg Val Glu Ile Asp Glu Arg Asp
370     375     380
Arg Ser Ala Phe His Phe Arg Phe Ile Pro Ala Gln Pro Ser Gly Ser
385     390     395     400
Tyr Pro Leu Ile Val Asp Asp Leu Ala Lys Ala Tyr Gly Asp His Gln
405     410     415
Val Phe Ser Gly Ala Thr Tyr Thr Ile Glu Arg Gly Glu Lys Val Ala
420     425     430
Phe Val Gly Lys Asn Gly Ala Gly Lys Ser Thr Met Val Lys Cys Ile
435     440     445
Met Gly Glu Leu Thr Asp Tyr Thr Gly Lys Leu Glu Glu Gly His Asn
450     455     460
Val Gln Leu Gly Tyr Phe Ala Gln Asn Glu Ala Gln Glu Leu Arg Gly
465     470     475     480
Asp Leu Thr Val Phe Asp Thr Ile Asp Arg Glu Ala Val Gly Asp Ile
485     490     495
Arg Leu Arg Leu Asn Asp Leu Leu Gly Ala Phe Leu Phe Gly Gly Glu
500     505     510
Ala Ser Glu Lys Lys Val Ser Val Leu Ser Gly Gly Glu Arg Ala Arg
515     520     525
Leu Ala Ile Ile Arg Leu Leu Gln Pro Ala Asn Phe Leu Ile Leu
530     535     540
```

```

Asp Glu Pro Thr Asn His Leu Asp Met Arg Ser Lys Asp Val Leu Lys
545          550          555          560
Glu Ala Ile Lys Asn Phe Asp Gly Thr Val Ile Val Val Ser His Asp
          565          570          575
Arg Glu Phe Leu Asp Gly Leu Val Ser Lys Val Tyr Glu Phe Ala Asp
          580          585          590
Gly Gln Val Asn Glu His Leu Gly Gly Ile Tyr Asp Tyr Leu Arg Thr
          595          600          605
Arg Arg Met Gln Thr Leu Thr Glu Leu Glu Arg Thr Thr Thr Ile Glu
610          615          620
Thr Lys Thr Thr Arg Glu Ala Ile Pro Glu Thr Glu Ala Lys Ala Asp
625          630          635          640
Tyr Arg Arg Gln Lys Glu Val Ala Lys Gln Leu Arg Thr Leu Glu Arg
          645          650          655
Thr Val Ala Thr Cys Glu Glu Arg Ile Gly Lys Leu Glu Ser Glu Leu
          660          665          670
Gln Ala Ile Glu Met Leu Leu Gln Asp Pro Lys His Ala Thr Asp Ala
675          680          685
Asn Leu Phe Glu Arg Tyr Ala Gly Met Lys Gln Glu Leu Glu Lys Ala
690          695          700
Met Glu Asp Trp Glu Gln Ala Ser Glu Ala Leu Ser Glu Ala Gln Gly
705          710          715          720

```

(2) INFORMATION FOR SEQ ID NO:279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

```

Tyr Leu Lys Leu Leu Ile Leu Gln Ile Ala Leu Met Asn Phe Leu Lys
1          5          10          15
Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr Leu Leu Leu Asp Thr
          20          25          30
Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val Ile Asn Leu Ala Asn
          35          40          45
Asn Leu His Ala Asn Gly His Arg Val Ser Leu Val Ser Val Cys Thr
50          55          60
Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys Gly Ile Glu Val His
65          70          75          80
His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu Ala Arg Lys Thr Val
          85          90          95
Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu Tyr Lys Lys Arg Glu
100          105          110
Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile Asn Thr Ile Leu Ser
115          120          125
Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile Gly Cys Glu His Ile
130          135          140
Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg Ile Arg Gly Phe Leu
145          150          155          160
Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr Lys Arg Asp Gln Gln
          165          170          175
Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys Ala Tyr Val Ile Pro
180          185          190
Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp Ala Thr Thr His Lys
195          200          205
Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln Lys Gly Phe Glu Phe
210          215          220
Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu Arg Pro Asp Trp Lys
225          230          235          240
Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser Met Leu Arg Lys Glu
          245          250          255
Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu Ile His Pro Ser Thr
260          265          270

```

```

Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala Ile Tyr Leu Met Thr
  275                280                285
Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu Glu Ala Glu Ala Tyr
  290                295                300
Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr Gly Pro Arg Glu Leu
  305                310                315                320
Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro Met Glu Ala His Glu
  325                330                335
Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp Asp Glu Thr Leu Arg
  340                345                350
Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val Lys Ser Tyr Ser Pro
  355                360                365
Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe Val Glu Ile Gly Tyr
  370                375                380
Met Asn
385

```

(2) INFORMATION FOR SEQ ID NO:280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

```

Thr Thr Lys Glu Asn Glu Thr Thr Thr Lys Asn Glu Tyr Arg Ile Met
1          5          10          15
Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val Ser
  20          25          30
Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly Lys
  35          40          45
Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg Lys
  50          55          60
Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys Thr
  65          70          75          80
Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val Ser
  85          90          95
Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn Asn
  100         105         110
Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu Ile
  115         120         125
Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr Leu
  130         135         140
Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe Asn
  145         150         155         160
Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly Leu
  165         170         175
Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr
  180         185         190
Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp Leu
  195         200         205
Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly Val
  210         215         220
Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp Asp
  225         230         235         240
Phe Asp His Val Ile Ile Asp Trp Leu Ala Glu Glu Phe Lys Ser Gln
  245         250         255
Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu Lys
  260         265         270
Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser Thr
  275         280         285
Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys His
  290         295         300
Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp Arg
  305         310         315         320

```

Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp Ala
 325 330 335
 Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly Ser
 340 345 350
 Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly Lys
 355 360 365
 Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala
 370 375 380
 Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu Leu
 385 390 395 400
 Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly Val
 405 410 415
 Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys Ser
 420 425 430
 Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile His
 435 440 445
 Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile Gly
 450 455 460
 Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro Gln
 465 470 475 480
 Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Thr
 485 490 495
 Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu Ala
 500 505 510
 Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu Ala
 515 520 525
 Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp Lys
 530 535 540
 Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu Lys
 545 550 555 560
 Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp Thr
 565 570 575
 Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala Ala
 580 585 590
 Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala Gly
 595 600 605
 Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln Pro
 610 615 620
 Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln Pro
 625 630 635 640
 Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys
 645 650 655

(2) INFORMATION FOR SEQ ID NO:281

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

Lys Trp Ala Arg Thr Thr Thr Leu Arg Ile Ser Asn Ala Thr Ile Tyr
 1 5 10 15
 Lys Thr Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly
 20 25 30
 Tyr Thr Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu
 35 40 45
 Ile Glu Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile
 50 55 60
 Pro Thr Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala
 65 70 75 80
 Thr Ala Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu
 85 90 95
 Gly Lys Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala
 100 105 110

Gly Ile Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala
 115 120 125
 Glu Ala Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr
 130 135 140
 Ala Gly Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly
 145 150 155 160
 Ser Glu Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr
 165 170 175
 Trp Thr Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu
 180 185 190
 Val Ile Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe
 195 200 205
 Asn Gly Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile
 210 215 220
 Leu Asn Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr
 225 230 235 240
 Glu Lys Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val
 245 250 255
 Arg Asn Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile
 260 265 270
 Glu Gly Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln
 275 280 285
 Gly Phe Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr
 290 295 300
 Asn Glu Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp
 305 310 315 320
 Ile Thr Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu
 325 330 335
 Val Ala Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr
 340 345 350
 Arg Ala Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val
 355 360 365
 Gly Glu Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val
 370 375 380
 Arg Arg Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu
 385 390 395 400
 Gln Gly Asn Gly Glu Cys Lys Leu Leu Leu Asp Glu Glu Asn Arg Leu
 405 410 415
 Ile Gly Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr
 420 425 430
 Ala Ala Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg
 435 440 445
 Ile Ile Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu
 450 455 460
 Ala Gly Gly
 465

(2) INFORMATION FOR SEQ ID NO:282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

Pro Lys Ile Leu Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu
 1 5 10 15
 Leu Val Gly Phe Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro
 20 25 30
 Leu Pro Thr Asp Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu
 35 40 45
 Thr Tyr Phe Ile Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe
 50 55 60
 Phe Ile Ala Gln Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser
 65 70 75 80

Gly Leu Ala His Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn
 85 90 95
 Phe Pro Gly Lys Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg
 100 105 110
 Phe Gly Gln Asn Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr
 115 120 125
 Thr Ile Met Asp Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys
 130 135 140
 Leu Leu Ile Leu His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His
 145 150 155 160
 Glu Ile Asp Glu Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg
 165 170 175
 Arg Asp Ala Asn Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met
 180 185 190
 Pro Gly Asn Lys Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val
 195 200 205
 Val Leu Asn Phe Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp
 210 215 220
 Tyr Arg Pro Asp Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val
 225 230 235 240
 Asp Tyr Val Glu Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala
 245 250 255
 Pro Val Asn Pro Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp
 260 265 270
 Glu Pro Ile Val Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln
 275 280 285
 Leu Ser Ile Ser Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly
 290 295 300
 Ser Ile Phe Gly Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr
 305 310 315 320
 Ala Val Asn Glu Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro
 325 330 335
 Phe Leu Ser Ala Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln
 340 345 350
 Thr Lys Asp Ala Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala
 355 360 365
 Glu Lys Ala Met Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln
 370 375 380
 Phe Gly Ile Thr Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu
 385 390 395 400
 Lys Arg Tyr Glu Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn
 405 410 415
 Ala Tyr Ala Asn Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile
 420 425 430
 Pro Gly Ile Glu Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln
 435 440 445
 Val Pro Leu Glu Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro
 450 455 460
 Val Lys Asn Ala Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala
 465 470 475 480
 Lys Ile Pro Ser Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg
 485 490 495
 Gln Gln Lys Val Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu
 500 505 510
 Met Glu Lys Ala Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp
 515 520 525
 Gln Lys Phe Gly Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val
 530 535 540
 Tyr Leu Lys Lys Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala
 545 550 555 560
 Leu Ser Pro Gly Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser
 565 570 575
 Val Met Asn Ser Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala
 580 585 590
 Ile Gln Leu Asp Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro
 595 600 605
 Ser Leu Ser Leu Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu
 610 615 620
 Asp Met Glu Thr Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn
 625 630 635 640
 Arg Lys Asp Pro Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn
 645 650 655
 Asn Leu Lys Asn Gln Glu Ala Asn Pro Met Ala Ala Leu Met Asp Ser
 660 665 670
 Ile Arg His Thr Met Tyr Gly Asp Asn Pro Met Met Lys Pro Met Lys
 675 680 685
 Ala Ala Asp Val Glu Lys Val Asn Tyr Asp Gln Val Met Ala Phe Tyr

690	695	700
Asn Glu Arg Phe Ala Asp	Ala Gly Asp Phe Met	Phe Phe Phe Ile Gly
705	710	715
Asn Leu Asp Glu Ala Lys	Met Lys Pro Leu Ile	Glu Thr Tyr Leu Ala
720	725	730
Ser Leu Pro Asn Leu Lys	Arg Gly Asp Lys Met	Asn Lys Ala Gln Val
735	740	745
Pro Ala Ala Arg Ser Gly	Lys Ile Asp Cys Lys	Phe Glu Lys Glu Met
750	755	760
Asp Thr Pro Ser Thr Thr	Ile Phe Asp Val Val	Ser Gly Asn Val Glu
765	770	775
Tyr Thr Leu Lys Asn Ser	Leu Leu Leu Glu Val	Phe Ser Ala Val Met
780	785	790
Asp Gln Val Tyr Thr Ala	Thr Val Arg Glu Lys	Glu Gly Gly Ala Tyr
795	800	805
Ser Val Ala Ala Phe Gly	Gly Leu Glu Gln Tyr	Pro Gln Pro Lys Ala
810	815	820
Leu Met Gln Ile Tyr Phe	Pro Thr Asp Pro Ala	Arg Ala Glu Glu Met
825	830	835
Asn Ala Ile Val Phe Ala	Glu Leu Glu Lys Leu	Ala Lys Glu Gly Pro
840	845	850
Asn Val Glu Tyr Phe Lys	Thr Ile Glu Asn Leu	Asn Lys Gln His
855	860	865
Lys Glu Ser Leu Arg Glu	Asn Arg Phe Trp Leu	Glu Ala Met Lys Ala
870	875	880
Ser Phe Phe Glu Gly Asn	Asp Phe Ile Thr Asp	Tyr Glu Ser Val Leu
885	890	895
Asn Gly Leu Thr Pro Ala	Glu Leu Gln Lys Phe	Ala Ala Asp Leu Leu
900	905	910
Lys Gln Gln Asn Arg Val	Val Val Met Met Ala	Pro Val Ala Lys Ala
915	920	925
Gln	930	935
940	945	

(2) INFORMATION FOR SEQ ID NO:283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

Tyr Thr Met Ser Lys Lys Gly Thr Ile Gly Val Thr Ser Asp Asn Ile	1	5	10	15
Phe Pro Val Ile Lys Lys Phe Leu Tyr Ser Asp His Glu Ile Phe Leu	20	25	30	
Arg Glu Ile Val Ser Asn Ala Val Asp Ala Thr Gln Lys Leu Lys Thr	35	40	45	
Leu Thr Ser Val Gly Glu Phe Lys Gly Glu Thr Gly Asp Leu Arg Val	50	55	60	
Thr Val Ser Val Asp Glu Val Ala Arg Thr Ile Thr Val Ser Asp Arg	65	70	75	80
Gly Val Gly Met Thr Glu Glu Glu Val Glu Lys Tyr Ile Asn Gln Ile	85	90	95	
Ala Phe Ser Ser Ala Glu Glu Phe Leu Glu Lys Tyr Lys Asp Asp Lys	100	105	110	
Ala Ala Ile Ile Gly His Phe Gly Leu Gly Phe Tyr Ser Ala Phe Met	115	120	125	
Val Ser Glu Arg Val Asp Val Ile Thr Arg Ser Phe Arg Glu Asp Ala	130	135	140	
Thr Ala Val Lys Trp Ser Cys Asp Gly Ser Pro Glu Tyr Thr Leu Glu	145	150	155	160
Pro Ala Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp	165	170	175	
Glu Glu Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu				

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

```
Asp Ile Arg Gln Lys Arg Pro Cys Phe Asn Ala Asn Leu Tyr Phe Tyr
1      5      10      15
Arg Ala Met Glu Lys Leu Ile Asp Ile Leu Val Val Asp Asp Asp Val
20      25      30
Ala Val Cys Ala Ala Leu Arg Leu Val Leu Lys Arg Ala Gly Tyr Asn
35      40      45
Pro Val Ile Ala Asn Ser Pro Asp Glu Ala Leu Ser Ile Met Arg Asn
50      55      60
Pro Asp Gly Gly Cys Lys Pro Ala Val Ile Leu Met Asp Met Asn Phe
65      70      75      80
Ser Leu Ser Thr Ser Gly Arg Glu Gly Leu Glu Leu Leu Glu Lys Met
85      90      95
Gln Ile Phe Thr Ser Cys Pro Val Ile Leu Met Thr Ala Trp Ala Ser
100      105      110
Ile Pro Leu Ala Val Glu Gly Met Arg Leu Gly Ala Phe Asp Phe Ile
115      120      125
Gly Lys Pro Trp Asp Asn Asp Arg Leu Leu Arg Thr Ile Asp Thr Ala
130      135      140
Leu His Leu Ala Ala Pro Ser Ala Val Ala Asn Pro Ser Glu Gln Ser
145      150      155      160
Asp Arg Asp Thr Ala Arg Gln Pro Lys Ala Thr Val Gln Glu Asn Asp
165      170      175
Pro Cys Ala His Ile Ile Gly Arg Ser Asp Ala Ile Cys Lys Ile Lys
180      185      190
Glu Arg Ile Arg Arg Ile Ala Pro Thr His Ala Ser Val Leu Ile Thr
195      200      205
Gly Glu Ser Gly Thr Gly Lys Glu Leu Ile Ala Glu Ala Leu His Arg
210      215      220
Gly Ser Lys Arg Ala Ser Ala Pro Phe Val Lys Val Asn Leu Gly Gly
225      230      235      240
Ile Pro Glu Ser Leu Phe Glu Ser Glu Leu Phe Gly His Lys Lys Gly
245      250      255
Ala Phe Thr Asn Ala Phe Ser Asp Arg Lys Gly Arg Phe Glu Leu Ala
260      265      270
Asp Gly Gly Thr Ile Phe Leu Asp Glu Ile Gly Glu Leu Pro Val Gly
275      280      285
Asn Gln Val Lys Leu Leu Arg Val Leu Gln Glu Gln Thr Phe Glu Pro
290      295      300
Leu Gly Glu Ser Val Ser His Arg Val Asp Ile Arg Val Val Ser Ala
305      310      315      320
Thr Asn Ala Ser Leu Glu Arg Met Val Ala Glu Gly Arg Phe Arg Glu
325      330      335
Asp Leu Tyr Tyr Arg Ile Asn Leu Ile His Leu His Leu Pro Pro Leu
340      345      350
Arg Glu Arg Gln Glu Asp Ile Gln Leu Leu Val Glu Ala Phe Ser Glu
355      360      365
Ala Phe Ala Gln Ser Asn Gly Leu Pro His Ala Val Trp Ser Ala Glu
370      375      380
Ala Met Arg Arg Ile Cys Ala Met Pro Leu Pro Gly Asn Val Arg Glu
385      390      395      400
Leu Lys Asn Val Val Glu Arg Thr Leu Leu Leu Ser Gly Ser Arg Glu
405      410      415
Ile Ser Ala Arg Asp Val Ala Asp Phe Gly Ser Gln Val Thr Ala Ala
420      425      430
Asp His Ser Asp Glu Arg Ala Leu Thr Asp Met Glu Glu Ala Ala Ile
435      440      445
Arg Glu Thr Leu Thr Lys Tyr Asn Gly Asn Val Ser Arg Ala Ala Arg
450      455      460
Ala Leu Gly Leu Ser Arg Ala Ala Leu Tyr Arg Arg Met Glu Lys Tyr
465      470      475      480
Gly Leu
```

(2) INFORMATION FOR SEQ ID NO:285

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

```

Arg Ser Leu Gln Ser Phe Gln Asn Lys Lys His Ser Ser Met Leu Lys
1      5      10      15
Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile Leu Lys Gly
      20      25      30
Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile Met Gly Pro
      35      40      45
Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val Gly His Pro
      50      55      60
Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly Ile Asp Leu
      65      70      75      80
Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu Phe Leu Ser
      85      90      95
Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val Asn Phe Met
      100     105     110
Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala Glu Pro Val
      115     120     125
Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg Ala Ile Val
      130     135     140
Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu Gly Phe Ser
      145     150     155     160
Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala Met Leu Glu
      165     170     175
Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu Asp Ile Asp
      180     185     190
Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg Ser Pro Glu
      195     200     205
Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu Glu Tyr Ile
      210     215     220
Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile Val Lys Ser
      225     230     235     240
Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly Tyr Asp Trp
      245     250     255
Ile Lys Glu Glu Ile Gly Glu
      260

```

(2) INFORMATION FOR SEQ ID NO:286

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

```

Ser Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr
1      5      10      15
Lys Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn
      20      25      30
Cys Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala
      35      40      45
Ala Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu
      50      55      60
Gln Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu

```

```

65          70          75          80
Glu Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val
85          90          95
Leu Leu Gly Gly Glu Pro Gly Ile Gly Lys Ser Thr Leu Ile Leu Gln
100         105         110
Thr Val Leu Arg Leu Pro Gln Leu Arg Thr Leu Tyr Val Ser Gly Glu
115         120         125
Glu Ser Ala Arg Gln Leu Lys Met Arg Ala Glu Arg Leu Gly Gln Ala
130         135         140
Met Asn Gly Cys Tyr Val Tyr Cys Glu Thr Asn Ile Glu Arg Ile Leu
145         150         155
Ser Arg Ala Glu Glu Leu Thr Pro Asp Leu Leu Val Ile Asp Ser Ile
165         170         175
Gln Thr Val Tyr Thr Glu Glu Met Glu Ser Ser Ala Gly Ser Val Gly
180         185         190
Gln Ile Arg Glu Cys Ala Ala Leu Leu Leu Lys Tyr Cys Lys Thr Thr
195         200         205
Gly Ile Pro Val Ile Val Ile Gly His Ile Thr Lys Glu Gly Ser Ile
210         215         220
Ala Gly Pro Lys Val Leu Glu His Ile Val Asp Thr Val Leu Leu Phe
225         230         235
Asp Gly Asp Lys His His Leu Tyr Arg Ile Leu Arg Gly Gln Lys Asn
245         250         255
Arg Tyr Gly Ser Thr Ser Glu Leu Gly Ile Tyr Glu Met Arg Gln Asp
260         265         270
Gly Leu Arg Gly Val Glu Asn Pro Ser Glu His Leu Ile Thr Arg Asn
275         280         285
Arg Glu Asp Leu Ser Gly Ile Ala Ile Ala Val Ala Met Glu Gly Ile
290         295         300
Arg Pro Ile Leu Ile Glu Ala Gln Ala Leu Val Ser Ser Ala Ile Tyr
305         310         315
Ala Asn Pro Gln Arg Ser Ala Thr Gly Phe Asp Ile Arg Arg Met Asn
325         330         335
Met Leu Leu Ala Val Leu Glu Lys Arg Ala Gly Phe Lys Leu Ile Gln
340         345         350
Lys Asp Val Phe Leu Asn Ile Ala Gly Gly Ile Lys Ile Ala Asp Pro
355         360         365
Ala Thr Asp Leu Ala Val Ile Ser Ala Val Leu Ala Ser Ser Leu Asp
370         375         380
Ile Val Ile Pro Pro Ala Val Cys Met Thr Gly Glu Val Gly Leu Ser
385         390         395
Gly Glu Ile Arg Pro Val Ser Arg Ile Glu Gln Arg Ile Thr Glu Ala
405         410         415
Arg Arg Ile Gly Phe Lys Glu Ile Leu Val Pro Ala Asp Asn Phe Arg
420         425         430
Gln Glu Asp Ala Gly Arg Phe Gly Ile Arg Leu Val Pro Val Arg Lys
435         440         445
Val Glu Glu Ala Phe Arg His Leu Phe Ser Lys Gly Arg Glu
450         455         460

```

(2) INFORMATION FOR SEQ ID NO:287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

```

Gly Ser Cys Gly Ser Ser Pro Ala Ile Gly Arg Ser Gly Cys Ser Arg
1          5          10          15
Cys Asp Arg Arg Ile Gly His Gly Leu Ser Thr Ser Ala Phe Arg Thr
20         25         30
Tyr Ala Gly Leu Val Cys His Ser Arg Leu Arg Asp Gln Ser Ser Cys
35         40         45
Arg Val Cys Gly Met Arg Pro Ile Gly Gln Leu Phe Phe Pro Ser Cys

```

```

      50              55              60
Pro Arg Arg Ser Ala Ser Asp Ala Gly Arg Thr Glu Arg Ile Gln Ser
65              70              75              80
Pro Leu Gln Asn Leu Leu Gln Glu Met Gln Phe Ser Pro Thr Asn Arg
      85              90              95
Arg Asn Pro Phe Asp Asn Met Asn Ser Arg His Leu Thr Ile Thr Ile
      100              105              110
Ile Ala Gly Leu Ser Leu Phe Val Leu Thr Leu Gly Gly Cys Ser Val
      115              120              125
Ala Gln Gln Asp Thr Gln Trp Thr Leu Gly Gly Lys Leu Phe Thr Ser
      130              135              140
Ala Trp Ile Gln Arg Ser Ala Glu Tyr Gln Ala Leu Cys Ile Gln Ala
      145              150              155              160
Tyr Asn Ile Ala Thr Glu Arg Val Asp Ala Leu Pro Ala Glu Arg Lys
      165              170              175
Gln Gly Asp Arg Pro Tyr Ala Ile Val Thr Asp Ile Asp Glu Thr Ile
      180              185              190
Leu Asp Asn Thr Pro Asn Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp
      195              200              205
Tyr Asp Glu Glu Thr Trp Gly Lys Trp Cys Ala Gln Ala Asp Ala Asp
      210              215              220
Thr Leu Ala Gly Ala Leu Ser Phe Phe Leu His Ala Ala Asn Lys Gly
      225              230              235              240
Ile Glu Val Phe Tyr Val Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala
      245              250              255
Thr Leu Gln Asn Leu Gln Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu
      260              265              270
His Leu Leu Thr Thr His Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu
      275              280              285
Lys Ile Gln Glu Gln Tyr Glu Ile Val Leu Leu Ile Gly Asp Asn Leu
      290              295              300
Gly Asp Phe His His Phe Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys
      305              310              315              320
Gln Ala Leu Gly Leu Thr Ala Gly Glu Phe Gly Arg His Phe Ile Met
      325              330              335
Leu Pro Asn Pro Asn Tyr Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly
      340              345              350
Lys Tyr Pro Pro Leu Pro Glu Arg Asp Lys Ala Leu Lys Gln Leu His
      355              360              365
Ser Gln Asn Ser Arg
      370

```

(2) INFORMATION FOR SEQ ID NO:288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

```

Arg Trp Gly Phe Ser Asn Phe Val Ala Met Ser Thr Asn Ile Asp Val
1              5              10              15
Gln Gln Ile Lys Gln Arg Phe Gly Ile Ile Gly Ser Ser Pro Leu Met
      20              25              30
Glu His Ala Ile Arg Val Ala Ala Gln Val Ala Pro Thr Asp Met Ser
      35              40              45
Val Leu Val Thr Gly Glu Ser Gly Ser Gly Lys Glu Phe Phe Pro Gln
      50              55              60
Ile Ile His Tyr Tyr Ser Ala Arg Lys His His Ser Tyr Ile Ala Val
      65              70              75              80
Asn Cys Gly Ala Ile Pro Glu Gly Thr Ile Asp Ser Glu Leu Phe Gly
      85              90              95
His Arg Lys Gly Ser Phe Thr Gly Ala Val Ser Asp Arg Lys Gly Tyr
      100              105              110
Phe Glu Glu Ala Ser Gly Gly Thr Ile Phe Leu Asp Glu Val Gly Glu

```

115	120	125
Leu Pro Leu Pro Thr Gln Ala Arg Leu Leu Arg Val Leu Glu Thr Gly		
130	135	140
Glu Phe Ile Pro Val Gly Ala Ser Gln Ser Gln Lys Thr Asp Val Arg		
145	150	155
Ile Val Ala Ala Thr Asn Val Asn Leu Lys Glu Ala Val Ala Asn Gly		160
	165	170
Lys Phe Arg Glu Asp Leu Phe Phe Arg Leu Asn Thr Val Pro Ile Glu		175
	180	185
Val Pro Ala Leu Arg Met Arg Pro Asp Asp Val Pro Leu Leu Phe Arg		190
	195	200
Arg Phe Ala Ala Asp Ser Ala Glu Lys Tyr Arg Met Pro Pro Leu Arg		205
	210	215
Leu Ser Asp Glu Ala Arg Thr Ile Leu Met Arg Tyr Arg Trp Pro Gly		220
225	230	235
Asn Val Arg Glu Leu Arg Asn Ile Thr Asp Arg Leu Ser Ile Leu Glu		240
	245	250
Glu Glu Arg Thr Val Ser Ala Glu Thr Ile Thr Arg Tyr Leu Asp Ala		255
	260	265
Glu Gly Met Gln Asp Leu His Pro Val Val Ile Arg Arg Asn Glu Thr		270
	275	280
Thr Glu Ala Asp Lys Gln Ile Pro His Tyr Glu Arg Glu Ile Ile Tyr		285
	290	295
Gln Val Leu Tyr Asp Met Lys Lys Glu Ile Ala Asp Leu Lys Gly Met		300
305	310	315
Met Asn Arg Leu Ala His His Glu Gln Pro Ser Trp Pro Val Gly Ser		320
	325	330
Asp Val Trp Gly Asn Asp Asp Lys Arg Thr Ala Asp Pro Lys Trp Gly		335
	340	345
Val Ser Thr His Lys Ala Pro Ile Ala Asn Ala Ala Glu Pro Val Glu		350
	355	360
Pro Ile Gln Glu Ala Ser Glu Tyr Thr Glu Asp Pro Val Ser Leu Glu		365
	370	375
Glu Val Glu Lys Lys Met Ile Ser Leu Ala Leu Glu Arg His Gly Gly		380
385	390	395
Arg Arg Lys Gln Thr Ala Glu Glu Leu Lys Ile Ser Glu Arg Thr Leu		400
	405	410
Tyr Arg Lys Ile Lys Glu Tyr Gly Leu Glu		415
	420	425

(2) INFORMATION FOR SEQ ID NO:289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

Lys Asn Leu Pro Arg Tyr Ala Pro Ala Phe Gly Arg Asn Arg Lys Arg	
1	5
Glu Gln Pro Asp Pro Asp Asn Asp Asp Ser Arg Gly Arg Ser His Arg	10
	15
	20
Gln Ser Gly Arg Ala Val Thr Val Val Cys Arg Arg Ile Gln Thr Pro	25
	30
	35
Leu Pro His Met Ile Leu Leu Phe Gly Gly Thr Thr Glu Gly Arg Ala	40
	45
	50
Ala Ala Arg Val Leu Asp Glu Ala Gly Ser Pro Phe Phe Tyr Ser Thr	55
	60
	65
Lys Gly Asn Leu Gln Glu Ile Gln Ser Ser His Gly His Arg Leu Thr	70
	75
	80
	85
Gly Ala Met Thr Val Ala Asp Met Val Ser Phe Cys Arg Lys Glu Glu	90
	95
	100
Ile Arg Leu Ile Val Asp Ala Ala His Pro Phe Ala Glu Leu His	105
	110
	115
Ala Ser Val Ala Glu Ala Ser Glu Gln Thr Gly Ile Pro Val Val Arg	120
	125

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

```
Gln Gln Arg Pro His Arg Ile Ile Met Leu Arg Thr Phe Arg Ile Gly
1      5      10      15
Gly Ile His Pro Pro Glu Asn Lys Leu Ser Ala Gly Lys Pro Val Glu
      20      25      30
Val Leu Pro Ile Pro Ser Gln Val Val Ile Pro Leu Gly Gln His Ile
      35      40      45
Gly Ala Pro Ala Thr Ala Thr Val Lys Lys Gly Asp Glu Val Lys Val
      50      55      60
Gly Thr Ile Ile Ala Gln Ala Gly Gly Phe Val Ser Ala Asn Ile His
65      70      75      80
Ser Ser Val Ser Gly Lys Val Leu Lys Ile Asp Asn Val Tyr Asp Ser
      85      90      95
Ser Gly Tyr Pro Lys Pro Ala Val Phe Ile Ser Val Glu Gly Asp Glu
      100     105     110
Trp Glu Glu Gly Ile Asp Arg Ser Pro Ala Ile Val Lys Glu Cys Asn
      115     120     125
Leu Asp Ala Lys Glu Ile Val Ala Lys Ile Ser Ala Ala Gly Ile Val
      130     135     140
Gly Leu Gly Gly Ala Thr Phe Pro Thr His Val Lys Leu Ser Pro Pro
145     150     155     160
Pro Gly Asn Lys Ala Glu Ile Leu Ile Ile Asn Ala Val Glu Cys Glu
      165     170     175
Pro Tyr Leu Thr Ser Asp His Val Leu Met Leu Glu His Gly Glu Glu
      180     185     190
Ile Met Ile Gly Val Ser Ile Leu Met Lys Ala Ile Gln Val Asn Lys
      195     200     205
Ala Val Ile Gly Val Glu Asn Asn Lys Lys Asp Ala Ile Ala His Leu
      210     215     220
Thr Lys Leu Ala Thr Ala Tyr Pro Gly Ile Glu Val Met Pro Leu Lys
225     230     235     240
Val Gln Tyr Pro Gln Gly Gly Glu Lys Gln Leu Ile Asp Ala Val Ile
      245     250     255
Arg Lys Gln Val Lys Ser Gly Ala Leu Pro Ile Ser Thr Gly Ala Val
      260     265     270
Val Gln Asn Val Gly Thr Val Phe Ala Val Tyr Glu Ala Val Gln Lys
      275     280     285
Asn Lys Pro Leu Val Glu Arg Ile Val Thr Val Thr Gly Lys Lys Leu
      290     295     300
Ser Arg Pro Ser Asn Leu Leu Val Arg Ile Gly Thr Pro Ile Ala Ala
305     310     315     320
Leu Ile Glu Ala Ala Gly Gly Leu Pro Glu Asn Thr Gly Lys Ile Ile
      325     330     335
Gly Gly Gly Pro Met Met Gly Arg Ala Leu Leu Ser Pro Asp Val Pro
      340     345     350
Val Thr Lys Gly Ser Ser Gly Val Leu Ile Leu Asp Arg Glu Glu Ala
      355     360     365
Val Arg Lys Pro Met Arg Asp Cys Ile Arg Cys Ala Lys Cys Val Gly
      370     375     380
Val Cys Pro Met Gly Leu Asn Pro Ala Phe Leu Met Arg Asp Thr Leu
385     390     395     400
Tyr Lys Ser Trp Glu Thr Ala Glu Lys Gly Asn Val Val Asp Cys Ile
      405     410     415
Glu Cys Gly Ser Cys Ser Phe Thr Cys Pro Ala Asn Arg Pro Leu Leu
      420     425     430
Asp Tyr Ile Arg Gln Ala Lys Lys Thr Val Met Gly Ile Gln Arg Ala
      435     440     445
Arg Lys Gln
450
```

(2) INFORMATION FOR SEQ ID NO:291

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

Met	Asn	Ser	Gln	Lys	Lys	Glu	Ala	Phe	Asn	Met	Lys	Arg	Ile	Gln	Leu
1				5					10					15	
Thr	Leu	Ile	Ala	Leu	Phe	Ala	Ala	Val	Ala	Gly	Leu	Val	Ala	Gln	Asn
			20					25					30		
Ala	Tyr	Glu	Gly	Val	Ile	Ser	Tyr	Lys	Ile	Ser	Leu	Asp	Lys	Thr	Gly
		35					40					45			
Asn	Lys	Val	Val	Leu	Asn	Gly	Ala	Ala	Asp	Met	Ser	Asn	Leu	Lys	Leu
50						55					60				
Lys	Ser	Thr	Gln	Met	Ile	Val	Thr	Pro	Ile	Leu	Arg	Ser	Glu	Asp	
65				70					75					80	
Gly	Thr	Ser	Arg	Val	Glu	Phe	Pro	Ser	Val	Val	Ile	Thr	Gly	Arg	Asn
			85						90					95	
Arg	Thr	Lys	Ala	Leu	Lys	Arg	Glu	Ile	Ala	Phe	Ser	Ser	Ala	Leu	Pro
			100					105					110		
Gln	Ala	Lys	His	Ala	Ala	Gln	Tyr	Ile	Arg	Arg	His	Asn	Gly	Lys	Ser
		115					120					125			
Glu	Gln	Phe	Ala	Phe	Thr	Gly	Glu	His	Ala	Tyr	Ala	Ser	Trp	Met	Met
130						135					140				
Asp	Ala	Lys	Phe	Val	Val	Arg	Glu	Glu	Val	Arg	Gly	Cys	Ala	Lys	Cys
145				150						155				160	
Pro	Val	Gly	Leu	Ser	Ser	Asn	Ile	Val	Pro	Phe	Asp	Pro	Leu	Phe	Asn
			165						170					175	
Pro	Ala	Glu	Ala	Pro	Tyr	Leu	Leu	Ala	His	Ile	Thr	Pro	Ala	Glu	Glu
			180					185					190		
Val	Glu	Lys	Gln	Arg	Glu	Ser	Ser	Phe	Asp	Ala	Tyr	Ile	Asn	Phe	Lys
			195					200				205			
Val	Asn	Lys	Ala	Asp	Val	Leu	Pro	Glu	Tyr	Arg	Asn	Asn	Lys	Ala	Glu
210						215					220				
Leu	Glu	Lys	Ile	Lys	Glu	Phe	Val	Ser	Thr	Val	Lys	Ala	Asn	Pro	Asn
225					230					235				240	
Tyr	Ser	Val	Asn	Lys	Met	Ile	Ile	Glu	Gly	Phe	Ala	Ser	Pro	Glu	Ala
			245						250					255	
Ser	Ile	Ala	His	Asn	Lys	Ala	Leu	Ser	Glu	Arg	Arg	Ala	Lys	Arg	Leu
			260					265					270		
Ala	Glu	Glu	Leu	Val	Arg	Lys	Tyr	Gly	Lys	Thr	Leu	Pro	Asn	Ile	Thr
		275					280					285			
Thr	Glu	Phe	Gly	Gly	Glu	Asp	Trp	Lys	Gly	Leu	Lys	Leu	Ala	Ile	Glu
290						295					300				
Lys	Ser	Asp	Ile	Ala	Asp	Arg	Asp	Arg	Val	Leu	Glu	Ile	Ile	Asn	Ser
305					310					315				320	
Asp	Lys	Tyr	Ala	Asp	Asp	Ala	Arg	Glu	Gln	Ala	Leu	Lys	Gln	Leu	
			325						330					335	
Ser	Ser	Tyr	Arg	Tyr	Ile	Leu	Asp	Gln	Ile	Tyr	Pro	Asn	Leu	Arg	Arg
			340					345					350		
Asn	Thr	Ile	Thr	Met	Gly	Tyr	Ile	Val	Arg	Asp	Tyr	Thr	Leu	Glu	Glu
			355				360					365			
Ala	Arg	Glu	Ile	Ile	Lys	Thr	Ala	Pro	Lys	Glu	Leu	Ser	Glu	Ala	Glu
370						375					380				
Met	Tyr	Arg	Val	Ala	Met	Ser	Tyr	Pro	Glu	Gly	His	Gln	Glu	Arg	Leu
385					390					395				400	
Phe	Ala	Leu	Asn	Thr	Thr	Leu	Lys	Tyr	Phe	Pro	Glu	Ser	Val	Thr	Gly
			405						410					415	
Arg	Ile	Asn	Leu	Ala	Val	Ala	Ala	Phe	Asn	Gly	Gly	Asp	Val	Gln	Gln
			420					425					430		
Ala	Ile	Ala	Leu	Leu	Ser	Pro	Ile	Gln	Thr	Glu	Lys	Gly	Val	Ser	Asn
		435					440					445			
Ile	Leu	Gly	Ala	Ala	Tyr	Ala	Arg	Thr	Gly	Asp	Phe	Ala	Arg	Ala	Glu
450						455					460				
Thr	Phe	Phe	Arg	Lys	Ala	Val	Ala	Glu	Gly	Asp	Ala	Asn	Ala	Gln	Arg
465					470					475				480	
Asn	Leu	Asp	Met	Leu	Leu	Gly	Lys	Lys							
				485											

(2) INFORMATION FOR SEQ ID NO:292

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

Asp	Met	Ala	Glu	Lys	Arg	Asp	Tyr	Tyr	Glu	Val	Leu	Gly	Val	Ser	Lys
1			5					10						15	
Asn	Ala	Thr	Asp	Asp	Glu	Leu	Lys	Lys	Ala	Tyr	Arg	Lys	Lys	Ala	Ile
		20					25						30		
Gln	Tyr	His	Pro	Asp	Lys	Asn	Pro	Gly	Asp	Lys	Glu	Ala	Glu	Glu	His
		35				40						45			
Phe	Lys	Glu	Val	Ala	Glu	Ala	Tyr	Asp	Val	Leu	Ser	Asp	Pro	Gln	Lys
	50					55				60					
Arg	Ser	Gln	Tyr	Asp	Gln	Phe	Gly	His	Ala	Gly	Leu	Gly	Gly	Ala	Ala
65					70					75					80
Gly	Gly	Gly	Phe	Ser	Gly	Gly	Gly	Met	Ser	Met	Glu	Asp	Ile	Phe	Ser
			85					90						95	
Arg	Phe	Gly	Asp	Leu	Phe	Gly	Gly	Phe	Gly	Gly	Phe	Gly	Gly	Phe	Ser
		100					105						110		
Asp	Met	Gly	Gly	Gly	Ser	Arg	Arg	Arg	Val	Arg	Arg	Gly	Ser	Asp	Leu
		115					120					125			
Arg	Val	Arg	Val	Lys	Leu	Ser	Leu	Ala	Asp	Ile	Ser	Lys	Gly	Val	Glu
	130					135					140				
Lys	Lys	Val	Lys	Val	Lys	Lys	Gln	Val	Val	Cys	Ser	Lys	Cys	Arg	Gly
145					150					155					160
Asp	Gly	Thr	Glu	Glu	Ala	Asn	Gly	Lys	Thr	Thr	Cys	Gln	Thr	Cys	His
			165					170						175	
Gly	Thr	Gly	Val	Val	Thr	Arg	Val	Ser	Asn	Thr	Phe	Leu	Gly	Ala	Met
		180						185					190		
Gln	Thr	Gln	Ser	Thr	Cys	Pro	Thr	Cys	His	Gly	Glu	Gly	Glu	Ile	Ile
	195					200						205			
Thr	Lys	Pro	Cys	Ser	Lys	Cys	Lys	Gly	Glu	Gly	Val	Glu	Ile	Gly	Glu
	210					215					220				
Glu	Val	Ile	Ser	Phe	His	Ile	Pro	Ala	Gly	Val	Ala	Glu	Gly	Met	Gln
225					230					235					240
Met	Ser	Val	Asn	Gly	Lys	Gly	Asn	Ala	Ala	Pro	Arg	Gly	Gly	Val	Asn
			245					250						255	
Gly	Asp	Leu	Ile	Val	Val	Ile	Ala	Glu	Glu	Pro	Asp	Pro	Asn	Leu	Ile
		260						265					270		
Arg	Asn	Gly	Asn	Asp	Leu	Ile	Tyr	Asn	Leu	Leu	Ile	Ser	Val	Pro	Leu
		275					280					285			
Ala	Ile	Lys	Gly	Gly	Ser	Val	Glu	Val	Pro	Thr	Ile	Asp	Gly	Arg	Ala
	290					295						300			
Lys	Ile	Arg	Ile	Glu	Ala	Gly	Thr	Gln	Pro	Gly	Lys	Met	Leu	Arg	Leu
305					310					315					320
Arg	Asn	Lys	Gly	Leu	Pro	Ser	Val	Asn	Gly	Tyr	Gly	Met	Gly	Asp	Gln
			325					330					335		
Leu	Val	Asn	Val	Asn	Val	Tyr	Ile	Pro	Glu	Ser	Ile	Asp	Ala	Lys	Asp
		340						345					350		
Glu	Gln	Ala	Ile	Ala	Ala	Met	Glu	Asn	Ser	Asp	Ser	Phe	Lys	Pro	Thr
		355				360						365			
Asp	Ala	Ala	Arg	Lys	Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Glu	Met	Leu	Asp
	370					375						380			

(2) INFORMATION FOR SEQ ID NO:293

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

```
Arg Phe Asp Ser Thr Thr Asn Val Ser Gln Ile Asn Leu Arg Thr Glu
1      5      10      15
Met Lys Lys Leu Ile Leu Ala Thr Leu Gly Leu Met Ala Ile Ala Met
      20      25      30
Leu Ser Cys Ser Ser Asn Asn Lys Asp Leu Glu Asn Lys Gly Glu Ala
      35      40      45
Thr Leu Leu Val Thr Phe Gly Ser Ser Tyr Lys Ala Pro Arg Glu Thr
      50      55      60
Tyr Ala Lys Ile Glu Lys Thr Phe Ala Ala Tyr Pro Asp Gln Arg
65      70      75      80
Ile Ser Trp Thr Tyr Thr Ser Ser Ile Ile Arg Lys Lys Leu Ala Gln
      85      90      95
Gln Gly Ile Tyr Ile Asp Ala Pro Asp Glu Ala Leu Glu Lys Leu Ala
      100      105      110
Arg Leu Gly Tyr Lys Lys Ile Asn Val Gln Ser Leu His Val Ile Pro
      115      120      125
Gly Arg Glu Tyr Asp Glu Met Ile Asp Phe Val Asn Lys Phe Lys Ala
      130      135      140
Ala His Ser Asp Ile Thr Val Lys Val Gly Ala Pro Leu Phe Asp Thr
145      150      155      160
Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln
      165      170      175
Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr
      180      185      190
Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys
      195      200      205
Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser
      210      215      220
Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val
225      230      235      240
Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp
      245      250      255
Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala
      260      265      270
Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala
      275      280      285
Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys
      290      295      300
Ala Thr Ser Ala Arg
305
```

(2) INFORMATION FOR SEQ ID NO:294

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

```
Arg Arg Asp Ala Arg Arg Gln Leu Val Arg Arg Arg Arg Lys Glu Leu
1      5      10      15
Ser Gly Thr Ala Asn Thr Arg Cys Arg Arg Arg Val Phe Pro Glu Arg
      20      25      30
Arg Ser Ala Ile Arg Trp Cys Phe Pro Arg Leu Arg Asp Gly Leu Gln
      35      40      45
Pro Ile Arg Phe Gly Ser Leu Leu Ala Asn Pro Gln Gln Leu Ser Arg
```

50		55		60
Gly Val Arg Leu Arg Ser Phe Glu Ser Arg Arg Gln Pro Ile Cys Arg				
65		70	75	80
Phe Gln Gly Ile Gln Gly Lys Arg Arg Asp Ile Leu Gln Pro Glu Gly				
	85	90	95	
Asn Ser Leu Leu Arg Thr His Ala His Ala Ser Arg Leu Gly Ala Gly				
	100	105	110	
Arg Ser Tyr Arg Tyr Leu Ala Pro Arg Thr Thr Ser Arg Pro Pro Thr				
	115	120	125	
Ala Phe Leu Leu Phe Ala Pro Met Thr Ser Val Ser His Leu Arg Thr				
	130	135	140	
Ile Ser Val Ala Gly Ile Leu Ala Ala Leu Gly Gly Ala Val Leu Ile				
145		150	155	160
Leu Phe Gly Val Asn Leu Phe Leu Gly Ser Val Ala Ile Pro Met Ser				
	165	170	175	
Glu Ile Phe Arg His Leu Phe Ser Asp Arg Pro Glu Gly Gly Glu Ala				
	180	185	190	
Leu Val His Tyr Asn Ile Leu Trp Lys Ser Arg Leu Pro Glu Ala Leu				
	195	200	205	
Thr Ala Ala Phe Ala Gly Ala Gly Leu Ser Val Ser Gly Leu Gln Met				
	210	215	220	
Gln Thr Val Phe Arg Asn Pro Leu Ala Gly Pro Ser Val Leu Gly Ile				
225		230	235	240
Ser Ser Gly Ala Ser Leu Gly Val Ala Leu Val Val Leu Leu Ser Gly				
	245	250	255	
Ser Leu Gly Gly Val Ala Leu Ser Ser Leu Gly Tyr Met Gly Glu Val				
	260	265	270	
Ala Met Asn Ile Ala Ala Ala Val Gly Ser Leu Ala Val Met Gly Leu				
	275	280	285	
Ile Val Phe Val Ser Thr Lys Val Arg Ser His Val Thr Leu Leu Ile				
	290	295	300	
Ile Gly Val Met Ile Gly Tyr Val Ala Thr Ala Val Ile Gly Val Phe				
305		310	315	320
Lys Phe Phe Ser Ile Glu Glu Asp Ile Arg Ala Tyr Val Ile Trp Gly				
	325	330	335	
Leu Gly Ser Phe Ser Arg Ala Thr Asp Ser Gln Leu Ser Phe Phe Ala				
	340	345	350	
Ile Leu Met Leu Ile Phe Ile Pro Ala Gly Met Leu Leu Val Lys Gln				
	355	360	365	
Leu Asn Leu Leu Leu Gly Glu Ser Tyr Ala Arg Asn Leu Gly Leu				
	370	375	380	
Asn Thr Arg Arg Ala Arg Leu Leu Val Ile Ser Ser Ala Gly Leu Leu				
385		390	395	400
Ile Ala Thr Val Thr Ala Tyr Cys Gly Pro Ile Gly Phe Leu Gly Met				
	405	410	415	
Ala Val Pro His Leu Ala Arg Val Ile Phe His Thr Ser Asp His Arg				
	420	425	430	
Ile Leu Met Pro Ala Thr Cys Leu Ile Gly Ser Ala Leu Ala Leu Phe				
	435	440	445	
Cys Asn Ile Ile Ala Arg Met Pro Gly Phe Glu Gly Ala Leu Pro Val				
	450	455	460	
Asn Ser Val Thr Ala Leu Val Gly Ala Pro Ile Ile Val Thr Val Leu				
465		470	475	480
Phe Arg Arg Arg Arg Phe Lys Glu Glu Thr Asp				
	485	490		

(2) INFORMATION FOR SEQ ID NO:295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

His Phe Leu Val Thr Ile Met Arg Thr Lys Thr Ile Phe Phe Ala Ile

1				5					10					15	
Ile	Ser	Phe	Ile	Ala	Leu	Leu	Ser	Ser	Ser	Leu	Ser	Ala	Gln	Ser	Lys
			20					25					30		
Ala	Val	Leu	Thr	Gly	Ser	Val	Ser	Asp	Ala	Glu	Thr	Gly	Glu	Pro	Leu
		35					40					45			
Ala	Gly	Ala	Arg	Ile	Glu	Val	Lys	His	Thr	Asn	Ile	Val	Ala	Gly	Ala
	50					55					60				
Asp	Ala	Gly	Gly	His	Phe	Glu	Ile	Lys	Asn	Leu	Pro	Ala	Gly	Gln	His
65				70					75					80	
Thr	Ile	Ile	Cys	Ser	Leu	Gly	Gly	Tyr	Gly	Gln	Lys	Glu	Glu	Val	Val
			85					90					95		
Ala	Ile	Glu	Ala	Gly	Gln	Thr	Lys	Thr	Ile	Ser	Phe	Ala	Leu	Arg	Leu
		100					105						110		
Arg	Thr	Asn	Asn	Leu	Glu	Glu	Val	Val	Thr	Gly	Thr	Gly	Thr	Arg	
		115					120					125			
Tyr	Arg	Leu	Val	Asp	Ala	Pro	Val	Ala	Thr	Glu	Val	Leu	Thr	Ala	Lys
	130				135						140				
Asp	Ile	Ala	Ser	Phe	Ser	Ala	Pro	Thr	Ser	Glu	Ala	Leu	Leu	Gln	Gly
145				150						155				160	
Leu	Ser	Pro	Ser	Phe	Asp	Phe	Gly	Pro	Asn	Leu	Met	Gly	Ser	Phe	Met
			165					170						175	
Gln	Leu	Asn	Gly	Leu	Ser	Ser	Lys	Tyr	Ile	Leu	Ile	Leu	Ile	Asp	Gly
		180					185						190		
Lys	Arg	Val	Tyr	Gly	Asp	Val	Gly	Gly	Gln	Ala	Asp	Leu	Ser	Arg	Ile
		195				200						205			
Ser	Pro	Asp	Gln	Ile	Glu	Arg	Ile	Glu	Leu	Val	Lys	Gly	Ala	Ser	Ser
	210					215					220				
Ser	Leu	Tyr	Gly	Ser	Asp	Ala	Ile	Ala	Gly	Val	Ile	Asn	Val	Ile	Thr
225				230						235				240	
Lys	Lys	Asn	Thr	Asn	Arg	Leu	Ser	Ala	Tyr	Thr	Ser	His	Arg	Ile	Ser
			245					250						255	
Lys	Tyr	Asn	Asp	Arg	Gln	Thr	Asn	Thr	Ser	Leu	Asp	Ile	Asn	Ile	Gly
		260					265						270		
Lys	Phe	Ser	Ser	Asn	Thr	Asn	Tyr	Phe	Phe	Tyr	His	Thr	Asp	Gly	Trp
	275						280					285			
Gln	Asn	Ser	Pro	Phe	Glu	Ile	Lys	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Pro
	290					295					300				
Val	Leu	Glu	Glu	Thr	Tyr	Lys	Lys	Thr	Phe	Arg	Ala	Gln	Glu	Asn	Gln
305				310						315				320	
Gly	Val	Ser	Gln	Ser	Leu	Ser	Tyr	Tyr	Ala	Thr	Asn	Asn	Leu	Ser	Phe
			325						330					335	
Ser	Gly	Asn	Val	Gln	Tyr	Asn	Lys	Arg	Gln	Ile	Phe	Thr	Pro	Thr	Phe
		340					345						350		
Ser	Glu	Lys	Lys	Ala	Tyr	Asp	Met	Asp	Tyr	Arg	Ala	Leu	Thr	Ala	Ser
	355						360					365			
Leu	Gly	Thr	Asn	Tyr	Leu	Phe	Pro	Asn	Gly	Leu	His	Thr	Leu	Ser	Phe
	370					375					380				
Asp	Ala	Val	Tyr	Asp	Arg	Phe	Arg	Phe	Gly	Tyr	Leu	Tyr	His	Asp	Lys
385				390						395				400	
Asp	Ser	Ser	Glu	Ser	Leu	Ile	Asn	Asn	Gln	Gly	Gln	Thr	Glu	Gln	Pro
			405						410					415	
Thr	Phe	Phe	Pro	Gly	Gln	Leu	Arg	Asn	Lys	Asn	Asp	Gln	Ile	Arg	Tyr
	420							425					430		
Thr	Ala	Glu	Ala	Arg	Gly	Val	Phe	Thr	Leu	Pro	Tyr	Ala	Gln	Lys	Leu
	435						440					445			
Thr	Gly	Gly	Leu	Glu	Tyr	Phe	Arg	Glu	Glu	Leu	Ile	Ser	Pro	Tyr	Asn
	450					455					460				
Leu	Ile	Thr	Asp	Lys	Ala	Asp	Ala	Ser	Thr	Leu	Ser	Ala	Tyr	Val	Gln
465				470						475				480	
Asp	Glu	Trp	Lys	Pro	Leu	Asp	Trp	Phe	Asn	Met	Thr	Ala	Gly	Phe	Arg
			485					490						495	
Leu	Val	His	His	Gln	Glu	Phe	Gly	Thr	Arg	Met	Thr	Pro	Lys	Val	Ser
	500						505						510		
Ile	Leu	Ala	Lys	Tyr	Gly	Pro	Leu	Asn	Phe	Arg	Ala	Thr	Tyr	Ala	Asn
	515						520					525			
Gly	Tyr	Lys	Thr	Pro	Thr	Leu	Lys	Glu	Leu	Phe	Ala	Arg	Asn	Glu	Leu
	530					535					540				
Thr	Thr	Met	Gly	Ser	His	Asn	Leu	Tyr	Leu	Gly	Asn	Ala	Asp	Leu	Lys
545				550						555				560	
Pro	Gln	Met	Ser	Asp	Tyr	Tyr	Ala	Leu	Gly	Leu	Glu	Tyr	Asn	Gln	Gly
			565						570					575	
Pro	Ile	Ser	Phe	Ser	Ala	Thr	Val	Tyr	Asp	Asn	Glu	Leu	Arg	Asn	Leu
	580							585					590		
Ile	Ser	Phe	Met	Asp	Ile	Pro	Thr	Ser	Pro	Glu	His	Glu	Ala	Gln	Gly
	595					600					605				
Ile	Lys	Lys	Thr	Lys	Gln	Tyr	Ala	Asn	Ile	Gly	Lys	Ala	Arg	Ser	Arg
	610					615						620			

Gly	Leu	Asp	Val	Leu	Cys	Asp	Ala	Ser	Ile	Gly	Trp	Gly	Ile	Lys	Leu
625					630					635					640
Gly	Ala	Gly	Tyr	Ser	Leu	Val	Glu	Ala	Lys	Asn	Leu	Gln	Thr	Asp	Glu
				645					650						655
Trp	Leu	Glu	Gly	Ala	Ala	Arg	His	Arg	Ala	Asn	Val	His	Ala	Asp	Trp
			660					665					670		
Val	His	Tyr	Trp	Gly	Gln	Tyr	Arg	Leu	Gly	Val	Ser	Leu	Phe	Gly	Arg
		675					680					685			
Ile	Gln	Ser	Glu	Arg	Tyr	Tyr	Lys	Asp	Gly	Asn	Ala	Pro	Asp	Tyr	Thr
	690					695				700					
Leu	Trp	Arg	Leu	Ala	Thr	Ser	His	Arg	Phe	Ala	His	Phe	Arg	His	Ile
705					710					715					720
Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Asn	Leu	Phe	Asp	Tyr	Val	Asp
			725					730						735	
Asp	Arg	Pro	Met	Gly	Val	Asn	Tyr	Ala	Thr	Val	Thr	Pro	Gly	Arg	Thr
		740					745						750		
Phe	Phe	Ala	Gln	Ile	Ala	Ile	Arg	Phe	Asn	Asn					
		755					760								

(2) INFORMATION FOR SEQ ID NO:296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

Cys	Cys	Ala	Arg	Leu	Arg	Asp	Thr	Ser	Pro	Arg	Lys	Lys	Ser	Phe	Arg
1				5					10					15	
Asn	Asp	Thr	Val	Phe	Pro	Tyr	Phe	Val	Ile	His	Leu	Ile	Lys	His	Ile
			20					25					30		
Ile	Ile	Met	Thr	Asp	Asn	Lys	Gln	Arg	Asn	Ile	Val	Phe	Pro	Ala	Phe
		35					40					45			
Leu	Leu	Leu	Leu	Gly	Val	Ile	Ala	Val	Val	Thr	Ile	Val	Gly	Phe	Phe
	50					55					60				
Met	Leu	Arg	Pro	Ala	Glu	Glu	Ile	Ile	Gln	Gly	Gln	Ile	Glu	Val	Thr
65					70					75				80	
Glu	Tyr	Arg	Val	Ser	Ser	Lys	Val	Pro	Gly	Arg	Ile	Lys	Glu	Leu	Arg
			85						90					95	
Val	Ser	Glu	Gly	Gln	Gln	Val	Gln	Ala	Gly	Asp	Thr	Leu	Ala	Val	Ile
			100					105					110		
Glu	Ala	Pro	Asp	Val	Ala	Ala	Lys	Met	Glu	Gln	Ala	Lys	Ala	Ala	Glu
	115						120					125			
Ala	Ala	Ala	Gln	Ala	Gln	Asn	Ala	Lys	Ala	Leu	Lys	Gly	Ala	Arg	Ser
	130					135						140			
Glu	Gln	Ile	Gln	Ala	Ala	Tyr	Glu	Met	Trp	Gln	Lys	Ala	Gln	Ala	Gly
145					150					155					160
Val	Ala	Ile	Ala	Thr	Lys	Thr	His	Gln	Arg	Val	Gln	Asn	Leu	Tyr	Asp
			165					170						175	
Gln	Gly	Val	Val	Pro	Ala	Gln	Lys	Leu	Asp	Glu	Ala	Thr	Ala	Gln	Arg
		180						185					190		
Asp	Ala	Ala	Ile	Ala	Thr	Gln	Lys	Ala	Ala	Glu	Ala	Gln	Tyr	Asn	Met
	195						200					205			
Ala	Arg	Asn	Gly	Ala	Glu	Arg	Glu	Asp	Lys	Leu	Ala	Ala	Ser	Ala	Leu
	210					215						220			
Val	Asp	Arg	Ala	Arg	Gly	Ala	Val	Ala	Glu	Val	Glu	Ser	Tyr	Ile	Asn
225					230					235					240
Glu	Thr	Tyr	Leu	Ile	Ala	Pro	Arg	Ala	Gly	Glu	Val	Ser	Glu	Ile	Phe
			245						250					255	
Pro	Lys	Ala	Gly	Glu	Leu	Val	Gly	Thr	Gly	Ala	Pro	Ile	Met	Asn	Ile
		260						265					270		
Ala	Glu	Met	Gly	Asp	Met	Trp	Ala	Ser	Phe	Ala	Val	Arg	Glu	Asp	Phe
	275						280					285			
Leu	Ser	Ser	Met	Thr	Met	Gly	Ala	Val	Leu	Glu	Thr	Val	Val	Pro	Ala
	290					295						300			

```

Leu Asn Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met
305                               310                315                320
Gly Thr Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp
                               325                330                335
Leu Lys Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala
                               340                345                350
Gln Lys Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys
                               355                360                365

```

(2) INFORMATION FOR SEQ ID NO:297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

```

Pro Gln Ser Ser Pro Asp Arg Arg Ser Phe Gln Asn Val Met Asn Lys
1                               5                10                15
Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly Ile Val Ile
                               20                25                30
Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro Pro Phe Leu
                               35                40                45
Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser
                               50                55                60
Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val
65                               70                75                80
Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys
                               85                90                95
Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val
                               100               105               110
Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr
                               115               120               125
Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly
130                               135               140
Phe Leu Val Asp Ser Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln
145                               150               155               160
Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln
                               165               170               175
Lys Arg Ile Ile Ser Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val
                               180               185               190
Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val Asn His Pro
                               195               200               205
Gly Ser Met Ser Val Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile
210                               215               220
Gly Met Ala Gly Asp Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe
225                               230               235               240
Val Ile Arg Glu Thr Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu
                               245               250               255
Arg Lys Ala Asp Leu Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn
260                               265               270
Asp Val Ile Tyr Val Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu
275                               280               285
Ile Asn Gln Asn Asn Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr
290                               295               300
Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
305                               310               315                320

```

(2) INFORMATION FOR SEQ ID NO:298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

Ser	Lys	Ile	Val	Leu	Arg	Lys	Phe	Cys	Thr	Leu	Ala	Arg	Met	Lys	Lys
1			5						10					15	
Thr	Asn	Leu	Phe	Leu	Ser	Leu	Leu	Val	Ile	Phe	Ile	Thr	Gly	Ser	Phe
			20					25					30		
Met	Thr	Ala	Cys	Ala	Gln	Lys	Ser	Lys	Thr	Asn	Lys	Leu	Thr	Glu	Glu
		35					40					45			
Asp	Arg	Ser	Arg	Asn	Glu	Tyr	Val	Gln	Ser	Met	Asp	Val	Leu	Ser	Asn
		50				55					60				
Ile	Ile	Gly	Asn	Val	Arg	Leu	Tyr	Phe	Val	Asp	Thr	Ile	Ser	Ile	Lys
65					70					75					80
His	Met	Thr	Arg	Arg	Gly	Ile	Asp	Ala	Met	Leu	Gly	Gly	Leu	Asp	Pro
			85						90					95	
Tyr	Thr	Glu	Tyr	Ile	Pro	Tyr	Glu	Glu	Met	Asp	Glu	Leu	Lys	Leu	Met
		100						105					110		
Thr	Thr	Gly	Glu	Tyr	Ala	Gly	Val	Gly	Ala	Ile	Ile	Ser	Gln	Arg	Pro
		115					120					125			
Asp	Ser	Ala	Val	Ile	Ile	Gln	Arg	Pro	Met	Glu	Gly	Met	Pro	Ala	Asp
		130				135					140				
Glu	Ala	Gly	Leu	Ile	Ala	Gly	Asp	Arg	Ile	Leu	Thr	Ile	Asp	Gly	Lys
145					150					155					160
Asp	Phe	Arg	Lys	Ser	Thr	Thr	Pro	Lys	Val	Ser	Gln	Ala	Leu	Lys	Gly
			165						170					175	
Ile	Ala	Gly	Thr	Val	Ala	Lys	Val	Thr	Val	Met	Arg	Tyr	Gly	Glu	Thr
		180						185					190		
Lys	Pro	Arg	Thr	Phe	Ser	Val	Lys	Arg	Gln	Lys	Val	Ile	Met	Asn	Ser
		195					200					205			
Val	Thr	Tyr	Ser	Gly	Met	Leu	Asp	Gly	Ser	Ile	Gly	Tyr	Ile	Arg	Leu
		210				215					220				
Asn	Asn	Phe	Thr	Asp	Lys	Ser	Ala	Glu	Glu	Val	Arg	Thr	Ala	Leu	Leu
225					230					235					240
Asp	Leu	Arg	Asp	Lys	Gln	Gly	Ala	Lys	Gly	Leu	Ile	Leu	Asp	Leu	Arg
			245						250					255	
Gly	Asn	Gly	Gly	Gly	Leu	Met	Gln	Ala	Ala	Ile	Glu	Ile	Val	Asn	Leu
		260					265						270		
Phe	Val	Pro	Lys	Gly	Lys	Glu	Val	Val	Thr	Thr	Lys	Gly	Arg	Ile	Ala
		275					280					285			
Glu	Ser	Ala	Ser	Val	Phe	Arg	Thr	Leu	Thr	Glu	Pro	Ile	Asp	Thr	Lys
		290				295					300				
Leu	Pro	Ile	Val	Val	Leu	Ile	Asp	Gly	Gln	Ser	Ala	Ser	Ser	Ser	Glu
305					310					315					320
Ile	Val	Ala	Gly	Ala	Leu	Gln	Asp	Met	Asp	Arg	Ala	Val	Leu	Met	Gly
			325						330					335	
Gln	Lys	Ser	Tyr	Gly	Lys	Gly	Leu	Val	Gln	Thr	Thr	Arg	Gln	Leu	Pro
		340						345					350		
Tyr	Asn	Gly	Val	Ile	Lys	Leu	Thr	Thr	Ala	Lys	Tyr	Tyr	Ile	Pro	Ser
		355					360					365			
Gly	Arg	Cys	Ile	Gln	Arg	Leu	Asp	Tyr	Ser	Arg	Thr	Asn	Arg	Thr	Gly
		370				375					380				
Met	Ala	Thr	Ala	Ile	Pro	Asp	Ser	Leu	His	Lys	Ile	Phe	Tyr	Thr	Ala
385					390					395					400
Ala	Gly	Arg	Arg	Val	Glu	Asp	Ala	Gly	Gly	Ile	Leu	Pro	Asp	Ile	Glu
			405						410					415	
Val	Lys	Gln	Asp	Thr	Ala	Ala	Thr	Leu	Leu	Tyr	Tyr	Met	Ala	Ile	Asn
		420						425					430		
Asn	Asp	Val	Phe	Asp	Phe	Val	Thr	Gly	Tyr	Val	Leu	Lys	His	Lys	Thr
		435					440					445			
Ile	Ala	Lys	Pro	Glu	Asp	Phe	Ser	Ile	Thr	Asn	Glu	Asp	Tyr	Ala	Ala
		450				455					460				
Phe	Cys	Lys	Met	Met	Glu	Gly	Lys	Lys	Phe	Asp	Tyr	Asp	Arg	Gln	Ser
465					470					475					480
Gly	Lys	Met	Leu	Asp	Lys	Leu	Glu	Glu	Leu	Ala	Lys	Ile	Glu	Gly	Tyr
			485						490					495	
Leu	Pro	Glu	Ala	Asn	Ser	Glu	Leu	Lys	Ala	Leu	Arg	Glu	Lys	Leu	Lys
			500					505					510		

Pro Asn Leu Ser Arg Asp Leu Leu Arg Phe Lys Lys Glu Ile Thr Asn
515 520 525
Tyr Leu Asn Asn Glu Ile Val Thr Arg Tyr Tyr Tyr Glu Arg Gly Ser
530 535 540
Ile Arg Gln Ser Leu Pro Glu Asp Lys Val Val Lys Glu Ala Ile Lys
545 550 555 560
Leu Leu Lys Asp His Pro Glu Gln Ile Arg Gln Ile Leu Ala Ala Pro
565 570 575
Lys Ala Glu Asn Lys Gly
580

(2) INFORMATION FOR SEQ ID NO:299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

Val Thr Asp Lys Met Gln Asn Lys Gly Phe Val Ile Val Ile Thr Ser
1 5 10 15
Ala Leu Ala Ile Cys Ala Phe Tyr Leu Ser Phe Ser Phe Val Thr
20 25 30
Asn Arg Tyr Glu Lys Lys Ala Lys Ala Met Gly Asp Val Ala Gly Met
35 40 45
Ala Tyr Leu Asp Ser Met Ser Asn Glu Lys Val Trp Phe Gly Tyr Thr
50 55 60
Leu Lys Glu Ala Gln Ala Gln Gln Ile Gly Leu Gly Leu Asp Leu Lys
65 70 75 80
Gly Gly Met Asn Val Ile Leu Lys Leu Asn Ala Ser Asp Leu Leu Arg
85 90 95
Asn Leu Ser Asn Lys Ser Leu Asp Pro Asn Phe Asn Lys Ala Leu Glu
100 105 110
Asn Ala Ala Lys Ser Thr Glu Gln Ser Asp Phe Ile Asp Ile Phe Val
115 120 125
Lys Glu Tyr Arg Lys Leu Asp Pro Asn Gly Arg Leu Ala Val Ile Phe
130 135 140
Gly Ser Gly Asp Leu Arg Asp Gln Ile Thr Ala Lys Ser Thr Asp Ala
145 150 155 160
Asp Val Val Arg Leu Leu Lys Glu Lys Tyr Asn Ser Ala Val Glu Ala
165 170 175
Ser Phe Asn Val Leu Arg Ala Arg Ile Asp Ala Phe Gly Val Val Ala
180 185 190
Pro Asn Leu Gln Arg Leu Glu Gly Gln Gly Arg Ile Leu Val Glu Leu
195 200 205
Pro Gly Val Lys Asp Pro Glu Arg Val Arg Thr Leu Leu Gln Arg Ser
210 215 220
Ala Asn Leu Gln Phe Trp Arg Thr Tyr Lys Phe Glu Glu Val Ser Gly
225 230 235 240
Asp Leu Ile Ala Ala Asn Asp Arg Leu Ser Glu Leu Ala Met Asn Asn
245 250 255
Thr Asp Ala Thr Pro Glu Thr Glu Pro Ala Thr Thr Asp Ser Val Ala
260 265 270
Ala Thr Ala Asp Ser Ala Ala Val Gln Ala Val Ala Asp Ser Ala Thr
275 280 285
Val Ala Gln Lys Glu Ala Lys Asp Ala Thr Arg Lys Asp Ala Leu Phe
290 295 300
Ser Leu Leu Thr Pro Val Asn Arg Gly Gly Ala Val Val Gly Val Ala
305 310 315 320
Arg Arg Ala Asn Met Ala Gln Ile Ser Glu Met Leu Gln Gln Ala His
325 330 335
Asp Leu Lys Val Thr Arg Glu Asp Val Leu Phe Leu Trp Gly Ala Lys
340 345 350
Ala Ile Glu Asp Pro Glu Thr Lys Lys Glu Thr Asp Leu Tyr Glu Leu
355 360 365

Tyr	Ala	Ile	Arg	Thr	Asn	Arg	Thr	Gly	Asp	Pro	Asp	Leu	Gly	Gly	Asp
370						375					380				
Val	Val	Thr	Ser	Ala	Lys	Ser	Asp	Ile	Gln	Asn	Asp	Phe	Gly	Arg	Ser
385					390					395					400
Glu	Pro	Ile	Val	Ser	Met	Thr	Met	Asn	Glu	Glu	Gly	Ala	Arg	Lys	Trp
				405					410					415	
Ala	Arg	Ile	Thr	Lys	Asp	Asn	Val	Gly	Arg	Ala	Ile	Ala	Ile	Val	Leu
			420					425					430		
Asp	Gly	Val	Val	Tyr	Ser	Ala	Pro	Asn	Val	Asn	Asp	Glu	Ile	Thr	Gly
	435					440					445				
Gly	Arg	Ser	Gln	Ile	Ser	Gly	His	Phe	Thr	Val	Glu	Glu	Ala	Gly	Asp
450					455						460				
Leu	Ala	Asn	Val	Leu	Asn	Ser	Gly	Lys	Met	Asp	Ala	Thr	Val	Ser	Ile
465					470					475					480
Glu	Gln	Glu	Asn	Val	Ile	Gly	Pro	Thr	Leu	Gly	Ala	Glu	Ser	Ile	Lys
			485						490					495	
Ala	Gly	Phe	Leu	Ser	Phe	Leu	Leu	Ala	Leu	Val	Ile	Leu	Met	Cys	Tyr
			500					505					510		
Met	Cys	Leu	Ala	Tyr	Gly	Phe	Leu	Pro	Gly	Leu	Ile	Ala	Asn	Gly	Ala
	515						520					525			
Leu	Ile	Val	Asn	Ser	Phe	Phe	Thr	Leu	Gly	Val	Leu	Ala	Ser	Phe	His
	530					535					540				
Ala	Val	Leu	Thr	Leu	Ser	Gly	Ile	Ala	Gly	Leu	Val	Leu	Thr	Leu	Gly
545					550					555					560
Met	Ala	Val	Asp	Ala	Asn	Val	Leu	Ile	Phe	Glu	Arg	Ile	Lys	Glu	Glu
			565						570					575	
Leu	Arg	Ala	Gly	Lys	Thr	Pro	Ile	Arg	Ala	Val	Thr	Asp	Gly	Tyr	Gly
			580					585					590		
Asn	Ala	Phe	Ser	Ala	Ile	Phe	Asp	Ser	Asn	Val	Thr	Thr	Ile	Ile	Thr
	595					600					605				
Gly	Ile	Ile	Leu	Phe	Leu	Tyr	Gly	Thr	Gly	Pro	Ile	Arg	Gly	Phe	Ala
610					615						620				
Thr	Thr	Leu	Ile	Ile	Gly	Leu	Ile	Ala	Ser	Phe	Ile	Thr	Ala	Val	Phe
625					630					635					640
Leu	Thr	Arg	Ile	Val	Phe	Glu	Lys	Leu	Ala	Lys	Lys	Gly	Arg	Leu	Asp
			645						650					655	
Lys	Ile	Thr	Phe	Thr	Thr	Ser	Ile	Thr	Arg	Asn	Leu	Leu	Val	Asn	Pro
		660						665					670		
Ser	Tyr	Asn	Ile	Leu	Gly	Lys	Arg	Lys	Thr	Gly	Phe	Ile	Ile	Pro	Val
	675						680					685			
Ile	Ile	Ile	Val	Leu	Gly	Leu	Ile	Ala	Ser	Phe	Thr	Ile	Gly	Leu	Asn
	690					695					700				
Arg	Gly	Ile	Glu	Phe	Ser	Gly	Gly	Arg	Asn	Tyr	Val	Val	Lys	Phe	Asp
705					710					715					720
Gln	Pro	Val	Ser	Ser	Glu	Ala	Val	Arg	Ser	Ala	Leu	Ser	Ser	Pro	Leu
			725						730					735	
Gln	Glu	Lys	Val	Leu	Val	Thr	Ser	Ile	Gly	Thr	Glu	Gly	Thr	Glu	Val
			740						745					750	
Arg	Ile	Ser	Thr	Asn	Tyr	Lys	Ile	Gln	Glu	Glu	Ser	Glu	Glu	Thr	Glu
		755							760				765		
Ala	Glu	Ile	Thr	Asp	Lys	Leu	Tyr	Gln	Ser	Leu	Lys	Gly	Phe	Tyr	Thr
770						775					780				
Gln	Gln	Pro	Thr	Ala	Asp	Gln	Phe	Leu	Asp	Asn	Ile	Ile	Ser	Ser	Gln
785					790					795					800
Lys	Val	Ser	Pro	Ser	Met	Ser	Ser	Asp	Ile	Thr	Arg	Gly	Ala	Ile	Trp
			805						810					815	
Ala	Val	Leu	Leu	Ser	Met	Ile	Phe	Met	Ala	Ile	Tyr	Ile	Leu	Ile	Arg
		820						825					830		
Phe	Arg	Asp	Ile	Ser	Phe	Ser	Ala	Gly	Val	Phe	Val	Ser	Val	Ala	Ala
	835						840					845			
Thr	Thr	Phe	Cys	Ile	Ile	Ala	Leu	Tyr	Ala	Leu	Leu	Trp	Lys	Ile	Leu
850						855					860				
Pro	Phe	Thr	Met	Glu	Ile	Asp	Gln	Asn	Phe	Ile	Ala	Ala	Ile	Leu	Ala
865					870					875					880
Ile	Ile	Gly	Tyr	Ser	Leu	Asn	Asp	Thr	Val	Val	Val	Phe	Asp	Arg	Ile
			885						890					895	
Arg	Glu	Thr	Met	Lys	Leu	Tyr	Pro	Asn	Arg	Asp	Arg	Tyr	Gln	Val	Ile
		900						905					910		
Asn	Asp	Ala	Leu	Asn	Ser	Thr	Leu	Gly	Arg	Thr	Leu	Asn	Thr	Ser	Leu
		915						920					925		
Thr	Thr	Phe	Ile	Val	Met	Leu	Val	Ile	Phe	Ile	Phe	Gly	Gly	Ala	Thr
		930						935				940			
Met	Arg	Ser	Phe	Thr	Phe	Ser	Ile	Leu	Leu	Gly	Ile	Val	Ile	Gly	Thr
945					950					955					960
Tyr	Ser	Thr	Leu	Phe	Val	Ala	Thr	Pro	Leu	Ala	Tyr	Glu	Ile	Gln	Lys
			965						970					975	
Arg	Lys	Leu	Asn	Lys	Ala	Ala	Lys	Lys							

(2) INFORMATION FOR SEQ ID NO:300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300

```

Asp Phe Pro Trp Val Arg Val Lys Pro Glu Lys Lys Arg Lys Gln His
1      5      10      15
Asn Ser Asn Asn Phe Lys Phe Asn Ala Lys Glu Lys Ser Met Lys Arg
      20      25      30
Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly Trp Ala Met
      35      40      45
Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser Glu Asp Asn
      50      55      60
Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn Thr Thr Ile
65      70      75      80
Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser Val Pro Ala
      85      90      95
Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr Thr Lys Glu
      100     105     110
Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro Asp Ser Lys
      115     120     125
Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly Gln Lys Leu
130     135     140
Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu Lys Leu Ala
145     150     155     160
Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly Gln Val Ala
      165     170     175
Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala Val Ala Ser
      180     185     190
Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser Ala Pro Leu
195     200     205
Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val Ala Thr Met
210     215     220
Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp Ala Ser Ala
225     230     235     240
Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val Phe Ile Gln
      245     250     255
Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr Phe Asn Ala
260     265     270
Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu Asp Asn Met
275     280     285
Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala Gly Phe Trp
290     295     300
Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile Leu Ala Gly
305     310     315     320
Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp Glu Tyr Gly
      325     330     335
Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp Trp Leu Lys
      340     345     350
Ala Leu Phe Lys Thr Ala Pro Thr Ser Gln Gly Asp Ile Ser Phe Ser
355     360     365
Gly Gly Ser Gln Gly Thr Ser Tyr Tyr Ala Ser Ile Gly Tyr Phe Asp
370     375     380
Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg Tyr Ser Gly
385     390     395     400
Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys Val Gly Ala
      405     410     415
Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp Tyr Phe Gly
420     425     430
Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr Met Pro Arg

```

		435						440						445					
Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp	Val	Tyr	Tyr				
	450					455					460								
Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr	Phe	Ala	Lys				
465					470					475					480				
Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val	Asn	Gly	Phe				
			485						490					495					
Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala	Gln	Ala	Gly				
			500					505					510						
Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met	Pro	Asn	Asn				
	515						520					525							
Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg	Ala	Tyr	Arg				
	530					535					540								
Asp	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys	Phe	Ser	Ile				
545					550					555					560				
Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu	Tyr	Ile	Glu				
				565					570					575					
Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe	Glu	Ser	Asp				
			580					585					590						
Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser	Leu	Ser	Leu				
	595					600						605							
Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe	Phe	Ser	Arg				
	610					615					620								
Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe	Ser	Val	Arg				
625					630					635					640				
Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser	Ala	Trp	Phe				
			645						650					655					
Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe	Ile	Gln	Glu				
			660				665						670						
Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr	Gly	Thr	Thr				
	675					680					685								
Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu	Val	Thr	Val				
	690					695				700									
Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser	Thr	Ala	Gly				
705					710					715					720				
Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn	Phe	Gly	Leu				
			725						730					735					
Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val	Asp	Phe	Tyr				
			740					745					750						
Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met	Pro	Tyr	Ile				
	755						760					765							
Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met	Lys	Asn	Thr				
	770					775				780									
Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn	Lys	Asp	Trp				
785					790														

(2) INFORMATION FOR SEQ ID NO:301

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 869 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301

Trp	His	Arg	Asn	Ile	Phe	Ile	Phe	Ala	Ser	Thr	Phe	Ser	Pro	Lys	Asn
1			5						10					15	
Met	Leu	Pro	Leu	Pro	Tyr	Arg	Tyr	Ala	Lys	Thr	Glu	His	Leu	Phe	Leu
			20					25					30		
Ala	Lys	Gly	Tyr	Cys	Lys	Asn	Pro	Ile	Thr	Asn	Ile	Ile	Ile	Leu	Phe
		35					40					45			
Met	Lys	Lys	Lys	Asn	Phe	Leu	Leu	Leu	Gly	Ile	Phe	Val	Ala	Leu	Leu
	50					55					60				
Thr	Phe	Ile	Gly	Ser	Met	Gln	Ala	Gln	Gln	Ala	Lys	Asp	Tyr	Phe	Asn
65					70				75						80
Phe	Asp	Glu	Arg	Gly	Glu	Ala	Tyr	Phe	Ser	Phe	Lys	Val	Pro	Asp	Arg
			85						90					95	
Ala	Val	Leu	Gln	Glu	Leu	Ala	Leu	Ile	Met	Ser	Ile	Asp	Glu	Phe	Asp
			100					105					110		
Pro	Val	Thr	Asn	Glu	Ala	Ile	Ala	Tyr	Ala	Ser	Glu	Glu	Glu	Phe	Glu
			115				120					125			
Ala	Phe	Leu	Arg	Tyr	Gly	Leu	Lys	Pro	Thr	Phe	Leu	Thr	Pro	Pro	Ser
	130					135					140				
Met	Gln	Arg	Ala	Val	Glu	Met	Phe	Asp	Tyr	Arg	Ser	Gly	Glu	Lys	Tyr
145					150					155					160
Glu	Trp	Asn	Ala	Tyr	Pro	Thr	Tyr	Glu	Ala	Tyr	Ile	Ser	Met	Met	Glu
				165					170					175	
Glu	Phe	Gln	Thr	Lys	Tyr	Pro	Ser	Leu	Cys	Thr	Thr	Ser	Val	Ile	Gly
			180					185					190		
Lys	Ser	Val	Lys	Asp	Arg	Lys	Leu	Met	Ile	Cys	Lys	Leu	Thr	Ser	Ser
	195						200					205			
Ala	Asn	Thr	Gly	Lys	Lys	Pro	Arg	Val	Leu	Tyr	Thr	Ser	Thr	Met	His
	210					215						220			
Gly	Asp	Glu	Thr	Thr	Gly	Tyr	Val	Val	Leu	Leu	Arg	Leu	Ile	Asp	His
225					230					235					240
Leu	Leu	Ser	Asn	Tyr	Glu	Ser	Asp	Pro	Arg	Ile	Lys	Asn	Ile	Leu	Asp
			245						250					255	
Lys	Thr	Glu	Val	Trp	Ile	Cys	Pro	Leu	Thr	Asn	Pro	Asp	Gly	Ala	Tyr
		260						265					270		
Arg	Ala	Gly	Asn	His	Thr	Val	Gln	Gly	Ala	Thr	Arg	Tyr	Asn	Ala	Asn
		275					280					285			
Asn	Val	Asp	Leu	Asn	Arg	Asn	Phe	Lys	Asp	Asp	Val	Ala	Gly	Asp	His
	290					295					300				
Pro	Asp	Gly	Lys	Pro	Trp	Gln	Pro	Glu	Ala	Thr	Ala	Phe	Met	Asp	Leu
305					310					315					320
Glu	Gly	Asn	Thr	Ser	Phe	Val	Leu	Gly	Ala	Asn	Ile	His	Gly	Gly	Thr
			325						330					335	
Glu	Val	Val	Asn	Tyr	Pro	Trp	Asp	Asn	Lys	Lys	Glu	Arg	His	Ala	Asp
			340					345					350		
Asp	Glu	Trp	Tyr	Lys	Leu	Ile	Ser	Arg	Asn	Tyr	Ala	Ala	Ala	Cys	Gln
		355					360					365			
Ser	Ile	Ser	Ala	Ser	Tyr	Met	Thr	Ser	Glu	Thr	Asn	Ser	Gly	Ile	Ile
	370					375					380				
Asn	Gly	Ser	Asp	Trp	Tyr	Val	Ile	Arg	Gly	Ser	Arg	Gln	Asp	Asn	Ala
385					390					395					400
Asn	Tyr	Phe	His	Arg	Leu	Arg	Glu	Ile	Thr	Leu	Glu	Ile	Ser	Asn	Thr
			405						410					415	
Lys	Leu	Val	Pro	Ala	Ser	Gln	Leu	Pro	Lys	Tyr	Trp	Asn	Leu	Asn	Lys
			420					425					430		
Glu	Ser	Leu	Leu	Ala	Leu	Ile	Glu	Glu	Ser	Leu	Tyr	Gly	Ile	His	Gly
		435					440						445		

Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu
 450 455 460
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr
 465 470 475 480
 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys
 485 490 495
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys
 500 505 510
 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro
 515 520 525
 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly
 530 535 540
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp
 545 550 555 560
 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn
 565 570 575
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys
 580 585 590
 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile
 595 600 605
 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr
 610 615 620
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn
 625 630 635 640
 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser
 645 650 655
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp
 660 665 670
 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys
 675 680 685
 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala
 690 695 700
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr
 705 710 715 720
 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe
 725 730 735
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr
 740 745 750
 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu
 755 760 765
 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu
 770 775 780
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg
 785 790 795 800
 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile
 805 810 815
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr
 820 825 830
 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu
 835 840 845
 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu
 850 855 860
 Lys Ile His Ile Gly
 865

(2) INFORMATION FOR SEQ ID NO:302

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

Leu Ser Tyr Ser Gly Glu Ser Asp Ala Lys Glu Ser Asp Gln Asn Cys
 1 5 10 15

Arg	Lys	Cys	Thr	Phe	Ile	Gly	Phe	Glu	Lys	Arg	Val	Asn	Thr	Met	Arg
			20					25					30		
Leu	Ile	Lys	Ala	Phe	Leu	Val	Gln	Leu	Leu	Leu	Pro	Ile	Phe	Phe	
		35					40				45				
Tyr	Lys	Arg	Phe	Ile	Ser	Pro	Leu	Thr	Pro	Pro	Ser	Cys	Arg	Phe	Thr
	50				55					60					
Pro	Ser	Cys	Ser	Ser	Tyr	Ala	Ile	Glu	Ala	Leu	Arg	Lys	Tyr	Gly	Pro
65					70					75					80
Gly	Lys	Gly	Leu	Leu	Leu	Ser	Ile	Lys	Arg	Ile	Leu	Arg	Cys	His	Pro
			85						90					95	
Trp	Gly	Gly	Ser	Gly	Tyr	Asp	Pro	Val	Pro						
			100					105							

(2) INFORMATION FOR SEQ ID NO:303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

Leu	Glu	Met	Ala	Tyr	Asp	Phe	Thr	Gln	Thr	Phe	Arg	Asn	Ser	Leu	Glu
1				5					10					15	
Tyr	Ser	Tyr	Gln	Glu	Ala	Thr	Arg	Leu	Gly	Val	Val	Ala	Val	Thr	Gln
			20					25					30		
Asp	Met	Leu	Val	Leu	Gly	Ile	Ile	Arg	Asp	Gly	Asp	Asn	Gly	Ala	Ile
		35				40					45				
Asp	Ile	Met	Arg	His	Tyr	Gly	Ile	Asn	Leu	Tyr	Glu	Leu	Lys	Arg	Leu
	50				55					60					
Ile	Glu	Leu	Glu	Ala	Ile	Ala	Glu	Ser	Leu	Pro	Ala	Ser	Pro	Glu	Gly
65					70					75					80
Ser	Pro	Ile	Phe	Thr	Pro	Ser	Ala	Arg	Glu	Ala	Ile	Asp	Asp	Ala	Thr
			85					90						95	
Asp	Ile	Cys	Ala	Asp	Met	Glu	Asp	Glu	Ala	Val	Ser	Pro	Val	His	Leu
		100					105						110		
Leu	Leu	Ser	Ile	Leu	Asn	Ser	Thr	Gln	Glu	Ser	Leu	Val	Gln	Lys	Ile
		115					120					125			
Phe	Met	Lys	Gln	Gly	Ile	Lys	Tyr	Asp	Thr	Ile	Leu	Ser	Asp	Tyr	Phe
	130				135						140				
Gly	Gln	Arg	Asn	Pro	Ser	Glu	Gly	Lys	Ser	Pro	Ser	Glu	Met	Glu	Ile
145					150					155					160
Leu	Asp	Gly	Tyr	Gln	Asp	Asn	Asp	Phe	Asp	Asp	Glu	Glu	Asp	Glu	Ser
			165					170						175	
Ser	Pro	Pro	Ser	Gly	Asn	Ser	Gly	Thr	Gly	Gly	Gly	Ser	Gly	Asp	Ala
		180					185						190		
Pro	Glu	Gln	Asn	Thr	Gly	Gly	Gly	Asp	Thr	Thr	Thr	Thr	Thr	Arg	Ser
		195					200					205			
Gly	Gly	Asp	Thr	Pro	Ala	Leu	Asp	Thr	Phe	Gly	Thr	Asp	Ile	Thr	Ala
	210				215					220					
Met	Ala	Ala	Ala	Gly	Lys	Leu	Asp	Pro	Val	Val	Gly	Arg	Glu	Gln	Glu
225					230					235					240
Ile	Glu	Arg	Val	Ile	Gln	Ile	Leu	Ser	Arg	Arg	Lys	Lys	Asn	Asn	Pro
			245						250					255	
Val	Leu	Ile	Gly	Glu	Pro	Gly	Val	Gly	Lys	Ser	Ala	Ile	Val	Glu	Gly
		260					265						270		
Leu	Ala	Glu	Arg	Ile	Val	Asn	Arg	Lys	Val	Ser	Arg	Ile	Leu	Phe	Asp
		275				280					285				
Lys	Arg	Ile	Ile	Ser	Leu	Asp	Leu	Ala	Gln	Met	Val	Ala	Gly	Thr	Lys
	290				295					300					
Tyr	Arg	Gly	Gln	Phe	Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Leu
305					310					315					320
Lys	Lys	Asn	Pro	Gln	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile
			325					330					335		
Val	Gly	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Met	Asp	Thr	Ala	Asn	Met	Leu
			340				345						350		

Lys Pro Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr
 355 360 365
 Leu Asp Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg
 370 375 380
 Arg Phe Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu
 385 390 395 400
 Thr Ile Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val
 405 410 415
 Arg Tyr Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg
 420 425 430
 Tyr Val Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp
 435 440 445
 Glu Ala Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu
 450 455 460
 Ile Glu Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu
 465 470 475 480
 Ser Ala Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp
 485 490 495
 Gln Glu Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp
 500 505 510
 Glu Glu Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val
 515 520 525
 Ala His Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser
 530 535 540
 Thr Gly Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr
 545 550 555 560
 Lys Val Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile
 565 570 575
 Gln Arg Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser
 580 585 590
 Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys
 595 600 605
 Lys Leu Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val
 610 615 620
 Asp Met Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly
 625 630 635 640
 Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu
 645 650 655
 Arg Val Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu
 660 665 670
 Lys Ala His Ala Asp Val Phe Asn Leu Leu Leu Gln Val Met Asp Glu
 675 680 685
 Gly Gln Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr
 690 695 700
 Val Ile Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe
 705 710 715 720
 Gly Gln Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Glu Ala Asn Lys
 725 730 735
 Glu His Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser
 740 745 750
 Pro Glu Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu
 755 760 765
 Gly Lys Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val
 770 775 780
 Leu Ala Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu
 785 790 795 800
 Ala Lys Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala
 805 810 815
 Arg Pro Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr
 820 825 830
 Asp Leu Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu
 835 840 845
 Ser Ala Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala
 850 855 860

(2) INFORMATION FOR SEQ ID NO:304

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

```
Arg Gly Gly Gln Ile Arg Arg His His Thr Asp Ser Ser Arg Gly Ser
1      5      10      15
Asp Ser Lys Ala Cys Arg Phe Ser Phe His Ala Glu Thr Ile Gly Phe
20      25      30
Ser Asn His Gln Arg Ala Lys Met Asn Tyr Leu Tyr Ile Leu Ile Thr
35      40      45
Leu Leu Leu Ser Gly Phe Phe Ser Gly Ala Glu Ile Ala Phe Leu Ser
50      55      60
Ser Asp Lys Leu Arg Leu Glu Leu Asp Arg Asn Arg Gly Asp Leu Thr
65      70      75      80
Gly Arg Ala Leu Asn Leu Leu Tyr Arg His Pro Asp Gln Leu Val Thr
85      90      95
Thr Leu Leu Val Gly Asn Asn Ile Val Leu Val Val Tyr Gly Leu Leu
100      105      110
Met Ala Gly Leu Leu Ala Ala Pro Leu Ala Gln Trp Ile Asp Asn Asp
115      120      125
Ala Met Ile Val Val Leu Gln Ser Val Leu Ser Thr Ile Ile Ile Leu
130      135      140
Phe Thr Gly Glu Phe Leu Pro Lys Ala Ile Phe Lys Thr Asn Ala Asn
145      150      155      160
Met Met Met Arg Val Phe Ala Leu Pro Ile Val Ala Ile Tyr Tyr Leu
165      170      175
Leu Tyr Pro Leu Ser Lys Leu Phe Thr Gly Leu Ser Arg Ser Phe Ile
180      185      190
Arg Leu Val Asp Lys Asn Tyr Val Pro Thr Thr Val Gly Leu Gly Arg
195      200      205
Val Asp Leu Asp His Tyr Leu Ala Glu Asn Met Ser Gly Glu Asn Glu
210      215      220
Gln Asn Asp Leu Thr Thr Glu Val Lys Ile Ile Gln Asn Ala Leu Asp
225      230      235      240
Phe Ser Gly Ile Gln Val Arg Asp Cys Met Ile Pro Arg Asn Glu Met
245      250      255
Ile Ala Cys Glu Leu Gln Thr Asp Ile Glu Val Leu Lys Thr Thr Phe
260      265      270
Ile Asp Thr Gly Leu Ser Lys Ile Ile Ile Tyr Arg Gln Asn Ile Asp
275      280      285
Asp Val Val Gly Tyr Ile His Ser Ser Glu Met Phe Arg Gly Gln Asp
290      295      300
Trp Gln Lys Arg Ile Asn Thr Thr Val Phe Val Pro Glu Ser Met Tyr
305      310      315      320
Ala Asn Lys Leu Met Arg Leu Leu Met Gln Arg Lys Lys Ser Ile Ala
325      330      335
Ile Val Ile Asp Glu Leu Gly Gly Thr Ala Gly Met Val Thr Leu Glu
340      345      350
Asp Leu Val Glu Glu Ile Phe Gly Asp Ile Glu Asp Glu His Asp Thr
355      360      365
Arg Lys Ile Ile Ala Lys Gln Leu Gly Pro His Thr Tyr Leu Val Ser
370      375      380
Gly Arg Met Glu Ile Asp Asp Val Asn Glu Arg Phe Gly Leu Ser Leu
385      390      395      400
Pro Glu Ser Asp Asp Tyr Leu Thr Val Ala Gly Phe Ile Leu Asn Ser
405      410      415
His Gln Asn Ile Pro Gln Ala Asn Glu Val Val Glu Ile Ala Pro Tyr
420      425      430
Thr Phe Thr Ile Leu Arg Ser Ser Thr Lys Ile Glu Leu Val Lys
435      440      445
Met Ser Ile Asp Asp Gln Ser Asn
450      455
```

(2) INFORMATION FOR SEQ ID NO:305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

```
Leu Lys Lys Glu Ile Thr Met Lys Gln Asn Tyr Phe Lys Arg Val Cys
1      5      10      15
Ser Leu Leu Trp Leu Val Leu Pro Met Leu Ile Met Pro Leu Glu Val
20      25      30
Ala Ala Gln Glu Ile Ile Pro Asn Glu Glu Val Leu Glu Ser Leu Thr
35      40      45
Phe Val Ala Pro Val Glu Glu Thr Asp Ala Ile Glu Ala Glu Val Glu
50      55      60
Ala Leu Gln Glu Ile Val Ala Thr Glu Glu Ile Ala Glu Gln Ala Val
65      70      75      80
Arg Ser Tyr Thr Tyr Thr Val Tyr Arg Asp Gly Val Lys Ile Ala Ser
85      90      95
Gly Leu Thr Glu Pro Thr Phe Leu Asp Glu Asp Val Pro Ala Gly Glu
100     105     110
His Thr Tyr Cys Val Glu Val Gln Tyr Gln Gly Gly Val Ser Asp Lys
115     120     125
Val Cys Val Asp Val Glu Val Lys Asp Phe Lys Pro Val Thr Asn Leu
130     135     140
Thr Gly Thr Ala Ser Asn Asp Glu Val Ser Leu Asp Trp Asp Gly Val
145     150     155     160
Glu Glu Lys Ala Glu Glu Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn
165     170     175
Val Tyr Lys Asn Gly Thr Leu Ile Gly Asn Thr Ala Glu Thr His Tyr
180     185     190
Val Glu Thr Gly Val Ala Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val
195     200     205
Lys Tyr Pro Asp Gly Val Ser Pro Lys Val Ala Val Thr Val Thr Val
210     215     220
Thr Asn Ser Ser Leu Ser Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu
225     230     235     240
Arg Val Glu Gly Lys Lys Ile Ile Ala Glu Ala His Gly Met Ile Thr
245     250     255
Leu Tyr Asp Ile Asn Gly Arg Thr Val Ala Val Ala Pro Asn Arg Leu
260     265     270
Glu Tyr Met Ala Gln Thr Gly Phe Tyr Ala Val Arg Phe Asp Val Gly
275     280     285
Asn Lys His His Val Ser Lys Ile Gln Val Arg
290     295
```

(2) INFORMATION FOR SEQ ID NO:306

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

```
Leu Phe Asn His Lys Lys Ser Trp Tyr Glu Thr Phe Gln Phe Tyr Leu
1      5      10      15
Val Val Phe Arg Ser Gly Phe Ile Leu Leu Cys Glu Asn Thr Leu Ala
20      25      30
Gln Gln Lys Thr Glu Glu Phe Ala Pro Val Ser Asp Leu Arg Ala Glu
35      40      45
Ala Tyr Gly Ser Thr Val Phe Leu His Trp Thr Pro Pro Tyr Asp Asn
50      55      60
```

```

Pro Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile
65      70      75      80
Trp Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu
      85      90      95
Thr Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr
      100      105      110
Ile Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro
      115      120      125
Glu Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val
      130      135      140
Cys Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser
      145      150      155      160
Ser Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu
      165      170      175
Glu Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly
      180      185      190
Asn Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn
      195      200      205
Asp Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe
      210      215      220
Trp Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg
      225      230      235      240
Arg Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg
      245      250      255
Asp Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp
      260      265      270
Thr Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr
      275      280      285
Leu Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn
      290      295      300
Ser Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val
      305      310      315      320
Gly Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr
      325      330      335
Asp Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr
      340      345      350
Lys Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr
      355      360      365
Val Tyr Thr Glu Lys Ile Gln Ile Gln
      370      375

```

(2) INFORMATION FOR SEQ ID NO:307

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

```

Phe Gly Ile Ser Pro Ser Met Lys Lys Ser Phe Leu Leu Ala Ile Val
1      5      10      15
Met Leu Phe Gly Ile Ala Met Gln Gly His Ser Ala Pro Val Thr Lys
      20      25      30
Glu Arg Ala Leu Ser Leu Ala Arg Leu Ala Leu Arg Gln Val Ser Leu
      35      40      45
Arg Met Gly Gln Thr Ala Val Ser Asp Lys Ile Ser Ile Asp Tyr Val
      50      55      60
Tyr Arg Gln Gly Asp Ala Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly
65      70      75      80
Ser Pro Ala Tyr Phe Tyr Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr
      85      90      95
Ala Leu Val Ala Ala Asp Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser
      100      105      110
Pro Ile Gly Arg Phe Asp Met Asp Ser Met Pro Asp Asn Leu Arg Met
      115      120      125

```

Trp	Leu	Gln	Ile	Tyr	Asp	Gln	Glu	Ile	Gly	Leu	Ile	Leu	Ser	Gly	Lys
130						135					140				
Ala	Gln	Leu	Asn	Glu	Glu	Ile	Leu	Arg	Thr	Glu	Gly	Val	Pro	Ala	Glu
145						150					155				160
Val	His	Ala	Leu	Met	Asp	Asn	Gly	His	Phe	Ala	Asn	Asp	Pro	Met	Arg
				165					170					175	
Trp	Asn	Gln	Gly	Tyr	Pro	Trp	Asn	Asn	Lys	Glu	Pro	Leu	Leu	Pro	Asn
		180						185				190			
Gly	Asn	His	Ala	Tyr	Thr	Gly	Cys	Val	Ala	Thr	Ala	Ala	Ala	Gln	Ile
	195						200					205			
Met	Arg	Tyr	His	Ser	Trp	Pro	Leu	Gln	Gly	Glu	Gly	Ser	Phe	Asp	Tyr
	210					215					220				
His	Ala	Gly	Ser	Leu	Val	Gly	Asn	Trp	Ser	Gly	Thr	Phe	Gly	Glu	Met
225					230					235					240
Tyr	Asp	Trp	Ile	Asn	Met	Pro	Gly	Asn	Pro	Asp	Leu	Asp	Asn	Leu	Thr
				245					250					255	
Gln	Ser	Gln	Val	Asp	Ala	Tyr	Ala	Thr	Leu	Met	Arg	Asp	Val	Ser	Ala
		260					265						270		
Ser	Val	Ser	Met	Ser	Phe	Tyr	Glu	Asn	Gly	Ser	Gly	Thr	Tyr	Ser	Val
	275						280					285			
Tyr	Val	Val	Gly	Ala	Leu	Arg	Asn	Asn	Phe	Arg	Tyr	Lys	Arg	Ser	Leu
	290					295				300					
Gln	Leu	His	Val	Arg	Ala	Leu	Tyr	Thr	Ser	Gln	Glu	Trp	His	Asp	Met
305					310					315					320
Ile	Arg	Gly	Glu	Leu	Ala	Ser	Gly	Arg	Pro	Val	Tyr	Tyr	Ala	Gly	Asn
			325						330					335	
Asn	Gln	Ser	Ile	Gly	His	Ala	Phe	Val	Cys	Asp	Gly	Tyr	Ala	Ser	Asp
		340					345						350		
Gly	Thr	Phe	His	Phe	Asn	Trp	Gly	Trp	Gly	Gly	Val	Ser	Asn	Gly	Phe
	355						360				365				
Tyr	Lys	Leu	Thr	Leu	Leu	Ser	Pro	Thr	Ser	Leu	Gly	Ile	Gly	Gly	Glu
	370					375					380				
Gly	Ile	Gly	Phe	Thr	Ile	Tyr	Gln	Glu	Ile	Ile	Thr	Gly	Ile	Glu	Pro
385					390					395					400
Ala	Lys	Thr	Pro	Ala	Glu	Ala	Gly	Thr	Asp	Ala	Leu	Pro	Ile	Leu	Ala
				405					410					415	
Leu	Lys	Asp	Ile	Glu	Ala	Glu	Tyr	Lys	Ser	Glu	Ser	Gly	Leu	Asn	Val
		420					425						430		
Gly	Tyr	Ser	Ile	Tyr	Asn	Thr	Gly	Glu	Glu	Gln	Ser	Asn	Leu	Asp	Leu
	435						440				445				
Gly	Tyr	Arg	Leu	Asn	Lys	Ala	Asp	Gly	Glu	Val	Ile	Glu	Val	Lys	Thr
	450				455					460					
Ser	Ser	Ile	Asn	Ile	Ser	Trp	Tyr	Gly	Tyr	Gly	Glu	His	Pro	Glu	Ser
465					470					475					480
Phe	Ser	Leu	Ala	Pro	Asn	Gln	Leu	Ser	Gln	Gly	Ile	Asn	Thr	Ile	Thr
			485						490					495	
Leu	Leu	Tyr	Arg	Arg	Thr	Gly	Thr	Glu	Gln	Trp	Glu	Pro	Val	Arg	His
		500					505						510		
Ala	Gln	Gly	Gly	Tyr	Val	Asn	Ser	Ile	Lys	Val	Asn	Thr	Thr	Asp	Pro
	515						520				525				
Asn	Asn	Val	Val	Val	Thr	Val	Asp	Asn	Asn	Glu	Gly	Lys	Leu	Ser	Ile
530						535					540				
Val	Pro	Asn	Ser	Phe	Val	Ala	Asp	Leu	Asn	Ser	Tyr	Glu	His	Ser	Thr
545					550					555					560
Ile	Thr	Val	Gln	Phe	Asn	Ser	Asp	Ser	Pro	Asp	Glu	Ile	Arg	Thr	Pro
			565						570					575	
Val	Ala	Phe	Ala	Leu	Ser	Thr	Gly	Ala	Thr	Ala	Asp	Asp	Val	Ile	Ser
		580					585						590		
Leu	Gly	Trp	Val	Met	Ala	Glu	Val	Pro	Gly	Gly	Ser	Ser	Asn	Tyr	Pro
	595						600					605			
Val	Val	Trp	Ser	Lys	Asp	Val	Leu	Thr	Leu	Ser	Glu	Gly	Asp	Tyr	Thr
	610					615					620				
Leu	Trp	Tyr	Arg	Phe	Ser	Ile	Asn	Asn	Gln	Lys	Asp	Glu	Trp	Lys	Lys
625					630					635					640
Ile	Gly	Ser	Val	Ser	Val	Lys	Thr	Pro	Thr	Glu	Tyr	Thr	His	Pro	Leu
			645						650					655	
Phe	Glu	Val	Gly	His	Asn	Gln	Thr	Ser	Thr	Tyr	Thr	Leu	Asp	Met	Ala
	660						665					670			
His	Asn	Arg	Val	Leu	Pro	Asp	Phe	Thr	Leu	Lys	Asn	Leu	Gly	Leu	Pro
	675						680					685			
Phe	Asn	Gly	Glu	Leu	Val	Val	Phe	Arg	Gln	Thr	Gln	Ser	Ser	Ser	Ser
	690					695				700					
Gly	Ser	Leu	Trp	Ala	Ala	Gln	Glu	Thr	Val	His	Ile	Lys	Gln	Gly	Glu
705					710					715					720
Thr	Phe	Val	Tyr	Lys	Pro	Val	Val	Glu	Gly	Pro	Ile	Pro	Asp	Gly	Ser
			725						730					735	
Tyr	Arg	Ala	Thr	Leu	His	Ala	Phe	Val	Asn	Gly	Gln	Gln	Gln	Leu	Tyr

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...230
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

```

Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser
1      5      10      15
Val Leu Ala Val Ala Leu Val Phe Ala Gly Cys Gly Leu Asn Asn Met
      20      25      30
Ala Lys Gly Gly Leu Ile Gly Ala Gly Val Gly Gly Ala Ile Gly Ala
      35      40      45
Gly Val Gly Asn Val Ala Gly Asn Thr Ala Val Gly Ala Ile Val Gly
      50      55      60
Thr Ala Val Gly Gly Ala Ala Gly Ala Leu Ile Gly Lys Lys Met Asp
      65      70      75      80
Lys Gln Lys Lys Glu Leu Glu Ala Ala Val Pro Asp Ala Thr Ile Gln
      85      90      95
Thr Val Asn Asp Gly Glu Ala Ile Leu Val Thr Phe Asp Ser Gly Ile
      100     105     110
Leu Phe Ala Thr Asn Ser Ser Thr Leu Ser Pro Asn Ser Arg Thr Ala
      115     120     125
Leu Thr Lys Phe Ala Ala Asn Met Asn Lys Asn Pro Asp Thr Asp Ile
      130     135     140
Arg Ile Val Gly His Thr Asp Asn Thr Gly Ser Asp Lys Ile Asn Asp
      145     150     155     160
Pro Leu Ser Glu Arg Arg Ala Ala Ser Val Tyr Ser Phe Leu Asn Ser
      165     170     175
Gln Gly Val Ser Met Ser Arg Met Ala Ala Glu Gly Arg Gly Ser His
      180     185     190
Glu Pro Val Ala Asp Asn Ser Thr Val Ala Gly Arg Ser Ala Asn Arg
      195     200     205
Arg Val Glu Val Tyr Ile Leu Pro Asn Ala Lys Met Ile Glu Gln Ala
      210     215     220
Gln Gln Gly Thr Leu Lys
      225     230

```

(2) INFORMATION FOR SEQ ID NO:310

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...342
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

```

Asn Arg Asn Arg Asn Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys
1      5      10      15
Ser Leu Cys Phe Ile Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn
      20      25      30
Val Arg Asn Ser Gln Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys
      35      40      45
Pro Ser Asp Ser Val Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu
      50      55      60

```

Glu Phe Arg Asn Lys Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu
 65 70 75 80
 Tyr Glu Asn Arg Leu Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp
 85 90 95
 Leu Tyr Gly Glu Asp Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly
 100 105 110
 Ala Gly Thr Asp Val Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser
 115 120 125
 Ser Phe Val Met Pro Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly
 130 135 140
 Tyr Arg Arg Arg Phe Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val
 145 150 155 160
 Asn Arg Gly Asp Thr Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val
 165 170 175
 Arg Ser Tyr Glu Ala Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His
 180 185 190
 Pro Asn Gly Leu Glu Thr Val Tyr Gly His Met Ser Arg Gln Leu Val
 195 200 205
 Asp Glu Asn Gln Ile Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly
 210 215 220
 Ser Thr Gly Arg Ser Thr Gly Pro His Leu His Phe Glu Thr Arg Phe
 225 230 235 240
 Met Gly Ile Pro Ile Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly
 245 250 255
 Val Pro Leu Arg Asp Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg
 260 265 270
 Tyr Ala Lys Ala Ser Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys
 275 280 285
 Lys Gly Arg Gln Ala Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly
 290 295 300
 Asp Thr Leu Glu Thr Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys
 305 310 315 320
 Leu Cys Ala Thr Asn Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly
 325 330 335
 Lys Ala Leu Arg Ile Lys
 340

(2) INFORMATION FOR SEQ ID NO:311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

Pro Ser Lys Thr Ile Ile Lys Thr Met Ala Lys Ile Asn Phe Tyr Ala
 1 5 10 15
 Glu Gly Val Ser Leu Pro Arg Ile Arg Arg Arg Ile Val Gly Lys Trp
 20 25 30
 Ile Ala Glu Val Cys Ser Arg Tyr Gly Lys Ala Val Gly Glu Ile Ser
 35 40 45
 Tyr Leu Phe Cys Asp Asp Glu Tyr Ile Leu Lys Ala Asn Gln Glu Phe
 50 55 60
 Leu Asp His Asp Tyr Tyr Thr Asp Ile Ile Thr Phe Asp Ser Cys Glu
 65 70 75 80
 Ala Asp Thr Val Asn Gly Asp Leu Leu Ile Ser Leu Asp Thr Val Arg
 85 90 95
 Ser Asn Ala Arg Ala Leu Asp Leu Arg Tyr Glu Asp Glu Leu His Arg
 100 105 110
 Val Ile Ile His Gly Ile Leu His Leu Cys Gly Leu Lys Asp Lys Ser
 115 120 125
 Lys Lys Asp Glu Ala Gln Met Arg Ala Ala Glu Glu Lys Ala Leu Val
 130 135 140
 Met Leu Arg Glu Thr Ile Gly Ser Glu Leu Ser Leu Leu His Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:312

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

```
Lys Ser Lys Thr Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly
1      5      10      15
Ala Ile Ala Leu Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr
      20      25      30
Gly Gln Leu Pro Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly
      35      40      45
Ser Asn Trp Phe Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu
      50      55      60
Asn Asp Asn Asn Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly
65      70      75      80
Ser Leu Ser Val Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu
      85      90      95
Gln Ile Asn Gly Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu
      100      105      110
Gln Glu Ile Asn Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe
      115      120      125
Asp Val Val Asn Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His
130      135      140
Leu Ile Pro Trp Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser
145      150      155      160
Glu Trp Ser Lys Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val
      165      170      175
Met Met Ala Phe Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala
      180      185      190
Gln Ala Ala His Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys
195      200      205
Lys Thr Pro Val Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe
210      215      220
Gln Gly Met Ala Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly
225      230      235      240
Phe Asn Ala Ile Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn
      245      250      255
Gly Gln Ile Asn Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg
260      265      270
Pro Val Ser Cys Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr
275      280      285
Glu Asn Ile Leu Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His
290      295      300
Val Val Asp Lys Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe
305      310      315      320
Val Lys Glu Thr Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro
      325      330      335
Thr Gly Asn Thr Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys
340      345      350
Ala Val Val Asp Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu
355      360      365
Ile Ser Val Glu Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys
370      375      380
Ala Trp Asn Arg Val Val Ile Val Arg Ser Lys
385      390      395
```

(2) INFORMATION FOR SEQ ID NO:313

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

```
Tyr Lys Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala
1      5      10      15
Leu Ala Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr
20      25      30
Thr Gln Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala
35      40      45
Ser Asp His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu
50      55      60
Ser Gly Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val
65      70      75      80
Pro Thr Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg
85      90      95
Leu Gln Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys
100     105     110
Glu Arg Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe
115     120     125
Asp Leu Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His
130     135     140
Ile Ile Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu
145     150     155     160
Asn Ala Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr
165     170     175
Val Asn Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp
180     185     190
Phe Asn Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly
195     200     205
Thr Lys Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu
210     215     220
Thr Phe Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp
225     230     235     240
Tyr Ala Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly
245     250     255
Gln Val Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro
260     265     270
Glu Pro Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val
275     280     285
Tyr Phe Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn
290     295     300
Val Tyr Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys
305     310     315     320
Val Val Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met
325     330     335
Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys
340     345     350
Tyr Gly Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser
355     360     365
Glu Gln Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr
370     375     380
Ala Ala Glu
385
```

(2) INFORMATION FOR SEQ ID NO:314

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

```
Val Ile Gly Ile Ile Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val
1      5      10      15
Phe Val Asn Asn Val Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe
      20      25      30
Leu Gly Val Ser Lys Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala
      35      40      45
Val Thr Phe Val Leu Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln
      50      55      60
Lys Phe Val Leu Asp Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala
65      70      75      80
Phe Ile Leu Val Ile Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu
      85      90      95
Lys Lys Val Ser Pro Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro
      100     105     110
Leu Ile Thr Thr Asn Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile
      115     120     125
Gln Lys Asp Tyr Thr Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr
130     135     140
Ala Ile Gly Phe Thr Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu
145     150     155     160
Gln Leu Asp Met Thr Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser
      165     170     175
Ala Leu Leu Ala Ala Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser
      180     185     190
Gly Ile Ala
      195
```

(2) INFORMATION FOR SEQ ID NO:315

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

```
Tyr Arg Ser Tyr Arg Gly Ile Gly Ser Gly Thr His Ser Pro Asn Leu
1      5      10      15
Lys Asn Arg Leu Lys Arg Ile Gly Ile Arg Ile Pro Asn Arg His Tyr
      20      25      30
Ile His Ile Lys Pro Ile Lys Pro Lys Asn Lys Met Lys Gln Leu Asn
      35      40      45
Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu Gly Thr Ser Ala Ser
      50      55      60
Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr Val Val Asp Lys Ser
65      70      75      80
Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe Val Lys Gly Thr Thr
      85      90      95
Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr Ser Ile Lys Gly Ile
      100     105     110
Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu Met Gly Tyr Ser Thr
      115     120     125
Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly Ser Arg His Val Asp
130     135     140
Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp Gly Val Val Val Ser
145     150     155     160
Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala Pro Ser Leu Val Thr
```

				165						170						175		
Val	Leu	Ser	Pro	Glu	Leu	Phe	Leu	Lys	Thr	Asn	Ser	Thr	Asn	Leu	Ser			
			180					185					190					
Gln	Gly	Leu	Lys	Phe	Gln	Pro	Gly	Leu	Arg	Val	Glu	Asp	Asn	Cys	Gln			
		195					200					205						
Asn	Cys	Gly	Phe	Asn	Gln	Val	Arg	Ile	Asn	Gly	Leu	Glu	Gly	Ala	Tyr			
	210					215				220								
Ser	Gln	Ile	Leu	Ile	Asp	Ser	His	Pro	Ile	Phe	Ser	Ser	Leu	Ala	Gly			
225					230					235					240			
Val	Tyr	Gly	Leu	Glu	Gln	Met	Pro	Ala	Asn	Met	Ile	Glu	Arg	Val	Glu			
				245					250						255			
Val	Ile	Arg	Gly	Gly	Gly	Ser	Ala	Leu	Phe	Gly	Ser	Asn	Ala	Val	Gly			
			260					265					270					
Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Glu	Pro	Leu	Arg	Asn	Ser	Ala	Glu			
		275					280					285						
Ile	Ser	His	Ser	Thr	Met	Thr	Phe	Asp	His	Ala	Lys	Gly	Trp	Gly	Ser			
	290					295					300							
Phe	Gln	Asn	Thr	Thr	Gln	Phe	Asn	Gly	Ser	Met	Leu	Thr	Glu	Asp	Arg			
305					310					315					320			
Lys	Ala	Gly	Val	Met	Val	Phe	Gly	Gln	His	Asn	Tyr	Arg	Pro	Gly	Gln			
				325					330					335				
Asp	Ile	Asp	Gly	Asp	Asn	Phe	Thr	Glu	Leu	Pro	Asn	Leu	Arg	Asn	Arg			
			340					345					350					
Ser	Leu	Gly	Phe	Arg	Ser	Tyr	Tyr	Lys	Thr	Gly	Leu	Tyr	Ser	Lys	Ala			
		355					360					365						
Thr	Leu	Glu	Tyr	His	Ser	Met	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Asp	Arg			
		370				375					380							
Leu	Asp	Asn	Pro	Pro	Phe	Glu	Ala	Gln	Ile	Ala	Glu	Tyr	Leu	Gln	His			
385					390					395					400			
Tyr	Ile	Asn	Gly	Gly	Ser	Phe	Lys	Phe	Asp	Gln	Gly	Phe	Ser	Gly	Gly			
			405						410					415				
Lys	Asp	Phe	Phe	Ser	Leu	Tyr	Ala	Ser	Ala	Gln	Asp	Val	Gln	Arg	Arg			
			420					425					430					
Ser	Tyr	Tyr	Gly	Gly	Gly	Asp	Tyr	Thr	Glu	Asn	Leu	Leu	Asn	Gly	Ala			
		435					440					445						
Val	Gln	Ser	Gly	Ser	Thr	Glu	Ser	Asp	Glu	Tyr	Asn	Asp	Ala	Phe	Thr			
		450				455					460							
Ala	Leu	Thr	Ser	Tyr	Gly	Thr	Thr	Lys	Gly	Phe	Asp	Leu	Gln	Gly	Gly			
465					470					475					480			
Gly	Met	Tyr	Arg	His	Thr	Phe	Gly	Glu	Asn	Trp	Asp	Phe	Thr	Gly	Gly			
				485					490					495				
Leu</																		

```

Gly Ser Phe Asp Phe Glu Met Asn Gly Gln Gln Phe Lys Gly Leu Ala
785          790          795          800
Glu Gly His Ala Lys Leu Val Lys Thr Pro Ala Phe Ala Asp Ile Asp
          805          810          815
Leu Lys Leu Ser His Asp Phe His Leu Ala Ser Thr Met Thr Leu Glu
          820          825          830
Leu Asn Ala Gly Ile Gln Asn Ile Phe Asn Ser Tyr Gln Lys Asp Thr
          835          840          845
Asp Lys Gly Pro Gly Arg Ala Ser Thr Tyr Val Tyr Gly Pro Met Gln
          850          855          860
Pro Arg Arg Ile Phe Val Gly Thr Lys Ile Asn Phe
865          870          875

```

(2) INFORMATION FOR SEQ ID NO:316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 899 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

```

Ile Leu Asn His Leu Arg Lys Thr Met Tyr Lys Lys Ile Ile Ala Val
1          5          10          15
Ala Ala Leu Phe Cys Ala Ser Ile Gly Ile Leu Lys Gly Gln Ser Ser
          20          25          30
Asp Leu Thr Pro Gln Asp Thr Ile Tyr Ser Pro Glu Ile Ser Tyr Ala
          35          40          45
Lys Pro Ile His Lys Thr Ile Ala Ser Ile Glu Ile Glu Gly Met Arg
          50          55          60
Ser Phe Asp Asp Phe Val Leu Arg Asn Leu Ser Gly Leu Ala Val Gly
65          70          75          80
Asp Glu Val Leu Ile Pro Gly Asp Ala Met Ser Ala Ala Val Asn Arg
          85          90          95
Ile Met Arg Gln Gly Tyr Phe Ser Asn Val Arg Ile Ile Ala Asp Lys
          100          105          110
Tyr Val Gly Asn Lys Val Tyr Leu Lys Ile Ile Val Thr Glu Arg Pro
          115          120          125
Arg Ile Ser Lys Val Thr Phe Ser Gly Val Lys Lys Ser Glu Arg Glu
          130          135          140
Asp Leu Glu Met Lys Ile Gly Leu Arg Glu Gly Ile Gln Met Thr Arg
145          150          155          160
Asn Asn Glu Asp Lys Val Arg Gln Ile Val Gln Lys Tyr Phe Ser Glu
          165          170          175
Lys Gly Tyr Arg Asp Ala Ser Ile Arg Ile Thr Gln Glu Pro Asp Leu
          180          185          190
Ser Lys Asp Gly Phe Val Asn Val Leu Ile Ser Ile Glu Lys Lys Ser
          195          200          205
Lys Thr Lys Val Asn Glu Ile Tyr Phe Ser Gly Asn Lys Ala Leu Ser
          210          215          220
Asn His Lys Leu Arg Met Ala Met Lys Asn Thr Asn Ala Lys Phe Ser
225          230          235          240
Leu Arg Lys His Ile Arg Ser Ser Phe Leu Lys Leu Phe Ser Thr His
          245          250          255
Lys Phe Val Glu Glu Ser Tyr Arg Glu Asp Leu Val Arg Leu Ile Glu
          260          265          270
Lys Tyr Gln Glu Tyr Gly Tyr Arg Asp Ala Glu Ile Leu Thr Asp Ser
          275          280          285
Val Val Lys Ala Pro Asp Gly Lys Arg Val Asp Ile Tyr Leu Asn Ile
          290          295          300
Glu Glu Gly Gln Lys Tyr Tyr Ile Lys Asp Val Asn Phe Val Gly Asn
305          310          315          320
Ser Gln Tyr Pro Ser Glu Tyr Leu Glu Arg Val Leu Gly Ile Lys Ser
          325          330          335
Gly Asp Val Tyr Asn Gln Arg Arg Leu Ala Lys Arg Leu Asn Glu Asp
          340          345          350

```

Glu Asp Ala Val Gly Asn Leu Tyr Tyr Asn Asn Gly Tyr Ile Phe Ala
 355 360 365
 Trp Val Asp Pro Val Glu Thr Asn Val Val Gly Asp Ser Val Ser Leu
 370 375 380
 Asp Ile Arg Ile Ala Glu Gly Lys Gln Ala Asn Ile Asn Lys Val Ile
 385 390 395 400
 Ile Lys Gly Asn Thr Val Val Tyr Glu Asp Val Val Arg Arg Glu Leu
 405 410 415
 Tyr Thr Lys Pro Gly Gln Leu Phe Ser Arg Glu Asp Ile Ile Asn Ser
 420 425 430
 Ile Arg Leu Ile Asn Gln Leu Gly His Phe Asp Ala Glu Lys Ser Ile
 435 440 445
 Pro Arg Pro Ile Pro Asn Pro Glu Thr Gly Thr Val Asp Ile Glu Tyr
 450 455 460
 Asp Leu Val Pro Arg Ser Ser Asp Gln Leu Glu Leu Ser Val Gly Trp
 465 470 475 480
 Ser Gln Ser Gly Leu Leu Phe Arg Gly Ala Ile Lys Phe Thr Asn Phe
 485 490 495
 Ser Val Gly Asn Leu Leu His Pro Ser Met Tyr Lys Lys Gly Ile Ile
 500 505 510
 Pro Gln Gly Asp Gly Gln Thr Leu Ser Leu Ser Ala Gln Thr Asn Gly
 515 520 525
 Lys Tyr Tyr Gln Gln Tyr Ser Val Thr Phe Met Asp Pro Trp Phe Gly
 530 535 540
 Gly Lys Arg Pro Asp Met Phe Ser Phe Ser Ala Phe Tyr Ser Lys Thr
 545 550 555 560
 Thr Ala Ile Asp Ser Lys Phe Tyr Asn Ser Asn Ala Gly Asn Tyr Tyr
 565 570 575
 Asn Ala Tyr Tyr Asn Ser Tyr Tyr Asn Asn Tyr Asn Ser Tyr Tyr Asn
 580 585 590
 Gly Met Ser Asn Tyr Thr Gly Asp Leu Tyr Thr Gln Ala Ser Asp Pro
 595 600 605
 Asp Arg Ser Leu Gln Met Leu Gly Thr Ser Ile Gly Tyr Gly Lys Arg
 610 615 620
 Leu Thr Trp Pro Asp Asn Trp Phe Gln Ile Tyr Thr Ser Leu Asn Tyr
 625 630 635 640
 Thr Tyr Tyr Arg Leu Arg Asn Trp Ser Tyr Asn Thr Phe Gln Asn Phe
 645 650 655
 His His Gly Ser Ala Asn Asp Leu Asn Leu Glu Leu Arg Leu Ser Arg
 660 665 670
 Thr Ser Ile Asp Asn Pro Ile Tyr Thr Arg Ser Gly Ser Asp Phe Met
 675 680 685
 Val Ser Val Ala Ala Thr Leu Pro Tyr Ser Leu Trp Asp Asn His Asp
 690 695 700
 Tyr Ala Ser Gln Asn Leu Ser Val Ser Asp Arg Tyr Arg Phe Ile Glu
 705 710 715 720
 Tyr His Lys Trp Lys Phe Arg Gly Arg Val Phe Thr Pro Leu Leu Asn
 725 730 735
 Pro Ala Thr His Lys Tyr Thr Pro Val Leu Met Ser Arg Val Glu Gly
 740 745 750
 Ala Val Leu Gly Ser Tyr Asn Ser Asn Lys Lys Ser Pro Phe Gly Thr
 755 760 765
 Phe Tyr Met Gly Gly Asp Gly Met Ser Ser Tyr Tyr Gly Gly Tyr Met
 770 775 780
 Asn Glu Thr Ile Gly Leu Arg Gly Tyr Lys Asn Gly Ser Ile Ala Gly
 785 790 795 800
 Asn Asn Tyr Asp Tyr Ala Tyr Ala Tyr Met Arg Leu Thr Met Glu Leu
 805 810 815
 Arg Phe Pro Ile Leu Phe Glu Asn Ser Phe Asn Ala Trp Leu Leu Ala
 820 825 830
 Phe Ala Glu Ala Gly Asn Ala Trp Arg Ser Ile Asp Asn Tyr Asn Pro
 835 840 845
 Phe Asn Leu Lys Arg Ser Ala Gly Val Gly Leu Arg Val Thr Leu Pro
 850 855 860
 Met Val Gly Met Leu Gly Ile Asp Trp Gly Tyr Gly Phe Asp Arg Pro
 865 870 875 880
 Asp Asn Ser Leu Gln Arg Gly Gly Ser Asn Val His Phe Val Leu Gly
 885 890 895
 Gln Glu Phe

(2) INFORMATION FOR SEQ ID NO:317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

```

Gln Ile Asn Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly
1           5           10           15
Phe Ala Leu Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu
          20           25           30
Val Asp Met Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met
          35           40           45
Asn Glu Gln Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu
          50           55           60
Ala Leu Glu Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp
65           70           75           80
Leu Val Phe Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile
          85           90           95
Val Lys Lys Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly
          100          105          110
Pro Glu Gly Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile
          115          120          125
Gln Asp Glu Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn
130          135          140
Tyr Gln Met Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser
145          150          155          160
Pro Ser Ile Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser
          165          170          175
Lys

```

(2) INFORMATION FOR SEQ ID NO:318

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

```

Arg Ile Asn Lys Gln His Glu Met Lys Lys Phe Phe Leu Met Leu Leu
1           5           10           15
Met Ala Leu Pro Leu Ser Leu Leu Ala Gln Lys Val Ala Val Val Asn
          20           25           30
Thr Glu Glu Ile Ile Ser Lys Met Pro Glu Gln Val Ala Ala Thr Lys
          35           40           45
Gln Leu Asn Glu Leu Ala Glu Lys Tyr Arg Leu Asp Leu Lys Ser Met
          50           55           60
Asp Asp Glu Phe Ala Lys Lys Thr Glu Glu Phe Val Lys Glu Lys Asp
65           70           75           80
Ser Leu Leu Glu Asn Ile Arg Asn Arg Arg Gln Gln Glu Leu Gln Asp
          85           90           95
Ile Gln Thr Arg Tyr Gln Gln Ser Tyr Gln Thr Met Gln Glu Asp Leu
          100          105          110
Gln Lys Arg Gln Gln Gln Leu Phe Ala Pro Ile Gln Gln Lys Val Ala
          115          120          125
Asp Ala Ile Lys Lys Val Gly Asp Glu Glu Asn Cys Ala Tyr Ile Met
130          135          140

```

Glu Ala Gly Met Met Leu Tyr Thr Gly Ala Thr Ala Ile Asp Leu Thr
 145 150 155 160
 Ala Lys Val Lys Ala Lys Leu Gly Ile Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:319

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

Ile Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn
 1 5 10 15
 Gly Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser
 20 25 30
 Gln Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp
 35 40 45
 Arg Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr
 50 55 60
 Gly Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met
 65 70 75 80
 Lys Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr
 85 90 95
 Gln Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu
 100 105 110
 Asn Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val
 115 120 125
 Gln Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg
 130 135 140
 Asp Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile
 145 150 155 160
 Ser Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr
 165 170 175
 Ser Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly
 180 185 190
 Val Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly
 195 200 205
 Leu Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala
 210 215 220
 Gly Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp
 225 230 235 240
 Ile Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly
 245 250 255
 Met Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser
 260 265 270
 Gln Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr
 275 280 285
 Thr Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr
 290 295 300
 Phe Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly
 305 310 315 320
 Asn Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr
 325 330 335
 Ser Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp
 340 345 350
 Gly Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met
 355 360 365
 Asn Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala
 370 375 380
 Phe Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe
 385 390 395 400
 Leu Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser
 405 410 415

Gly Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His
 420 425 430
 Ala Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly
 435 440 445
 Glu Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala
 450 455 460
 Gln Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp
 465 470 475 480
 Ser Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr
 485 490 495
 Asn Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala
 500 505 510
 Phe Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Gly Thr Phe Ser
 515 520 525
 Leu Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu
 530 535 540
 Leu Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro
 545 550 555 560
 Ala Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe
 565 570 575
 Tyr Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val
 580 585 590
 Val Val Leu Asn Glu Lys Ile Arg Ser Gln Gly Ala Phe His Ile Leu
 595 600 605
 Ala Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe
 610 615 620
 Thr Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile
 625 630 635 640
 Ile Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly
 645 650 655
 Tyr Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly
 660 665 670
 Val Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu
 675 680 685
 Asp Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe
 690 695 700
 Ser Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala
 705 710 715 720
 Thr Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser
 725 730 735
 Lys Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val
 740 745 750
 Asp Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala
 755 760 765
 Gly Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala
 770 775 780
 Asp Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp
 785 790 795 800
 Val Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr
 805 810 815
 Arg Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe
 820 825

(2) INFORMATION FOR SEQ ID NO:320

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

Pro Ile Pro Phe Leu Leu Asn Met Tyr Ser Gly His His Lys Ile His
 1 5 10 15
 Tyr Pro Phe Leu Ile Leu Leu Val Cys Leu Ala Phe Ala Ala Cys Lys
 20 25 30

Ser Val Lys Leu Lys Asp Ala Glu Lys Ala His Asp Arg Gln Glu Tyr
 35 40 45
 Thr Lys Ala Ala Asp Met Tyr Asn Thr Leu Tyr Arg Arg Thr Arg Arg
 50 55 60
 Lys Gln Val Glu Met Lys Ala Tyr Thr Ala Phe Arg Ser Gly Glu Asn
 65 70 75 80
 Tyr Arg Ala Ala Gly Arg Gln Ala Lys Ala Leu Arg Gly Tyr Leu Asn
 85 90 95
 Ala Arg Arg Tyr Gly Tyr Pro Asp Ser Val Val Leu Leu Arg Leu Ala
 100 105 110
 Gln Thr Tyr Gln Gln Gly Gly Asn Tyr Lys Glu Ala Glu Val Leu Phe
 115 120 125
 Arg Gly Tyr Leu Glu Ala Tyr Pro Lys Ser Tyr Phe Ala Ala Ile Gly
 130 135 140
 Leu Glu Gly Cys Leu Phe Ala Arg Gln Gln Lys Glu Tyr Pro Thr Arg
 145 150 155 160
 Tyr Arg Ile Arg Arg Ala Ala Glu Trp Asn Ser Ala Arg Gly Asp Phe
 165 170 175
 Gly Pro Ala Tyr Ala Pro Asp Ala Ser Ala Leu Tyr Phe Thr Ser Ser
 180 185 190
 Arg Ser Lys Asp Asp Gly Leu Asp Asn Ser Ser Ile Thr Gly Leu Lys
 195 200 205
 Pro Asn Asp Ile Tyr Ile Ile Lys Arg Asp Ala Gln Gly Arg Trp Gly
 210 215 220
 Arg Pro Asp Ser Val Ser Gly Gly Ile Asn Thr Pro Trp Asp Glu Gly
 225 230 235 240
 Val Pro Thr Ile Thr Pro Asp Gly Ser Thr Ile Tyr Tyr Thr Leu Ala
 245 250 255
 Gln Gln Gly Ala Asp Tyr Asp Arg Thr Val Gln Ile Tyr Ser Ala Ala
 260 265 270
 Arg Ser Gly Glu Gly Gly Trp Ser Asn Gly Ser Leu Val Asp Ile Met
 275 280 285
 Arg Asp Ser Leu Arg Met Ala Ala His Pro Ser Met Ser Ala Ser Gly
 290 295 300
 Asp Tyr Leu Tyr Phe Val Ser Asn Ile Gly Gly Ser Tyr Gly Gly Lys
 305 310 315 320
 Asp Ile Tyr Arg Val Lys Val Ser Asp Arg Ser Tyr Gly Ser Pro Glu
 325 330 335
 Asn Leu Gly Pro Asp Ile Asn Thr Pro Gly Asp Glu Met Phe Pro Phe
 340 345 350
 Ile Asp Gly Asp Ser Thr Leu Phe Phe Ala Ser Asp Gly His Ala Gly
 355 360 365
 Leu Gly Gly Leu Asp Ile Phe Lys Ala Thr Leu Asp Ser Thr Gly Gln
 370 375 380
 Trp His Val Val Asn Met Gly Gln Pro Val Asn Ser Ser Ala Asp Asp
 385 390 395 400
 Phe Gly Leu Ala Val Glu Pro Lys Gly Lys Asn Lys Glu Glu Ala Leu
 405 410 415
 Pro Asp Asn Gly Val Lys Gly Val Phe Cys Ser Asn Arg Gly Asp Ala
 420 425 430
 Arg Gly Trp Pro His Leu Phe His Phe Glu Leu Pro Ala Ile Tyr Thr
 435 440 445
 Glu Ile Gln Gly Tyr Val Met Asp Arg Glu Glu Asn Pro Ile Ala Gly
 450 455 460
 Ala Thr Val Arg Ile Val Gly Glu Arg Gly Pro Val Gly Gln Gly Phe
 465 470 475 480
 Val Thr Thr Arg Asp Asp Gly Ser Tyr Lys Met Ser Val Gln Gly Asp
 485 490 495
 Thr Arg Tyr Val Met Leu Ala Gly Ala Ser Gly Tyr Leu Asn Gln Tyr
 500 505 510
 Val Glu Leu Lys Thr Asp Thr Ala Lys Gln Ser Glu Thr Tyr Tyr Val
 515 520 525
 Asp Phe Phe Leu Ala Ser Arg Glu Lys Ala Glu Gly Leu Gln Asn Ile
 530 535 540
 Phe Tyr Asp Phe Asp Lys Ala Thr Leu Arg Pro Glu Ser Met Lys Ser
 545 550 555 560
 Leu Asp Glu Leu Ile Arg Ile Leu Thr Asp Asn Pro Asp Ile Arg Ile
 565 570 575
 Glu Leu Gly Ser His Ala Asp Arg Lys Gly Pro Asp Ala Tyr Asn Leu
 580 585 590
 Gly Leu Ser Asp Arg Arg Ala Lys Ser Val Val Asp Tyr Leu Thr Ser
 595 600 605
 Arg Gly Ile Ala Ala Asp Arg Leu Thr Trp Lys Gly Tyr Gly Lys Ser
 610 615 620
 Val Pro Lys Thr Val Thr Ala Lys Ile Ala Glu Arg His Asp Phe Leu
 625 630 635 640
 Lys Glu Gly Asp Val Leu Thr Glu Glu Phe Val Ala Pro Leu Thr Glu

	645		650		655										
Glu	Gln	Gln	Ser	Val	Cys	Asp	Gln	Leu	Asn	Arg	Arg	Thr	Glu	Phe	Arg
	660						665						670		
Val	Ile	Glu	Glu	Glu	Leu	Arg									
	675														

(2) INFORMATION FOR SEQ ID NO:321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

```

Pro Ala Gln Pro Lys Thr Tyr Cys Ile Arg Tyr Phe Arg Arg Glu Val
1      5      10      15
Ser Pro Arg Arg Gln Thr Glu Arg Thr Leu Tyr Ala Asp Lys Met Arg
20     25     30
Arg His Ile Val Lys Cys Cys Pro Ser Ala Ser Ile Leu Leu Gln Glu
35     40     45
Tyr Ser Thr Thr Glu Leu Phe Ile His His Phe Asn Ile Ser Ile Ile
50     55     60
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
65     70     75     80
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
85     90     95
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
100    105    110
Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
115    120    125
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
130    135    140
Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
145    150    155    160
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
165    170    175
Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
180    185    190
Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn
195    200    205
Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys
210    215    220
Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala
225    230    235    240
Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp
245    250    255
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser
260    265    270
Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val
275    280    285
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala
290    295    300
Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu
305    310    315    320
Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly
325    330    335
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser
340    345    350
Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln
355    360    365
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala
370    375    380
Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly
385    390    395    400
Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu

```


65	70	75	80
Thr Val Lys Val Ala Asp Met Asp Val Arg Lys Gln Glu Tyr Ala Arg			
	85	90	95
Arg Ala Ala Arg Ala Asp Leu Phe Pro Lys Val Asp Leu Asn Gly Val			
	100	105	110
Tyr Ser His Thr Leu Lys Lys Gln Val Leu Tyr Ile Asp Met Pro Gly			
	115	120	125
Phe Ser Ser Ser Glu Gly Ile Glu Met Gly Arg Thr His Asn Thr Gln			
	130	135	140
Gly Gly Val Asn Val Ser Met Pro Leu Val Ser Ala Gln Leu Trp Lys			
	145	150	155
Ser Ile Ala Met Thr Gly Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala			
	165	170	175
Arg Ser Ser Arg Ile Asp Leu Val Ala Glu Val Lys Lys Ala Tyr Leu			
	180	185	190
Ser Val Leu Leu Ala Glu Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr			
	195	200	205
Asp Asn Ala Leu Ala Asn Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg			
	210	215	220
Gly Leu Val Ala Glu Tyr Asp Lys Ile Arg Ala Asn Val Gln Val Arg			
	225	230	235
Asn Ile Glu Pro Asn Leu Leu Gln Ala Gln Asn Ser Val Ala Leu Ala			
	245	250	255
Leu Trp Gln Leu Lys Val Leu Met Ser Met Glu Val Glu Thr Pro Ile			
	260	265	270
Arg Leu Ser Gly Ser Leu Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly			
	275	280	285
Tyr Phe Ala Ala Asp Thr Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln			
	290	295	300
Leu Asp Ile Gln Arg Arg Leu Ala Val Ser Ala Asp Lys Leu Asn Lys			
	305	310	315
Tyr Ser Phe Leu Pro Thr Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser			
	325	330	335
Leu Asn Ser Asn Asp Ile Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr			
	340	345	350
Pro Phe Ser Thr Ile Ser Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly			
	355	360	365
Gly Lys Arg Leu Tyr Asn Val Lys Gln Ser Ala Leu Ser Ile Arg Gln			
	370	375	380
Ile Asp Leu Gln Arg Arg His Ile Glu Gln Ser Ile Arg Met Gly Ile			
	385	390	395
Lys Asn Gln Asn Asp Arg Leu Arg Thr Cys Met Gln Arg Phe Val Ala			
	405	410	415
Ser Glu Glu Ala Val Arg Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu			
	420	425	430
Lys Arg Tyr Gln Thr Gly Glu Gly Thr Leu Val Glu Leu Asn Asp Ala			
	435	440	445
Asp Val Ala Leu Leu Gln Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe			
	450	455	460
Asp Phe Met Thr Ala Lys Ala Glu Leu Asp Lys Met Asn Gly Met Gly			
	465	470	475
Ile Pro Glu Gln			480

(2) INFORMATION FOR SEQ ID NO:323

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

Phe	His	Asn	Phe	Asp	Phe	Leu	Asn	Gly	Ile	Lys	Leu	Phe	Ser	Met	Ala
1			5					10						15	
Asn	Asn	Thr	Leu	Leu	Ala	Lys	Thr	Arg	Arg	Tyr	Val	Cys	Leu	Val	Gly

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

```
Lys Ser Pro Ser Asp Ser Ala Leu Pro Ser Val Trp Ser Ala Asn Thr
1      5      10      15
Ile Ser Gly Leu Val Gly Gly Lys Arg Ile Thr Leu Leu Ile Leu Tyr
      20      25      30
Ser Met Ala Ile Arg Ser Ser Asn Ile Glu Ser Ile Gln Cys Phe Val
      35      40      45
Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
      50      55      60
Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
      65      70      75      80
Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
      85      90      95
Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
      100     105     110
Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
      115     120     125
Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
      130     135     140
Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
      145     150     155     160
Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
      165     170     175
Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
      180     185     190
Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
      195     200     205
Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
      210     215     220
Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
      225     230     235     240
Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
      245     250     255
Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
      260     265     270
Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
      275     280     285
Ser Phe Ala Leu Lys
      290
```

(2) INFORMATION FOR SEQ ID NO:325

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

```
Gly Lys Leu Gln Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu
1      5      10      15
Leu Ala Leu Gly Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala
      20      25      30
Val Ser Glu Lys Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly
      35      40      45
Gln Asp Phe Ala Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro
      50      55      60
Ile Asp Ser Val Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr
```

65		70		75		80									
Thr	Arg	Phe	Ser	Tyr	Asn	Leu	Gly	Ala	Ile	Tyr	Ala	Ser	Asn	Ile	Ala
			85						90					95	
Arg	Gln	Leu	Ala	His	Asp	Ser	Ile	Asp	Ile	Asp	Lys	Phe	Tyr	Ala	Ala
		100						105					110		
Met	Arg	Ala	Ala	Leu	Leu	Lys	Asp	Thr	Val	Ser	Ile	Ala	Met	Lys	Pro
		115					120					125			
Ala	Asp	Ala	Gln	Ala	Phe	Met	Gln	Arg	Ile	Gln	Ala	Lys	Lys	Gln	Arg
	130					135					140				
Glu	Asn	Asn	Met	Lys	Gln	Phe	Gly	Gln	Asn	Ile	Glu	Lys	Gly	Asn	Glu
145					150					155					160
Tyr	Ile	Asp	Thr	Phe	Lys	Lys	Glu	Asp	Gly	Val	Thr	Val	Thr	Thr	Thr
			165						170					175	
Gly	Leu	Ala	Tyr	Lys	Thr	Leu	Gln	Glu	Gly	Thr	Gly	Ala	Thr	Pro	Ser
		180						185					190		
Leu	Ala	Asp	Thr	Val	Arg	Val	Lys	Tyr	Val	Gly	Thr	Leu	Val	Asp	Gly
		195					200					205			
Lys	Glu	Phe	Asp	Lys	Asn	Glu	Gly	Ile	Glu	Phe	Ala	Val	Thr	Gly	
	210					215				220					
Val	Ile	Lys	Gly	Trp	Thr	Glu	Met	Leu	Gln	Leu	Met	Lys	Val	Gly	Gln
225					230					235					240
Lys	Val	Arg	Val	Val	Ile	Pro	Gln	Glu	Leu	Ala	Tyr	Gly	Glu	Thr	Gly
			245						250					255	
Asn	Tyr	Thr	Ile	Glu	Pro	Phe	Ser	Thr	Leu	Thr	Phe	Glu	Met	Glu	Leu
			260					265					270		
Ile	Gly	Ile	Lys	Pro	Gly	Lys	Lys								
		275					280								

(2) INFORMATION FOR SEQ ID NO:326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

Cys	Arg	Lys	Gln	Lys	Leu	Ser	Asn	Pro	Lys	Arg	Ser	Arg	Tyr	Pro	Cys
1			5						10				15		
Arg	Arg	Ile	Ser	Phe	Arg	Gln	Ser	Asp	Lys	Asn	Pro	Met	Lys	Val	Leu
		20						25					30		
Arg	Gln	Val	Phe	Leu	Pro	Ile	Leu	Phe	Val	Leu	Leu	Thr	Gly	Ala	Cys
		35					40					45			
Ser	Thr	Thr	Lys	Asn	Leu	Pro	Glu	Gly	Glu	Gln	Leu	Tyr	Ile	Gly	Met
	50					55					60				
Gly	Lys	Thr	Gln	Ile	Leu	Arg	Gln	Asp	Lys	Ser	His	Ala	Gly	Gln	Gln
65				70					75					80	
Ala	Leu	Thr	Glu	Val	Glu	Ser	Thr	Leu	Lys	Val	Thr	Pro	Asn	Gly	Ala
			85						90					95	
Ile	Phe	Gly	Ser	Ala	Ser	Ala	Ser	Leu	Pro	Lys	Ile	Pro	Phe	Gly	Leu
		100						105					110		
Trp	Leu	Tyr	Asn	Ser	Phe	Val	Gly	Asp	Ser	Thr	Val	Ile	Ser	Lys	Trp
		115					120					125			
Ile	Phe	Asp	Lys	Phe	Ala	Ala	Lys	Pro	Val	Phe	Ile	Ser	Gln	Val	Lys
	130					135					140				
Ser	Asp	Ser	Arg	Ala	Lys	Val	Ala	Thr	Asn	Ile	Leu	Arg	Glu	His	Gly
145					150					155					160
Tyr	Phe	Asp	Ala	Lys	Val	Lys	Ser	Ser	Val	Thr	Thr	Leu	Lys	Lys	Asp
			165						170					175	
Ser	Leu	Lys	Ala	Lys	Ile	Ser	Tyr	Thr	Val	Asp	Met	Ala	Ser	Pro	Tyr
		180					185						190		
His	Tyr	Asp	Ser	Ile	Ile	Pro	Leu	Pro	Ile	Ser	Thr	Phe	Pro	Asp	Ser
		195					200					205			
Ile	Leu	Ala	Tyr	Arg	Gln	Thr	Pro	Ser	Leu	Ile	Arg	Lys	Gly	Asp	Gln
	210					215					220				
Phe	Asn	Leu	Ala	Lys	Leu	His	Glu	Glu	Arg	Gln	Thr	Ile	Ser	Ala	Leu

225					230					235				240	
Leu	Arg	Asp	Asn	Gly	Tyr	Tyr	Tyr	Phe	Arg	Pro	Gln	Asp	Ile	Ile	Tyr
				245					250					255	
Glu	Ala	Asp	Thr	Leu	Leu	Val	Arg	Gly	Ala	Val	Cys	Leu	Arg	Ala	Lys
			260					265					270		
Leu	Ser	Glu	Asp	Thr	Pro	Pro	Gln	Ala	Met	Arg	Pro	Trp	Arg	Ile	Gly
		275					280					285			
Lys	Arg	Thr	Ala	Val	Leu	Leu	Gly	Met	Asn	Gly	Glu	Ser	Pro	Thr	Asp
	290					295					300				
Ser	Leu	Glu	Val	Glu	Asp	Met	Lys	Val	Leu	Tyr	Arg	Lys	Met	Pro	
305					310					315				320	
Val	Arg	Pro	Lys	Ile	Leu	Ala	Lys	Arg	Phe	Arg	Phe	Phe	Ser	Gly	Asn
				325					330					335	
Leu	Tyr	Arg	Gln	Lys	Asp	Asp	Glu	Thr	Thr	Arg	Lys	Ser	Leu	Ala	Arg
		340						345					350		
Leu	Gly	Ala	Phe	Ser	Val	Ile	Asp	Leu	Asn	Phe	Leu	Gln	Arg	Asp	Ser
	355						360					365			
Ile	Ser	Gly	Leu	Leu	Asp	Val	Arg	Leu	Leu	Thr	Thr	Leu	Asp	Lys	Pro
	370				375						380				
Trp	Asp	Ala	Ser	Leu	Glu	Thr	Leu	Phe	Thr	Ser	Lys	Ser	Asn	Asp	Phe
385					390					395					400
Ile	Gly	Pro	Gly	Leu	Asn	Phe	Ala	Leu	Ala	Arg	Arg	Asn	Val	Phe	Gly
				405					410					415	
Gly	Gly	Glu	Asn	Leu	Ser	Trp	Asn	Ile	Gly	Gly	Ser	Tyr	Glu	Trp	Glu
			420					425					430		
Thr	Gly	Asn	Arg	Pro	Glu	Asn	Ser	Asn	Arg	Leu	Ile	Asp	Ile	Asn	
	435					440					445				
Ser	Tyr	Asn	Met	Asn	Thr	Ala	Val	Asn	Leu	Ser	Phe	Pro	Ser	Ile	Val
	450					455					460				
Phe	Pro	Gly	Leu	Leu	Asp	Lys	Tyr	Tyr	Tyr	Tyr	Pro	Thr	Thr	Thr	Thr
465					470					475					480
Phe	Gln	Ala	Ser	Ala	Thr	Ala	Leu	Asn	Arg	Ala	His	Tyr	Phe	Ser	Met
				485					490					495	
Tyr	Ser	Phe	Gly	Phe	Ser	Thr	Thr	Tyr	Glu	Phe	Gln	Pro	Ser	Lys	Glu
		500						505					510		
His	Arg	His	Ala	Ile	Phe	Pro	Leu	Lys	Leu	Asn	Tyr	Asn	Leu	Leu	Gly
		515					520					525			
His	Gln	Thr	Glu	Thr	Phe	Gln	Ala	Ile	Thr	Ala	Asn	Asn	Pro	Pro	Leu
	530					535					540				
Leu	Leu	Ser	Leu	Gln	Ser	Gln	Phe	Leu	Ala	Gln	Met	Gly	Tyr	Ile	Tyr
545					550					555					560
Thr	Phe	Asn	Lys	Ser	Val	Ser	Glu	Lys	Ser	Pro	His	His	Leu	Trp	Met
			565						570					575	
Gln	Phe	Gly	Leu	Ser	Glu	Ala	Gly	Asn	Leu	Leu	Asn	Leu	Ile	Tyr	Leu
			580					585					590		
Ala	Ala	Gly	Lys	Lys	Tyr	Ser	Asp	Thr	Lys	Asn	Phe	Val	Gly	Val	Pro
		595					600					605			
Phe	Ser	Gln	Phe	Ile	Lys	Ala	Thr	Gly	Glu	Leu	Arg	Tyr	Ser	Tyr	Thr
	610					615					620				
Ile	Asp	Arg	Asn	Gln	Ser	Leu	Ala	Thr	Arg	Phe	Gly	Thr	Gly	Val	Ile
625					630					635					640
Tyr	Ser	Tyr	Gly	Asn	Met	Arg	Val	Ala	Pro	Tyr	Ser	Glu	Gln	Phe	Tyr
			645						650					655	
Val	Gly	Gly	Ala	Asn	Ser	Ile	Arg	Ala	Phe	Thr	Val	Arg	Ser	Ile	Gly
		660						665					670		
Pro	Gly	Arg	Phe	Asn	Pro	Asp	Ser	Asp	Asn	Gln	Tyr	Ser	Tyr	Leu	Asp
		675					680					685			
Gln	Val	Gly	Glu	Phe	Lys	Leu	Glu	Ala	Asn	Val	Glu	Tyr	Arg	Gly	Lys
	690					695					700				
Leu	Phe	Gly	Asp	Leu	His	Ala	Ala	Val	Phe	Leu	Asp	Ala	Gly	Asn	Val
705					710					715					720
Trp	Leu	Leu	Arg	Glu	Asp	Ser	Ser	Arg	Pro	Gly	Gly	Ala	Leu	Ser	Glu
			725						730					735	
Val	Gly	Ser	Val	Ser	Asn	Phe	Leu	Asn	Ser	Ile	Ala	Leu	Gly	Thr	Gly
		740					745						750		
Val	Gly	Leu	Arg	Tyr	Asp	Leu	Ala	Phe	Leu	Val	Val	Arg	Val	Asp	Val
		755					760					765			
Gly	Phe	Gly	Leu	His	Leu	Pro	Tyr	Asn	Thr	Gly	Lys	Lys	Gly	Tyr	Tyr
	770					775					780				
Asn	Ile	Pro	Arg	Phe	Lys	Asp	Ala	Ile	Gly	Phe	His	Leu	Ala	Val	Gly
785					790					795					800
Tyr	Pro	Phe													

(2) INFORMATION FOR SEQ ID NO:327

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

Ser	Leu	Ser	Pro	Tyr	Ile	Arg	Phe	Pro	Met	Ser	Ser	His	Ser	Val	Arg
1			5					10					15		
Tyr	Leu	Ile	Gly	Ile	Ala	Gly	Cys	Leu	Leu	Leu	Met	Leu	Ala	Ser	Ser
		20					25					30			
Cys	Ser	Val	Thr	Arg	Tyr	Val	Pro	Asp	Gly	Ser	Arg	Leu	Leu	Asp	Arg
		35					40				45				
Val	Thr	Ile	Ala	Ser	Glu	Thr	Gly	Ser	Ile	Ala	Leu	Pro	Glu	Asp	Ile
	50					55				60					
Arg	Asp	Tyr	Thr	Leu	Gln	Pro	Asn	Tyr	Arg	Leu	Phe	Gly	Met	Thr	
65					70			75						80	
Arg	Trp	Leu	Leu	Arg	Val	Tyr	Ser	Ser	Ser	Asn	Pro	Asn	Ser	Asn	Ser
			85					90						95	
Trp	Trp	Asn	Arg	Ser	Leu	Arg	Lys	Met	Gly	Glu	Pro	Pro	Val	Leu	Ile
		100						105					110		
Asp	Ser	Val	Leu	Thr	Asp	Arg	Thr	Ala	Asn	Arg	Leu	Ala	Lys	Ala	Met
		115					120					125			
Ala	Gly	Asp	Gly	Phe	Leu	Asp	Ala	Thr	Ala	Arg	Ala	Val	Val	Asp	Thr
	130					135					140				
Gly	Leu	Tyr	Lys	Lys	Ala	Arg	Ile	Thr	Tyr	Leu	Ile	Gln	Pro	Gly	Ser
145					150					155					160
Arg	Tyr	Tyr	Ile	Arg	Asn	Met	Ala	Leu	Asp	Val	Lys	Asn	Pro	Leu	Leu
			165						170					175	
Pro	Pro	Val	Ala	Leu	Gly	Asn	Ser	Leu	Pro	Ser	Ala	Tyr	Lys	Val	Gly
		180					185						190		
Ile	Ser	Glu	Gly	Ser	Pro	Leu	Ser	Pro	Ile	Val	Leu	Asp	Glu	Glu	Arg
		195					200					205			
Lys	Ala	Ile	Ala	Arg	His	Met	Arg	Asn	Asn	Gly	Phe	Trp	Lys	Phe	Ser
	210					215					220				
Ala	Glu	Asp	Val	Tyr	Tyr	Glu	Ala	Asp	Thr	Thr	Val	Ser	Gly	Gly	Ser
225					230					235					240
Gly	Thr	Lys	Ser	Ala	Asp	Leu	Lys	Leu	Val	Val	Asn	Gly	Ile	Gly	Arg
			245						250					255	
Tyr	Pro	Tyr	Arg	Ile	Gly	Arg	Val	Phe	Phe	His	Ala	Asp	Tyr	Asp	Pro
		260						265					270		
Leu	Glu	Ser	Asp	Phe	Arg	Val	Gln	Glu	Leu	Pro	Arg	Ile	Asp	Ser	Ile
		275					280					285			
Ser	Arg	Gly	Asp	Tyr	Thr	Val	Tyr	Tyr	Gly	Ser	Arg	Gly	Arg	Tyr	Ile
	290					295					300				
Arg	Ala	Ser	Ala	Leu	Thr	Arg	Ser	Val	Ser	Val	Thr	Pro	Gly	Ala	Phe
305					310					315					320
Phe	Cys	Glu	Asp	Asp	Val	Glu	Arg	Ser	Tyr	Ile	Lys	Leu	Asn	Ala	Leu
			325						330					335	
Pro	Ile	Val	Arg	Asn	Val	Asn	Ile	Arg	Phe	Val	Glu	His	Asn	Gly	Lys
		340						345					350		
Asp	Glu	Ile	Ala	Leu	Ala	Asp	Ser	Ser	Arg	Leu	Val	Asp	Cys	Tyr	Ile
		355					360					365			
Leu	Thr	Val	Pro	Ala	Lys	Ser	Lys	Ser	Phe	Glu	Ala	Glu	Val	Leu	Gly
	370					375					380				
Thr	Asn	Ser	Ala	Gly	Asp	Phe	Gly	Ala	Ala	Leu	Ser	Leu	Gly	Phe	Thr
385					390					395					400
Asp	Arg	Asn	Leu	Phe	Arg	Gly	Ala	Glu	Met	Phe	Asn	Ile	Lys	Leu	Lys
			405						410					415	
Gly	Ala	Tyr	Glu	Ala	Ile	Arg	Lys	Gly	Ser	His	Ser	Phe	Met	Glu	Tyr
		420					425						430		
Gly	Val	Glu	Ser	Ser	Leu	Arg	Phe	Pro	Arg	Leu	Leu	Phe	Pro	Phe	Ile
		435					440					445			
Ser	Asp	Glu	Thr	Arg	Arg	Arg	Leu	Arg	Ala	Ser	Thr	Glu	Trp	Lys	Ile
	450					455					460				
Gly	Tyr	Asn	Tyr	Gln	Thr	Arg	Pro	Glu	Phe	Asp	Arg	Val	Ile	Leu	Ser
465					470					475					480

Ala	Gln	Leu	Asn	Tyr	Ser	Trp	Gln	Thr	Tyr	Leu	His	Asn	Arg	Leu	Arg		
			485						490						495		
His	Thr	Ile	Arg	Leu	Leu	Asp	Val	Asp	Tyr	Leu	His	Leu	Pro	Tyr	Ile		
			500						505					510			
Asp	Pro	Asp	Phe	Ala	Gln	Ser	Leu	Pro	Pro	Thr	Thr	Ala	Leu	Tyr	Asn		
		515					520					525					
Tyr	Thr	Glu	Gln	Phe	Ile	Leu	Gly	Ser	Ala	Tyr	Ile	Leu	Asn	Tyr	Thr		
	530					535					540						
Thr	Ala	Ser	Ser	Met	Glu	Arg	Thr	Val	Ser	Asn	Pro	Phe	Thr	Ala	Arg		
545				550						555					560		
Phe	Ser	Ile	Gln	Thr	Ala	Gly	Asn	Leu	Leu	Gln	Ala	Ile	Ser	Tyr	Leu		
			565						570					575			
Thr	Asp	Ser	Pro	Lys	Asp	Glu	His	Gly	Leu	Tyr	Lys	Met	Phe	Gly	Leu		
		580						585					590				
His	Tyr	Ala	Gln	Phe	Val	Lys	Leu	Asp	Leu	Asp	Leu	Ala	Lys	Thr	Val		
	595						600					605					
Leu	Leu	Glu	Lys	Asp	Asn	Thr	Leu	Ala	Leu	His	Leu	Gly	Phe	Gly	Leu		
	610					615					620						
Ala	Phe	Pro	Tyr	Gly	Asn	Ala	Arg	His	Ile	Pro	Phe	Glu	Leu	Arg	Tyr		
625					630					635					640		
Phe	Ala	Gly	Gly	Ser	Asn	Ser	Val	Arg	Gly	Trp	Ser	Val	Arg	Thr	Leu		
			645						650					655			
Gly	Pro	Gly	Ser	Met	Lys	Met	Thr	Pro	Asp	Lys	Thr	Phe	Phe	Asp	Gln		
		660						665					670				
Met	Gly	Asp	Ile	Arg	Leu	Asp	Leu	Asn	Val	Glu	Tyr	Arg	Thr	Lys	Leu		
	675					680						685					
Phe	Trp	Lys	Phe	Arg	Ala	Ala	Phe	Val	Asp	Ala	Gly	Asn	Val	Trp			
	690					695				700							
Thr	Ile	Lys	Glu	Tyr	Glu	Asn	Gln	Glu	Asp	Gly	Leu	Phe	Arg	Phe	Asp		
705					710					715					720		
Arg	Phe	Tyr	Lys	Glu	Ile	Ala	Leu	Ala	Tyr	Gly	Leu	Gly	Leu	Arg	Leu		
			725						730					735			
Asp	Phe	Asp	Tyr	Phe	Leu	Val	Arg	Leu	Asp	Ala	Gly	Leu	Lys	Ala	Tyr		
		740						745					750				
Asp	Pro	Gln	Thr	Gly	Arg	Tyr	Lys	Trp	Ala	Ile	Thr	Arg	Pro	Asn			
	755					760					765						
Leu	Ser	Ser	Asn	Phe	Ala	Trp	His	Ile	Ala	Val	Gly	Tyr	Pro	Phe			
	770					775					780						

(2) INFORMATION FOR SEQ ID NO:328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

Val	Glu	Ser	Lys	Leu	Leu	Cys	Leu	Met	Arg	Lys	Arg	Ile	Leu	Gln	Leu		
1				5					10					15			
Phe	Leu	Thr	Ala	Leu	Leu	Leu	Ala	Leu	Gly	Ser	Ser	Leu	Ala	Ile	Ala		
			20					25					30				
Gln	Thr	Val	Val	Thr	Gly	Lys	Val	Ile	Asp	Ser	Glu	Thr	Ser	Glu	Pro		
		35				40						45					
Leu	Ile	Gly	Val	Ser	Val	Ser	Thr	Gly	Gln	Gly	Ala	Ser	Leu	Arg	Gly		
	50					55					60						
Val	Thr	Thr	Asp	Met	Asp	Gly	Gly	Phe	Arg	Phe	Glu	Val	Pro	Ala	Lys		
65				70					75					80			
Ser	Val	Leu	Thr	Phe	Arg	Cys	Val	Gly	Tyr	Ala	Thr	Val	Thr	Arg	Ser		
			85					90					95				
Ile	Gly	Arg	Gly	Ser	Gln	Glu	Asp	Leu	Gly	Thr	Ile	Leu	Leu	Asp	Pro		
		100						105					110				
Gln	Ala	Ile	Gly	Leu	Asp	Glu	Ile	Gln	Val	Ile	Ala	Ser	Val	Val	Pro		
		115						120				125					
Lys	Asp	Arg	Met	Thr	Pro	Val	Pro	Val	Ser	Asn	Ile	Arg	Val	Ala	Asp		
	130					135						140					

Ile Gln Ala Ala Ser Leu Asn Val Glu Phe Pro Glu Leu Val Lys Ser
 145 150 155 160
 Thr Pro Ser Thr Tyr Thr Thr Lys Gly Ser Gly Gly Phe Gly Asp Gly
 165 170 175
 Arg Thr Asn Val Arg Gly Phe Asp Thr Tyr Asn Phe Gly Val Leu Ile
 180 185 190
 Asn Gly Val Pro Val Asn Gly Met Glu Asp Gly Lys Val Tyr Trp Ser
 195 200 205
 Asn Trp Ser Gly Leu Met Asn Gln Ala Ser Thr Ile Gln Ile Gln Arg
 210 215 220
 Gly Leu Gly Ala Ser Lys Leu Gly Ile Ser Ser Val Gly Gly Thr Met
 225 230 235 240
 Asn Ile Ile Thr Lys Thr Thr Asp Ala Asn Thr Gly Gly Ser Ala Tyr
 245 250 255
 Val Gly Met Gly Asn Asp Gly Leu His Lys Glu Ser Phe Ser Ile Ser
 260 265 270
 Thr Gly Met Asn Asp Gly Trp Ala Ile Thr Ile Ala Gly Ser His Met
 275 280 285
 Thr Gly Leu Gly Tyr Val Lys Gly Leu Lys Gly Arg Ala Phe Ser Tyr
 290 295 300
 Phe Phe Asn Val Ser Lys Lys Phe Asn Glu Arg His Thr Leu Ser Leu
 305 310 315 320
 Thr Gly Phe Gly Ala Pro Gln Trp His Asn Gln Arg Ser Ser Lys Tyr
 325 330 335
 Ser Val Ala Asp Tyr Asp Lys Tyr Gly Ile Arg His Asn Gln Ser Phe
 340 345 350
 Gly Tyr Leu Arg Gly Glu Leu Thr Pro Thr Ala Tyr Ala Tyr Asn Thr
 355 360 365
 Tyr His Lys Pro Gln Phe Ser Leu Asn His Phe Trp Lys Met Asp Glu
 370 375 380
 Asn Thr Ser Leu Tyr Thr Ala Unk Tyr Ala Ser Leu Ala Thr Gly Gly
 385 390 395 400
 Gly Arg Arg Ala Tyr Gly Lys Asn Ser Lys Trp Val Leu Ile Asn Tyr
 405 410 415
 Asn Thr Gly Gln Pro Tyr Glu Gln Thr Lys Val Thr Pro Asp Gly Leu
 420 425 430
 Ile Asp Tyr Asp Ala Val Leu Ala Ala Asn Ala Ala Ala Ser Asn Gly
 435 440 445
 Ser Glu Ala Ile Phe Ala Leu Gly Ser Asn Ser His Lys Trp Phe Gly
 450 455 460
 Leu Leu Ser Ser Phe Lys Lys Lys Leu Asn Ser Ser Leu Thr Leu Thr
 465 470 475 480
 Ala Gly Tyr Asp Gly Arg Tyr Tyr Arg Gly Asp His Tyr Asp Lys Ile
 485 490 495
 Thr Asp Leu Leu Gly Gly Ser Tyr Tyr Ile Glu Asp Pro Lys Thr Lys
 500 505 510
 Leu Ala Tyr His Ala Glu Gly Gln Gln Leu Lys Val Gly Asp Ile Val
 515 520 525
 Asn Arg Asp Tyr Thr Gly Glu Ile Met Trp His Gly Leu Phe Ala Gln
 530 535 540
 Met Glu His Ser Ser Glu Trp Ile Asp Ala Phe Val Ser Gly Ser Ile
 545 550 555 560
 Asn Tyr Glu Leu Tyr Arg Asn His Asn Tyr Gly Gly Ser Lys Ser Thr
 565 570 575
 Gly Tyr Leu Pro Gly Val Ser Pro Trp Lys Ser Phe Leu Pro Trp Ser
 580 585 590
 Gly Lys Ala Gly Leu Ser Tyr Lys Phe Ala Gln Gly His Asn Val Phe
 595 600 605
 Ala Asn Gly Gly Phe Phe Thr Arg Ala Pro Leu Phe Gly Asn Ile Tyr
 610 615 620
 Ala Ala Gly Ala Ile Ile Pro Asn Asp Lys Ala Asn Met Glu Lys Val
 625 630 635 640
 Leu Thr Gly Glu Val Gly Tyr Gly Phe Thr Asn His Lys Asn Phe Glu
 645 650 655
 Phe Asn Ile Asn Gly Tyr Tyr Thr Lys Trp Met Asp Arg Val Thr Ser
 660 665 670
 Lys Arg Ile Gly Asn Glu Tyr Val Tyr Leu Asn Gly Val Asp Ala Val
 675 680 685
 His Cys Gly Val Glu Ala Glu Val Ser Tyr Arg Pro Ile Arg Gln Ile
 690 695 700
 Asp Leu Arg Gly Met Phe Ser Leu Gly Asp Trp Thr Trp Gln Asn Asn
 705 710 715 720
 Val Ser Tyr Thr Ser Tyr Asp Glu Ala Gly Asn Glu Thr Gly Gln Asp
 725 730 735
 Ile Thr Tyr Ile Lys Gly Leu His Val Gly Asp Ala Ala Gln Met Thr
 740 745 750
 Ala Ala Val Ser Ala Asp Ile Glu Leu Phe Lys Gly Phe His Val Ile

	755		760		765										
Gly	Lys	Tyr	Asn	Phe	Leu	Gly	Lys	Asn	Tyr	Ala	Gly	Phe	Asn	Pro	Ala
770						775					780				
Thr	Arg	Asn	Ala	Gln	Gln	Tyr	Glu	Ala	Asp	Gly	Lys	Glu	Ile	Val	Glu
785					790					795					800
Ser	Trp	Lys	Leu	Pro	Asp	Val	Gly	Leu	Phe	Asp	Leu	Ser	Ala	Ser	Tyr
			805						810					815	
Asn	Phe	Lys	Leu	Gly	Ser	Leu	Ser	Thr	Thr	Phe	Tyr	Phe	Asn	Met	Asp
			820					825					830		
Asn	Val	Ala	Asp	Lys	Arg	Tyr	Val	Ser	Asp	Ala	Asp	Asp	Asn	Ile	Ile
		835					840					845			
Gly	Lys	Lys	His	Asp	Glu	Ala	Ser	Ala	Leu	Val	Trp	Tyr	Gly	Phe	Gly
	850				855						860				
Arg	Thr	Trp	Ser	Thr	Gly	Ile	Arg	Val	Asn	Phe					
865					870					875					

(2) INFORMATION FOR SEQ ID NO:329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

Asn	Arg	Cys	Asn	Pro	Ser	Arg	Gln	Tyr	Phe	His	Leu	Ser	Gln	Asn	Asp
1			5					10					15		
Val	Gly	Arg	Ser	Leu	Arg	Ala	Phe	Leu	Ile	His	Leu	Ser	Met	Lys	Phe
			20				25						30		
Ser	Ile	Arg	Leu	Phe	Leu	Cys	Ile	Ile	Phe	Leu	Leu	Ser	Ala	Phe	Ile
		35				40						45			
Leu	Pro	Ala	Leu	Gly	Gln	Lys	Ser	Lys	Gln	Val	Gln	Arg	Leu	Glu	Lys
	50				55					60					
Gln	Arg	Lys	Glu	Ala	Leu	Lys	Ala	Ile	Glu	Lys	Thr	Asp	Arg	Glu	Leu
65				70					75					80	
Arg	Asn	Thr	Lys	Lys	Asp	Lys	Gln	Asp	Lys	Gln	Lys	His	Leu	Asn	Leu
			85				90						95		
Leu	Asn	Lys	Gln	Val	Ala	Gln	Arg	Lys	Gln	Met	Val	Gln	Leu	Leu	Asp
		100					105						110		
Asn	Glu	Val	Lys	Glu	Leu	Gln	Ser	Asp	Ile	Asp	Ser	Met	Thr	Gly	Val
		115				120						125			
Cys	His	Gln	Leu	Ser	Val	Glu	Glu	Lys	Ala	Arg	Ser	Asp	Glu	Tyr	Ala
	130					135					140				
Gln	Ala	Leu	Gln	Ser	Met	Gln	Lys	Arg	Lys	Arg	Ser	Leu	Asp	Arg	Ile
145				150					155					160	
Leu	Phe	Ile	Ser	Ser	Ala	Lys	Ser	Phe	Asp	Glu	Gly	Met	Arg	Arg	Met
			165					170					175		
Arg	Phe	Leu	Glu	Gln	Tyr	Ala	Ser	Ala	Tyr	Lys	Leu	Ala	Ser	Val	Arg
		180					185						190		
Leu	Arg	Asp	Thr	Arg	Ser	Lys	Leu	Glu	Thr	Glu	Arg	Ala	Thr	Val	Glu
		195				200						205			
Asp	Ala	Lys	Lys	Glu	Lys	Gly	His	Leu	Leu	Val	Ile	Arg	Glu	Glu	Glu
	210				215						220				
Lys	Lys	Lys	Leu	Glu	Gly	Gln	Gln	Ala	Glu	Gln	Arg	Arg	Gln	Val	Gln
	225				230				235					240	
Ala	Leu	Gly	Ala	Lys	Gln	Lys	Asp	Leu	Glu	Ala	Gln	Leu	Arg	Lys	Gln
			245					250					255		
Lys	Lys	Gln	Ala	Glu	Ala	Leu	Asn	Arg	Lys	Ile	Glu	Lys	Gln	Ile	Ala
		260				265						270			
Lys	Glu	Ile	Glu	Ala	Ala	Glu	Arg	Arg	Ala	Arg	Glu	Glu	Arg	Glu	Arg
	275					280						285			
Leu	Ala	Arg	Glu	Ala	Lys	Ala	Lys	Gly	Lys	Pro	Val	Pro	Ala	Glu	Pro
	290				295					300					
Glu	Arg	Lys	Ala	Glu	Thr	Lys	Gly	Gly	Tyr	Ala	Met	Asp	Ala	Ser	Glu
305				310					315					320	
Arg	Ala	Leu	Ser	Gly	Ser	Phe	Ala	Gln	Asn	Lys	Gly	Arg	Leu	Pro	Gly

				325					330					335		
Pro	Val	Arg	Gly	Arg	Tyr	Arg	Ile	Val	Ser	Asp	Phe	Gly	Val	His	Gln	
			340					345					350			
His	Ser	Glu	Leu	Lys	Lys	Val	Gln	Val	Asn	Asn	Gly	Gly	Ile	Asp	Ile	
		355					360					365				
Ala	Val	Ala	Thr	Gly	Ser	Asp	Ala	Thr	Ser	Val	Phe	Asp	Gly	Val	Val	
	370					375					380					
Ser	Ser	Val	Phe	Val	Ile	Pro	Gly	Tyr	Asn	Ser	Ala	Val	Met	Val	Arg	
385					390				395						400	
His	Gly	Asn	Tyr	Ile	Thr	Val	Tyr	Ala	Asn	Leu	Ser	Lys	Val	Tyr	Val	
			405						410				415			
Asn	Ser	Gly	Thr	Arg	Val	Lys	Thr	Gly	Gln	Ala	Leu	Gly	Arg	Ala	Tyr	
			420					425				430				
Thr	Asp	Pro	Ser	Asn	Asn	Gln	Thr	Ile	Ile	His	Phe	Glu	Ile	Trp	Lys	
	435					440					445					
Glu	Arg	Ser	Lys	Gln	Asn	Pro	Arg	Leu	Trp	Leu	Arg					
	450					455					460					

```

305          310          315          320
Leu Tyr Arg Leu Pro Leu Pro Asp Lys Ile Leu Arg Asn His Trp Tyr
          325          330          335
Lys Tyr Glu Val Glu Ile
          340

```

(2) INFORMATION FOR SEQ ID NO:331

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...329
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

```

Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile
1          5          10          15
Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly
          20          25          30
Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala Ala Thr
          35          40          45
Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr
          50          55          60
Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala
65          70          75          80
Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro
          85          90          95
Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala
          100          105          110
Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu
          115          120          125
Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly
130          135          140
Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr
145          150          155          160
Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser
          165          170          175
Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu
          180          185          190
Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp
          195          200          205
Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met
210          215          220
Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser
225          230          235          240
Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu
          245          250          255
Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp
          260          265          270
Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe
          275          280          285
Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala Arg Pro
290          295          300
Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile Leu His
305          310          315          320
Ile Ala Arg Ala Leu Ala His Glu Arg
          325

```

(2) INFORMATION FOR SEQ ID NO:332

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 878 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

```
Ala Asp Ser Ile Arg Tyr Pro Leu Tyr Phe Phe Gly Arg Asn Arg Lys
1      5      10      15
Lys Cys Phe Arg Glu Pro Ile Pro Thr Leu Tyr Asn Lys Asn Met Ile
20      25      30
Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe Ser Gly
35      40      45
Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp Ala Asn
50      55      60
Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu Val Gly
65      70      75      80
Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr Asp Ala
85      90      95
Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile Thr Leu
100     105     110
Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val Arg Val
115     120     125
Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu Asp Ala
130     135     140
Ile Asn Leu Asp Glu Val Val Ile Ser Ala Asn Arg Glu Leu Thr Leu
145     150     155     160
Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys Val Phe
165     170     175
Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe Gln Pro
180     185     190
Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn Gln Val
195     200     205
Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile Asp Ser
210     215     220
Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu Gln Ile
225     230     235     240
Pro Ala Asn Met Ile Glu Arg Val Glu Val Val Arg Gly Gly Gly Ser
245     250     255
Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile Ile Thr
260     265     270
Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu Ser Phe
275     280     285
Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala Ser Ile
290     295     300
Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln Ala Arg
305     310     315     320
Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu Leu Gly
325     330     335
Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg Leu Ser
340     345     350
Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu Phe Arg
355     360     365
Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly Val Ala
370     375     380
Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr Asp Leu
385     390     395     400
Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser Gly Gln
405     410     415
Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile Asp Val
420     425     430
Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln Asp Gln
435     440     445
Tyr Gly Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met Gly Gly
450     455     460
Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro Ser Gln
465     470     475     480
Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp Val Met
485     490     495
Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn Thr Ile
500     505     510
Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser Leu Phe
```

515					520					525									
Gly	Gln	Asn	Glu	Trp	Lys	Asn	Asp	Arg	Trp	Ser	Ile	Leu	Val	Gly	Ala				
530						535					540								
Arg	Leu	Asp	Lys	His	Ser	Glu	Val	Lys	Asp	Met	Ile	Leu	Ser	Pro	Arg				
545					550					555					560				
Thr	Thr	Leu	Arg	Phe	Asn	Val	Asn	Pro	Asp	Ile	Asn	Leu	Arg	Ala	Thr				
				565					570					575					
Tyr	Ala	Lys	Gly	Phe	Arg	Ala	Pro	Gln	Val	Phe	Asp	Glu	Asp	Leu	His				
				580				585					590						
Val	Gly	Val	Val	Gly	Gly	Glu	Ala	Gln	Lys	Val	Phe	Asn	Asp	Pro	Asn				
		595				600						605							
Leu	Lys	Pro	Glu	Ile	Ser	His	Ala	Phe	Ser	Leu	Ser	Ala	Asp	Met	Tyr				
610					615					620									
His	Arg	Phe	Gly	Asn	Val	Gln	Thr	Asn	Phe	Leu	Val	Glu	Gly	Phe	Tyr				
625				630						635					640				
Thr	Arg	Leu	Leu	Asp	Val	Phe	Thr	Asn	Glu	Glu	Gln	Pro	Asp	Gln	His				
				645					650					655					
Asp	Gly	Ile	Lys	Arg	Tyr	Thr	Arg	Ile	Asn	Gly	Ser	Gly	Ala	Lys	Val				
			660					665					670						
Phe	Gly	Leu	Asn	Leu	Glu	Gly	Lys	Val	Ala	Tyr	Lys	Ser	Phe	Gln	Leu				
		675				680						685							
Gln	Ala	Gly	Leu	Thr	Leu	Ala	Ser	Asn	Lys	Tyr	Asp	Glu	Ala	Gln	Glu				
		690				695					700								
Trp	Gly	Leu	Asn	Thr	Val	Lys	Asp	Thr	Asn	Gly	Ala	Phe	Val	Thr	Glu				
705				710						715				720					
Ala	Asn	Ala	Asn	Gly	Gln	Gln	Glu	Tyr	Lys	Asn	Glu	Ser	Met	Thr	Asp				
			725						730					735					
Thr	Gln	Ile	Thr	Arg	Thr	Pro	Ser	Val	Tyr	Gly	Tyr	Phe	Thr	Leu	Ala				
			740			745							750						
Tyr	Asn	Pro	Ala	His	Ser	Trp	Asn	Ile	Ala	Leu	Thr	Gly	Ala	Tyr	Thr				
		755				760						765							
Gly	Gln	Met	Tyr	Val	Pro	His	Ala	Ile	Glu	Tyr	Gly	Val	Lys	Ser	Ala				
		770				775					780								
Glu	Leu	Asp	Ile	Met	Gln	Asn	Asn	Pro	Glu	Ile	Thr	Asp	Glu	Thr	Gly				
785				790						795				800					
Lys	Ala	Pro	Arg	Ile	Asp	Glu	Leu	Lys	Lys	Thr	Pro	Ala	Phe	Phe	Asp				
			805						810					815					
Leu	Gly	Leu	Lys	Val	Gly	Tyr	Asp	Phe	His	Val	Phe	Gln	Ala	Thr	Glu				
			820					825					830						
Val	Gln	Leu	Tyr	Val	Gly	Met	Asn	Asn	Ile	Phe	Asn	Ser	Phe	Gln	Lys				
			835			840					845								
Asp	Phe	Asp	Arg	Gly	Ala	Ala	Arg	Asp	Ser	Gly	Tyr	Ile	Tyr	Gly	Pro				
		850				855					860								
Thr	Gln	Pro	Arg	Thr	Gly	Tyr	Met	Gly	Leu	Val	Val	Lys	Phe						
865				870					875										

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

Lys	Gln	Ile	Val	Met	Thr	Val	Lys	Arg	Ala	Val	Arg	Ile	Ala	Leu	Leu
1				5					10					15	
Thr	Leu	Ile	Gly	Ile	Leu	Phe	Ser	Ser	Pro	Ser	Leu	Val	Arg	Ala	Gln
			20					25					30		
Ser	Leu	Phe	Ser	Thr	Glu	His	Val	Leu	Gln	Leu	Tyr	Asn	Lys	Ile	Leu
		35				40					45				
Tyr	Gly	Glu	Ser	Ala	Ala	Asp	Thr	Val	Ala	Glu	Lys	Thr	Ala	Gly	Glu
		50			55					60					
Ser	Ala	Phe	Pro	Phe	Ile	Asp	Lys	Leu	Ile	Asn	Leu	Gly	Arg	Thr	Phe
65				70					75					80	
Leu	Gly	Lys	Pro	Tyr	Arg	Tyr	Arg	Gly	Pro	Ser	Pro	Trp	Pro	Met	Asp

[illegible]

Lys	Thr	Ser	Tyr	Arg	Asn	Asn	Met	Arg	Phe	Gln	His	Tyr	Leu	Ile	Cys
1				5					10					15	
Thr	Ala	Ala	Val	Ala	Ala	Leu	Ala	Ala	Asn	Pro	Leu	Thr	Gly	Gln	Ser
			20					25					30		
Asn	Met	Thr	Leu	Glu	Glu	Cys	Ile	Asp	Tyr	Ala	Arg	Arg	His	Ser	Ser
	35						40					45			
Ala	Val	Ala	Leu	Ser	Ala	Ala	Glu	Leu	Glu	Gln	Ser	Lys	Ala	Asp	Tyr
	50					55					60				
Leu	Gln	Ala	Val	Gly	Asn	Phe	Leu	Pro	Arg	Val	Ser	Ala	Gly	Thr	Gly
65				70					75						80
Ala	Ser	Trp	Asn	Phe	Gly	Arg	Gly	Leu	Asp	Ala	Glu	Thr	Asn	Thr	Tyr
			85						90				95		
Thr	Asp	Ile	Asn	Ser	Phe	Asn	Asn	Ser	Tyr	Ser	Ile	His	Ala	Thr	Met
	100							105					110		
Thr	Leu	Phe	Asp	Gly	Leu	Gln	Ser	Val	Tyr	Arg	Leu	Arg	Met	Ala	His
	115						120					125			
Ala	Arg	Arg	Glu	Ala	Ser	Arg	Leu	Ser	Val	Arg	Glu	Gln	Gln	Glu	Leu
	130					135					140				
Ala	Ala	Leu	Gly	Thr	Thr	Glu	Ala	Tyr	Tyr	Asp	Leu	Val	Tyr	Ala	Arg
145				150					155						160
Gln	Met	Gln	Glu	Leu	Ala	Met	Gln	Lys	Tyr	Glu	Glu	Ser	Ser	Arg	Leu
			165						170					175	
His	Arg	Gln	Thr	Ala	Arg	Met	Glu	Glu	Leu	Gly	Met	Lys	Ser	Arg	Pro
	180							185					190		
Asp	Val	Leu	Glu	Met	Gln	Ser	Arg	Met	Ala	Gly	Asp	Arg	Leu	Ala	Leu
	195						200					205			
Thr	Gln	Ala	Asp	Asn	Gln	Cys	Ile	Ile	Ala	Leu	Ile	Arg	Leu	Lys	Glu
	210					215						220			
Lys	Met	Asn	Phe	Pro	Ile	Asp	Asp	Glu	Leu	Val	Val	Asp	Asp	Met	Pro
225				230						235					240
Ala	Asp	Ser	Leu	Ser	Ala	Asp	Met	Ala	Glu	Ser	Asp	Ser	Ser	Ala	Gly
			245						250					255	
Val	Phe	Ala	Arg	Ala	Ala	His	His	His	Pro	Val	Leu	Leu	Arg	Ala	Lys
			260					265					270		
Leu	Asp	Glu	Gln	Ala	Ala	Thr	Asp	Arg	Leu	Arg	Ala	Ala	Arg	Gly	Ala
	275						280					285			
Phe	Leu	Pro	Ser	Val	Ser	Val	Ser	Gly	Gly	Trp	Asn	Thr	Gly	Phe	Ser

290	295	300
Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg		
305	310	315
Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe		
	325	330
Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg		
	340	345
Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser		
	355	360
Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr		
	370	375
Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala		
385	390	395
Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr		
	405	410
Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala		
	420	425
Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys		
	435	440
Leu Ser Asp		445
450		

(2) INFORMATION FOR SEQ ID NO:336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys	
1	5 10 15
Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln	
	20 25 30
Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser	
	35 40 45
Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser	
	50 55 60
Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro	
65	70 75 80
Asp Phe Asn Pro Glu Asp Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln	
	85 90 95
Arg Asp Gly Arg Pro Val Arg Ile Gly Gln Val Ile Pro Val Asp Val	
	100 105 110
Asp Phe Ala Ser Lys Ala Ser His Ile Ser Ser Ile Gly Asp Val Asp	
	115 120 125
Val Tyr Arg Leu Gln Phe Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu	
	130 135 140
Tyr Tyr Asp Ala Phe Asn Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr	
145	150 155 160
Thr Pro Asp His Glu Ile Val Leu Gly Ala Tyr Thr Asn Ala Thr His	
	165 170 175
Arg Arg Asn Gly Ala Phe Ala Thr Glu Pro Val Pro Gly Ser Glu Leu	
	180 185 190
Ile Met Asp Tyr Glu Val Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys	
	195 200 205
Ile Ser Gly Ala Gly Tyr Ile Phe Asp Lys Val Gly Gly Arg Pro Val	
	210 215 220
Thr Asp Asn His Tyr Gly Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys	
225	230 235 240
Glu Ile Asn Ile Asn Cys Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys	
	245 250 255
Asn Gly Val Val Gln Met Ile Met Val Lys Gly Gln Tyr Ile Ser Met	
	260 265 270
Cys Ser Gly Asn Leu Leu Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu	

275					280					285					
Ile	Ile	Ser	Ala	Gly	His	Cys	Ala	Ser	Ile	Thr	Thr	Asn	Phe	Gly	Val
290						295					300				
Thr	Gln	Ser	Glu	Leu	Asp	Lys	Trp	Ile	Phe	Thr	Phe	His	Tyr	Glu	Lys
305					310					315					320
Arg	Gly	Cys	Ser	Asn	Gly	Thr	Leu	Ala	Ile	Phe	Arg	Gly	Asn	Ser	Ile
				325					330					335	
Ile	Gly	Ala	Ser	Met	Lys	Ala	Phe	Leu	Pro	Ile	Lys	Gly	Lys	Ser	Asp
		340					345						350		
Gly	Leu	Leu	Leu	Gln	Leu	Asn	Asp	Glu	Val	Pro	Leu	Arg	Tyr	Arg	Val
	355					360					365				
Tyr	Tyr	Asn	Gly	Trp	Asp	Ser	Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Ala
	370					375					380				
Gly	Ile	His	His	Pro	Ala	Gly	Asp	Ala	Met	Lys	Ile	Ser	Ile	Leu	Lys
385					390					395					400
Lys	Thr	Pro	Ala	Leu	Asn	Thr	Trp	Ile	Ser	Ser	Ser	Gly	Ser	Gly	Gly
				405					410					415	
Thr	Asp	Asp	His	Phe	Tyr	Phe	Lys	Tyr	Asp	Gln	Gly	Gly	Thr	Glu	Gly
			420				425						430		
Gly	Ser	Ser	Gly	Ser	Ser	Leu	Phe	Asn	Gln	Asn	Lys	His	Val	Val	Gly
	435						440					445			
Thr	Leu	Thr	Gly	Gly	Ala	Gly	Asn	Cys	Gly	Gly	Thr	Glu	Phe	Tyr	Gly
	450					455					460				
Arg	Leu	Asn	Ser	His	Trp	Asn	Glu	Tyr	Ala	Ser	Asp	Gly	Asn	Thr	Ser
465					470					475					480
Arg	Met	Asp	Ile	Tyr	Leu	Asp	Pro	Gln	Asn	Asn	Gly	Gln	Thr	Thr	Ile
				485					490					495	
Leu	Asn	Gly	Thr	Tyr	Arg	Asp	Gly	Tyr	Lys	Pro	Leu	Pro	Ser	Val	Pro
	500						505						510		
Arg	Leu	Leu	Leu	Gln	Ser	Thr	Gly	Asp	Gln	Val	Glu	Leu	Asn	Trp	Thr
	515						520					525			
Ala	Val	Pro	Ala	Asp	Gln	Tyr	Pro	Ser	Ser	Tyr	Gln	Val	Glu	Tyr	His
	530					535					540				
Ile	Phe	Arg	Asn	Gly	Lys	Glu	Ile	Ala	Thr	Thr	Lys	Glu	Leu	Ser	Tyr
545					550					555					560
Ser	Asp	Ala	Ile	Asp	Glu	Ser	Ile	Ile	Gly	Ser	Gly	Ile	Ile	Arg	Tyr
				565					570					575	
Glu	Val	Ser	Ala	Arg	Phe	Ile	Tyr	Pro	Ser	Pro	Leu	Asp	Gly	Val	Glu
			580				585						590		
Ser	Tyr	Lys	Asp	Thr	Asp	Lys	Thr	Ser	Ala	Asp	Leu	Ala	Ile	Gly	Asp
	595						600					605			
Ile	Gln	Thr	Lys	Leu	Lys	Pro	Asp	Val	Thr	Pro	Leu	Pro	Gly	Gly	Gly
	610					615					620				
Val	Ser	Leu	Ser	Trp	Lys	Val	Pro	Phe	Leu	Ser	Gln	Leu	Val	Ser	Arg
625					630					635					640
Phe	Gly	Glu	Ser	Pro	Asn	Pro	Val	Phe	Lys	Thr	Phe	Glu	Val	Pro	Tyr
				645					650					655	
Val	Ser	Ala	Ala	Ala	Ala	Gln	Thr	Pro	Asn	Pro	Pro	Val	Gly	Val	Val
		660					665					670			
Ile	Ala	Asp	Lys	Phe	Met	Ala	Gly	Thr	Tyr	Pro	Glu	Lys	Ala	Ala	Ile
	675						680					685			
Ala	Ala	Val	Tyr	Val	Met	Pro	Ser	Ala	Pro	Asp	Ser	Thr	Phe	His	Leu
690					695					700					
Phe	Leu	Lys	Ser	Asn	Thr	Asn	Arg	Arg	Leu	Gln	Lys	Val	Thr	Thr	Pro
705					710					715					720
Ser	Asp	Trp	Gln	Ala	Gly	Thr	Trp	Leu	Arg	Ile	Asn	Leu	Asp	Lys	Pro
				725					730					735	
Phe	Pro	Val	Asn	Asp	His	Met	Leu	Phe	Ala	Gly	Ile	Arg	Met	Pro	
			740				745						750		
Asn	Lys	Tyr	Lys	Leu	Asn	Arg	Ala	Ile	Arg	Tyr	Val	Arg	Asn	Pro	Asp
	755						760					765			
Asn	Leu	Phe	Ser	Ile	Thr	Gly	Lys	Lys	Ile	Ser	Tyr	Asn	Asn	Gly	Val
	770					775					780				
Ser	Phe	Glu	Gly	Tyr	Gly	Ile	Pro	Ser	Leu	Leu	Gly	Tyr	Met	Ala	Ile
785					790					795					800
Lys	Tyr	Leu	Val	Val	Asn	Thr	Asp	Ala	Pro	Lys	Ile	Asp	Met	Ser	Leu
				805					810					815	
Val	Gln	Glu	Pro	Tyr	Ala	Lys	Gly	Thr	Asn	Val	Ala	Pro	Phe	Pro	Glu
			820				825					830			
Leu	Val	Gly	Ile	Tyr	Val	Tyr	Lys	Asn	Gly	Thr	Phe	Ile	Gly	Thr	Gln
			835				840					845			
Asp	Pro	Ser	Val	Thr	Thr	Tyr	Ser	Val	Ser	Asp	Gly	Thr	Glu	Ser	Asp
	850					855					860				
Glu	Tyr	Glu	Ile	Lys	Leu	Val	Tyr	Lys	Gly	Ser	Gly	Ile	Ser	Asn	Gly
865					870					875					880
Val	Ala	Gln	Ile	Glu	Asn	Asn	Asn	Ala	Val	Val	Ala	Tyr	Pro	Ser	Val
				885					890						895

Val	Thr	Asp	Arg	Phe	Ser	Ile	Lys	Asn	Ala	His	Met	Val	His	Ala	Ala
			900					905					910		
Ala	Leu	Tyr	Ser	Leu	Asp	Gly	Lys	Gln	Val	Arg	Ser	Trp	Asn	Asn	Leu
		915				920						925			
Arg	Asn	Gly	Val	Thr	Phe	Ser	Val	Gln	Gly	Leu	Thr	Ala	Gly	Thr	Tyr
	930					935					940				
Met	Leu	Val	Met	Gln	Thr	Ala	Asn	Gly	Pro	Val	Ser	Gln	Lys	Ile	Val
945				950						955					960
Lys	Gln														

(2) INFORMATION FOR SEQ ID NO:337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

Trp	Lys	Lys	Ser	Asn	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Ala	Asn	Tyr	Arg
1				5					10					15	
Asp	His	Tyr	Asn	Thr	Glu	Ser	Tyr	Leu	Ser	Leu	Arg	Arg	Asn	Gln	Thr
			20					25					30		
Met	Lys	Tyr	Leu	Ile	Arg	Leu	Phe	Leu	Ser	Leu	Met	Leu	Leu	Ser	Leu
		35				40					45				
Trp	Thr	Gly	Cys	Thr	His	Glu	Gly	Leu	Ser	Ile	Cys	Asp	Gly	Glu	Asn
	50					55				60					
Thr	Leu	Val	Leu	Arg	Val	Glu	Thr	Gly	Lys	Ala	Pro	Asn	Ala	Arg	Ala
65				70					75					80	
Thr	Glu	Pro	Gly	Gln	Gly	Ile	Tyr	Asn	Glu	Asn	Lys	Val	Gly	Ser	Ile
			85					90					95		
Ser	Val	Leu	Phe	Tyr	Leu	Glu	Gly	Gln	Leu	Arg	Trp	Gln	Val	Lys	Ser
		100					105					110			
Thr	Asp	Tyr	Gln	Ile	His	Glu	Gly	Ala	Tyr	Ile	Ile	Pro	Val	Lys	Glu
	115					120					125				
Gln	Met	Arg	Pro	Leu	Phe	Asn	Gly	Asn	Asn	Asn	Phe	Ser	Ile	Tyr	Val
	130				135						140				
Val	Ala	Asn	Leu	Asp	Phe	Asn	Ala	Pro	Ala	Thr	Glu	Ala	Ala	Leu	Ser
145				150					155					160	
Gln	Phe	Val	Val	Glu	Lys	Ser	Ile	Glu	Val	Ser	Ser	Thr	Thr	Ala	Pro
		165						170						175	
Ala	Asp	Phe	Val	Met	Leu	Ala	His	Gly	Asn	Lys	Gln	Ile	Asn	Met	Ala
	180						185						190		
Thr	Thr	Glu	Gly	Lys	Leu	Leu	Gly	Asp	Tyr	Lys	Leu	Lys	Arg	Val	Ala
	195					200					205				
Ala	Lys	Ile	Arg	Met	Ile	Lys	Pro	Thr	Ile	Asn	Val	Gln	Gly	Tyr	Glu
	210				215					220					
Val	Val	Gly	Asn	Ile	Gln	Ala	Lys	Phe	Arg	Asn	Ser	Val	Thr	Lys	Gly
225				230					235					240	
Phe	Leu	Thr	Thr	Glu	Ala	Gln	Glu	Ile	Pro	Ala	Ala	Ala	Ser	Tyr	Lys
			245					250					255		
Thr	Ser	Glu	Tyr	Leu	Asp	Ile	Ala	Glu	Ser	Ala	Pro	Ala	Asn	Ser	Ile
	260						265					270			
His	Phe	Tyr	Ser	Tyr	Tyr	Asn	Lys	Trp	Thr	Leu	Ser	Thr	Pro	Glu	Lys
	275					280					285				
Arg	Pro	Glu	Phe	Phe	Ile	Met	Val	Lys	Phe	Lys	Lys	Thr	Gly	Gln	Pro
	290				295						300				
Asp	Asn	Thr	Ala	Lys	Pro	Tyr	Tyr	Tyr	Arg	Val	Pro	Leu	Glu	Ser	Gln
305				310					315					320	
Asp	Asn	Gln	Val	Lys	Ser	Asn	Val	Leu	Tyr	Asn	Leu	Asn	Val	Lys	Ile
		325						330					335		
Glu	Ile	Leu	Gly	Ser	Leu	Gln	Glu	Pro	Glu	Ala	Val	Ser	Val	Asn	Gly
	340						345					350			
Thr	Leu	Ala	Ile	Glu	Glu	Trp	Ile	Leu	His	Gln	Asp	Ala	Phe	Asn	Leu
	355					360						365			

```

Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn
370          375          380
Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile
385          390          395          400
Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly
          405          410          415
Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr
          420          425          430
Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val
          435          440          445
Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala
          450          455          460
Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile
          465          470          475          480
Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu
          485          490          495
Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val
          500          505          510
Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr
          515          520          525
Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr
          530          535          540
Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr
          545          550          555          560
Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala
          565          570          575
Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu
          580          585          590
Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn
          595          600          605
Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys
          610          615          620
Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp
          625          630          635          640
Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly
          645          650          655
Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln
          660          665          670
Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val
          675          680          685
Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys
          690          695          700

```

(2) INFORMATION FOR SEQ ID NO:338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

```

Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala
1          5          10          15
Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg
          20          25          30
Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln
          35          40          45
Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser
          50          55          60
Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val
          65          70          75          80
Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe
          85          90          95
Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu
          100          105          110

```

Ala	Glu	Leu	Pro	Val	Leu	Lys	Lys	Met	Ile	Ala	Val	Pro	Glu	Phe	Ser
	115					120						125			
Thr	Ala	Asn	Val	Ala	Val	Lys	Ile	Lys	Glu	Thr	Glu	Thr	Phe	Asp	Asn
	130					135					140				
Tyr	Asn	Ile	Tyr	Pro	Asn	Pro	Thr	Tyr	Val	Val	Glu	Glu	Leu	Pro	Glu
	145				150					155					160
Gly	Gly	Thr	Tyr	Leu	Val	Glu	Ala	Phe	Ala	Ile	Asn	Asn	Asp	Tyr	Tyr
			165					170						175	
Ser	Gln	Asn	Val	Ser	Leu	Pro	Ser	Thr	His	Tyr	Val	Tyr	Ser	Gln	Asp
		180						185					190		
Gly	Tyr	Phe	Arg	Ser	Gln	Arg	Phe	Ile	Glu	Val	Thr	Leu	Tyr	Pro	Phe
		195					200					205			
Arg	Tyr	Asn	Pro	Val	Arg	Gln	Glu	Ile	Leu	Phe	Ala	Lys	Lys	Ile	Glu
	210					215					220				
Val	Thr	Ile	Thr	Phe	Asp	Asn	Pro	Gln	Pro	Pro	Leu	Gln	Lys	Asn	Thr
	225				230					235					240
Gly	Ile	Phe	Asn	Lys	Val	Ala	Ser	Ser	Ala	Phe	Ile	Asn	Tyr	Glu	Ala
			245						250					255	
Asp	Gly	Lys	Ser	Ala	Ile	Glu	Asn	Asp	Met	Val	Phe	Ser	Arg	Gly	Thr
		260						265					270		
Thr	Thr	Tyr	Ile	Ser	Gly	Asn	Val	Ala	Ser	Asn	Leu	Pro	Gln	Asn	Cys
		275				280						285			
Asp	Tyr	Leu	Val	Ile	Tyr	Asp	Asp	Met	Phe	Asn	Val	Asn	Gln	Gln	Pro
	290					295					300				
His	Asp	Glu	Ile	Lys	Arg	Leu	Cys	Glu	His	Arg	Ala	Phe	Tyr	Asn	Gly
	305				310					315					320
Phe	Asp	Val	Ala	Ala	Val	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ser	Phe	Pro
			325						330					335	
Ser	Asn	Ala	Thr	Ser	Tyr	Ile	Asn	Glu	Thr	Lys	Leu	Lys	Asn	Phe	Ile
		340						345					350		
Arg	Ser	Val	Tyr	Asn	Gln	Ser	Asn	Ala	Lys	Arg	Thr	Leu	Asp	Gly	Lys
		355					360					365			
Leu	Gly	Tyr	Val	Leu	Leu	Ile	Gly	Lys	Pro	Leu	Ser	Lys	Tyr	Leu	Ala
	370					375					380				
Asp	Thr	Asp	Asn	Thr	Lys	Val	Pro	Thr	Ser	Phe	Ile	His	Asn	Val	Ser
	385				390					395					400
Leu	Ile	Pro	Ser	His	Pro	Thr	Phe	Gly	Ser	Ile	Cys	Ala	Ser	Asp	Tyr
			405						410					415	
Phe	Phe	Ser	Cys	Val	Ser	Pro	Leu	Asp	Thr	Val	Gly	Asp	Leu	Phe	Ile
		420						425				430			
Gly	Arg	Phe	Ser	Val	Thr	Asn	Ala	His	Glu	Leu	His	Asn	Leu	Ile	Glu
		435					440					445			
Lys	Thr	Ile	Asn	Lys	Glu	Ile	Ser	Tyr	Asn	Pro	Ile	Ala	His	Lys	Asn
	450					455					460				
Ile	Leu	Tyr	Ala	Glu	Gly	Lys	Gly	Cys	Asp	Ala	Pro	Ile	Leu	Arg	Leu
	465				470					475					480
Phe	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Lys
			485					490						495	
Ser	Asn	Gln	Val	Ser	Ala	Ile	Asp	Ser	Ile	Phe	Asp	Cys	Leu	Asn	Asn
		500						505					510		
Gly	Ser	His	His	Phe	Tyr	Phe	Asn	Thr	His	Gly	Met	Pro	Thr	Val	Trp
		515					520					525			
Gly	Ile	Gly	Gln	Gly	Leu	Asp	Val	Asn	Thr	Leu	Thr	Ala	Arg	Leu	Asn
	530					535					540				
Asn	Thr	Ser	Ser	Gln	Gly	Leu	Cys	Thr	Ser	Leu	Ser	Cys	Ser	Ser	Ala
	545				550					555					560
Val	Ala	Asp	Ser	Thr	Ile	Arg	Ser	Leu	Gly	Glu	Val	Leu	Thr	Thr	Tyr
			565						570					575	
Ala	Pro	Asn	Lys	Gly	Phe	Ser	Ala	Phe	Leu	Gly	Gly	Ser	Arg	Ala	Thr
		580						585					590		
Gln	Tyr	Ala	Val	Tyr	Leu	Glu	Gly	Pro	Cys	Pro	Pro	Ser	Glu	Phe	Tyr
		595					600					605			
Glu	Tyr	Leu	Pro	Tyr	Ser	Leu	Tyr	His	Asn	Leu	Ser	Thr	Val	Val	Gly
	610					615					620				
Glu	Met	Leu	Leu	Ser	Ser	Ile	Ile	Asn	Thr	Asn	Ser	Val	Asp	Thr	Tyr
	625				630					635					640
Ser	Lys	Phe	Asn	Phe	Asn	Leu	Leu	Gly	Asp	Pro	Ala	Leu	Asn	Ile	Met
			645						650					655	
Ala	His	Gly	Met	Glu	Val	Ser	Asn	Cys	Ile	Thr	Leu	Pro	Asn	Asn	Thr
		660						665					670		
Ile	Ile	Ser	Ser	Pro	Ile	Thr	Ile	Lys	Asn	Gly	Gly	Cys	Leu	Lys	Ile
		675					680					685			
Pro	Glu	Lys	Gly	Val	Leu	His	Phe	Thr	Asn	Asn	Gly	Ser	Ile	Gln	Val
	690					695					700				
Met	Ser	Gly	Gly	Thr	Leu	Glu	Ile	Gly	Asn	Gln	Ala	Lys	Ile	Ser	Gly
	705				710					715					720
Glu	Thr	Gly	Ala	Asn	Pro	Thr	Phe	Ile	Thr	Val	Tyr	Gly	Asp	Gly	Leu

(A) LENGTH: 938 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

```
Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile
1      5      10      15
Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
      20      25      30
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
      35      40      45
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
      50      55      60
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
65      70      75      80
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
      85      90      95
Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
      100     105     110
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
      115     120     125
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
130     135     140
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
145     150     155     160
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
      165     170     175
Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala
      180     185     190
Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu
195     200     205
Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr
210     215     220
Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp
225     230     235     240
Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu
      245     250     255
Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln
      260     265     270
Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu
      275     280     285
Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp
290     295     300
Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr
305     310     315     320
Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly
      325     330     335
Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr
      340     345     350
Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser
      355     360     365
Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn
      370     375     380
Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp
385     390     395     400
Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met
      405     410     415
Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu
      420     425     430
Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile
      435     440     445
Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys
450     455     460
Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr
465     470     475     480
```


Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile
 485 490 495
 Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu
 500 505 510
 Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn
 515 520 525
 Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val
 530 535 540
 Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu
 545 550 555 560
 Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln
 565 570 575
 Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu
 580 585 590
 Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile
 595 600 605
 Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met
 610 615 620
 Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro
 625 630 635 640
 Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu
 645 650 655
 Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val
 660 665 670
 Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala
 675 680 685
 Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala
 690 695 700
 Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys
 705 710 715 720
 Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu
 725 730 735
 Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro
 740 745 750
 Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
 755 760 765
 Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
 770 775 780
 Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
 785 790 795 800
 Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
 805 810 815
 Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
 820 825 830
 Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
 835 840 845
 Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
 850 855 860
 Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
 865 870 875 880
 Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
 885 890 895
 Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
 900 905 910
 Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
 915 920 925
 Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
 930 935

(2) INFORMATION FOR SEQ ID NO:340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

```

Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser
1      5      10      15
Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val
20      25      30
Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro
35      40      45
Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu
50      55      60
Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro
65      70      75      80
Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe
85      90      95
Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu
100     105     110
Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile
115     120     125
Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp
130     135     140
Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys
145     150     155     160
Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg
165     170     175
Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu
180     185     190
Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg
195     200     205
Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val
210     215     220
Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly
225     230     235     240
Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg
245     250     255
Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His
260     265     270
Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile
275     280     285
Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn
290     295     300
Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu
305     310     315     320
Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp
325     330     335
Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe
340     345     350
Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu
355     360     365
Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val
370     375     380
Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu
385     390     395     400
Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln
405     410     415
Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr
420     425     430
Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu
435     440     445
Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu
450     455     460
Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu
465     470     475     480
Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly
485     490     495
Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu
500     505     510
Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val
515     520     525
Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly
530     535     540
Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser
545     550     555     560
Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys
565     570     575
Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro
580     585     590
Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe

```

(2) INFORMATION FOR SEQ ID NO:341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

```

Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys
1      5      10      15
Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His
      20      25      30
Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
      35      40      45
Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
      50      55      60
Gln Ala Leu Ala Ala Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
65      70      75      80
Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly
      85      90      95
Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met
      100     105     110
Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly
      115     120     125
Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln
      130     135     140
Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln
      145     150     155     160
Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser
      165     170     175
Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu
      180     185     190
Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser
      195     200     205
Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn
      210     215     220
Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg
      225     230     235     240
Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu
      245     250     255
Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met
      260     265     270
Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser
      275     280     285
Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp
      290     295     300
Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val
      305     310     315     320
Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr
      325     330     335
His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp
      340     345     350
Asp Lys Ser Ile Phe
      355

```

(2) INFORMATION FOR SEQ ID NO:342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

```
Pro Gln Pro Val Gly Leu Lys Glu Ile Thr Ile Lys Pro Met Cys Leu
1      5      10      15
Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu Gln Glu Leu
      20      25      30
Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly Asn Glu Ile
      35      40      45
Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys Glu Val Gly
      50      55      60
Arg Leu Arg Glu Glu Ala Phe Arg His Tyr Gly Gly Gly Thr Gly Lys
65      70      75      80
Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser Tyr Lys Gln
      85      90      95
Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly Gly Tyr Arg
      100     105     110
Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly Lys Pro Leu
      115     120     125
Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe Leu His Asp
      130     135     140
Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val Ser Leu Gln
145     150     155     160
Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val Leu Asp Asn
      165     170     175
Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro Glu Ala Leu
      180     185     190
Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp Arg Arg Ala
      195     200     205
Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser Asp Pro Glu
      210     215     220
Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile Ser Ala Glu
225     230     235     240
Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn Tyr Lys Thr
      245     250     255
Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro Pro Leu Val
      260     265     270
Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe Gly Thr Ala
      275     280     285
Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile Phe Ile Ala
      290     295     300
Val Gly Lys Ile Leu Glu Lys Lys Gln Arg His Ile Glu Ser Phe
305     310     315     320
Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser Asn Gly Arg
      325     330     335
Ser
```

(2) INFORMATION FOR SEQ ID NO:343

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

Tyr	Asp	Gly	Ala	Arg	Leu	Val	Tyr	Thr	Leu	Phe	Arg	Asn	Arg	Asn	Asp
1			5						10					15	
Ile	His	Pro	Met	Lys	Thr	Ile	Val	Arg	Tyr	Ser	Arg	Leu	Pro	Val	Ala
			20					25					30		
Leu	Phe	Phe	Cys	Leu	Leu	Gly	Ala	Val	His	Leu	Ser	Val	Glu	Ala	Gln
		35				40						45			
Met	Leu	Asn	Thr	Pro	Phe	Glu	Leu	Ser	Asp	Gln	Ile	Val	Leu	Ser	Pro
	50				55					60					
Thr	Glu	Arg	Gln	Tyr	Arg	Glu	Ile	Cys	Val	Gln	Thr	Lys	Glu	Lys	Arg
65				70					75					80	
Gly	Ala	Asp	Leu	Phe	Pro	Leu	Ser	Asp	Lys	Leu	Arg	Asp	Ser	Ala	Tyr
			85					90					95		
Val	Arg	Phe	Gly	Ser	Ala	Tyr	Gly	Asp	Ile	Ala	Gly	Asp	Tyr	Leu	Pro
		100					105					110			
Tyr	Asn	Gly	Asn	Asn	Tyr	Ser	Ser	Leu	Ser	Leu	Glu	Ser	Gly	Gly	Arg
	115					120					125				
Ile	Ser	Val	Arg	Asn	Tyr	Gly	Thr	Leu	Gln	Gly	Ser	Ala	Ser	Tyr	Ser
130				135						140					
Arg	Gly	Met	His	Lys	Arg	Ile	Gly	Trp	Asn	Ala	Leu	Arg	Asn	Ala	Glu
145				150					155					160	
Ala	Tyr	Tyr	Pro	Tyr	Leu	Val	Ser	Asp	Ser	Thr	Gly	Gly	Asp	Tyr	His
			165					170					175		
Phe	Glu	Asp	Tyr	Arg	Leu	Ala	Gly	Tyr	Tyr	Ser	Phe	Arg	Ala	Gly	Arg
	180					185						190			
Leu	Pro	Leu	Gly	Ile	Gly	Phe	Ser	Tyr	Arg	Gly	Glu	Val	Ala	Tyr	Arg
	195					200					205				
Leu	Thr	Asp	Pro	Arg	Thr	Thr	Asn	Thr	Thr	Gly	Ala	Leu	Glu	Leu	Ser
	210				215					220					
Cys	Ala	Thr	Ser	Leu	Thr	Leu	Pro	Arg	Glu	Asn	Arg	Leu	Ser	Leu	Ser
225				230					235					240	
Ala	Ala	Tyr	Leu	Tyr	His	Arg	Gln	His	Leu	Thr	Gln	Tyr	Asn	Trp	Arg
			245					250					255		
Pro	Gly	Gln	Gln	Asp	Lys	Phe	Phe	Val	Ser	Tyr	Gly	Phe	Gly	Gln	Val
	260					265						270			
Asp	Val	Ser	Asn	Ser	Pro	Ile	Trp	Phe	Gly	Ile	Ser	Arg	Met	Asn	Tyr
	275					280				285					
Val	Asn	Gly	Trp	Lys	Leu	Ser	Ser	Arg	Leu	Asp	Thr	Arg	Arg	Gly	Asp
	290				295					300					
Ala	Ile	Gly	Leu	Asp	Tyr	Ser	Gly	Tyr	Phe	Leu	Asp	Thr	Glu	Glu	Arg
305				310					315					320	
Ser	Ser	Ile	Asn	Leu	Phe	Ala	Leu	Leu	Tyr	Asn	Arg	Leu	Arg	Leu	Tyr
			325					330					335		
Gly	Ser	Trp	His	Leu	Ser	Asp	Phe	Asp	Phe	Ser	Phe	Ser	Ala	Asp	Tyr
	340					345						350			
Ala	Leu	Arg	Gln	Gly	Ile	Glu	Arg	Ile	Tyr	Glu	Asp	Tyr	Lys	Pro	Asp
	355					360					365				
Asp	Asn	Tyr	His	Ile	Tyr	Asp	Leu	Arg	Ile	Leu	Ala	Ile	Arg	Arg	Trp
370				375						380					
Tyr	Met	Leu	Asn	Glu	Phe	Ser	Ala	Gln	Ala	Gln	Ala	Ser	Tyr	Arg	Ile
385				390					395					400	
Arg	Thr	Asp	Arg	Gly	Cys	Ala	Leu	Arg	Val	Ser	Ala	Gly	Ser	Asp	Phe
			405					410					415		
Tyr	Gly	Tyr	Asp	Glu	Thr	Tyr	Arg	Lys	His	Gly	His	His	Thr	Met	Ser
	420					425						430			
Gly	Met	Leu	Arg	Pro	Phe	Ala	Gly	Ile	Ala	Tyr	Asp	His	Ala	Gly	Ser
	435					440					445				
Lys	Leu	Asp	Phe	Gly	Leu	Ser	Leu	Ser	Ala	Ala	Tyr	Arg	Met	Val	Leu
	450				455					460					
Thr	His	Ser	Tyr	Lys	Ile	Arg	Thr	Ile	Gln	Lys	Glu	Gln	Leu	Asp	Tyr
465				470					475					480	
Gln	Leu	Ala	Tyr	Leu	Pro	Tyr	Ala	Tyr	Arg	Asn	Arg	Glu	Gly	Val	Glu
			485					490					495		
Val	Arg	Ser	Ser	Leu	Tyr	Val	Ser	Ile	Pro	Met	Gln	Asn	Thr	His	Arg
	500					505						510			
Leu	Met	Thr	Glu	Leu	Arg	Leu	Tyr	Gly	Asp	Leu	Met	Lys	Arg	Lys	Asp
	515					520					525				
Gly	Ile	Ala	Tyr	Gly	Lys	Thr	Pro	Gly	Val	Ile	Ser	His	Ile	Leu	Ser
	530				535					540					
Asp	Pro	Gln	Ala	Glu	Arg	Thr	Ser	Gly	His	Thr	Ile	Gly	Ala	Ile	Cys
545				550					555					560	
Asn	Ile	Ser	Tyr	Leu	Phe										
				565											

(2) INFORMATION FOR SEQ ID NO:344

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

Arg	Thr	Asn	Val	Phe	Leu	Ser	Leu	Ser	His	Lys	Ile	Gly	Arg	Arg	Gly	
1			5						10					15		
Ala	Ser	Cys	Ser	Asn	Arg	Asn	Ala	Trp	Met	Ala	Glu	Asn	Lys	Pro	Ser	
			20					25					30			
Ser	Pro	Glu	Pro	Asp	Asn	Thr	Gly	Val	Gly	Asn	Ser	Pro	Ser	Asp	Tyr	
		35					40					45				
Leu	His	Gly	Glu	Ala	Ile	Ile	Pro	Pro	Leu	Ser	Ser	Leu	Ser	Asn	Phe	
	50					55					60					
Asn	Asp	Lys	Arg	Phe	Met	Lys	Lys	Leu	His	Met	Ile	Ala	Ala	Leu	Ala	
65				70					75					80		
Val	Leu	Pro	Phe	Cys	Leu	Thr	Ala	Gln	Ala	Pro	Val	Ser	Asn	Ser	Glu	
			85					90					95			
Ile	Asp	Ser	Leu	Ser	Asn	Val	Gln	Leu	Gln	Thr	Val	Gln	Val	Val	Ala	
		100					105					110				
Thr	Arg	Ala	Thr	Ala	Lys	Thr	Pro	Val	Ala	Tyr	Thr	Asn	Val	Arg	Lys	
	115						120					125				
Ala	Glu	Leu	Ser	Lys	Ser	Asn	Tyr	Gly	Arg	Asp	Ile	Pro	Tyr	Leu	Leu	
	130					135				140						
Met	Leu	Thr	Pro	Ser	Val	Val	Ala	Thr	Ser	Asp	Ala	Gly	Thr	Gly	Ile	
145				150					155					160		
Gly	Tyr	Ser	Gly	Phe	Arg	Val	Arg	Gly	Thr	Asp	Ala	Asn	Arg	Ile	Asn	
			165					170					175			
Ile	Thr	Thr	Asn	Gly	Val	Pro	Leu	Asn	Asp	Ser	Glu	Ser	Gln	Ser	Val	
	180						185					190				
Phe	Trp	Val	Asn	Met	Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln	
	195					200					205					
Val	Gln	Arg	Gly	Val	Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly	
	210				215					220						
Ala	Ser	Val	Asn	Met	Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly	
225				230					235					240		
Arg	Val	Asp	Leu	Ser	Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val	
			245					250					255			
Lys	Leu	Gly	Ser	Gly	Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg	
	260						265					270				
Leu	Ser	Lys	Ile	Gly	Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp	
	275					280				285						
Leu	Lys	Ser	Tyr	Phe	Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala	
	290				295					300						
Leu	Arg	Phe	Ile	Thr	Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp	
305				310					315					320		
Asn	Gly	Leu	Ser	Lys	Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn	
			325					330					335			
Ser	Ala	Gly	Leu	Met	Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr	
	340						345					350				
His	Asn	Thr	Asp	Asn	Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr	
	355					360					365					
His	Ser	Phe	Ser	Pro	Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr	
	370				375					380						
Ala	Gly	Tyr	Gly	Tyr	Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys	
385					390				395					400		
Glu	Tyr	Ala	Leu	Gln	Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys	
			405					410					415			
Thr	Asp	Leu	Ile	Arg	Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu	
	420						425					430				
Ile	Gly	Ser	Leu	Asn	Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly	
	435					440					445					
Ala	Ser	Gly	Asn	Ile	Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr	
	450					455				460						
Ile	Lys	Lys	Tyr	Asn	Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg	
465				470					475					480		
Asn	Arg	Ala	Asp	Lys	Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp	

												485			490			495		
Gln	Ile	Thr	Pro	Glu	Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr					
			500				505						510							
Ile	Gly	Tyr	Thr	Ile	Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln					
			515				520						525							
Gly	Ser	Met	Gln	His	Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn					
			530				535						540							
Pro	Lys	Ala	Gly	Leu	Thr	Tyr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr					
			545				550						555			560				
Ala	Ser	Val	Ala	Val	Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr					
			565				570						575							
Glu	Ala	Gly	Ile	Gly	Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr					
			580				585						590							
Glu	Leu	Gly	Tyr	Arg	Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly					
			595				600						605							
Leu	Tyr	Tyr	Met	Gln	Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu					
			610				615						620							
Ser	Asp	Val	Gly	Gln	Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg					
			625				630						635			640				
Met	Gly	Leu	Glu	Leu	Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu					
			645				650						655							
Arg	Trp	Asp	Ala	Ser	Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr					
			660				665						670							
Val	Gln	Tyr	Thr	Ser	Val	Tyr	Asp	Ala	Asp	Tyr	Asn	Trp	Leu	Glu	Leu					
			675				680						685							
Lys	Glu	Glu	Thr	Leu	Glu	Ser	Thr	Asp	Ile	Ala	Tyr	Ser	Pro	Asn	Val					
			690				695						700							
Ile	Ala	Gly	Ser	Met	Leu	Thr	Leu	Ser	His	Ala	Gly	Phe	Glu	Met	Ala					
			705				710						715			720				
Trp	Thr	Ser	Arg	Phe	Val	Ser	Lys	Gln	Tyr	Leu	Asp	Asn	Thr	Gln	Arg					
			725				730						735							
Ser	Asp	Arg	Met	Leu	Ser	Ser	Tyr	Trp	Val	Asn	Asp	Leu	Arg	Leu	Gly					
			740				745						750							
Tyr	Val	Leu	Pro	Val	His	Phe	Val	Lys	Arg	Val	Ala	Leu	Gly	Val	Gln					
			755				760						765							
Leu	Asn	Asn	Leu	Phe	Asn	Leu	Met	Tyr	Ala	Ser	Asn	Ala	Tyr	Ile	Tyr					
			770				775						780							
Asp	Ala	Gly	Tyr	Val	Gln	Ala	Ser	Gly	Glu	Leu	Ser	Ala	Tyr	Ala	Asp					
			785				790						795			800				
Leu	Arg	Tyr	Tyr	Pro	Gln	Ala	Gly	Phe	Asn	Ala	Leu	Gly	Ser	Leu	Thr					
			805				810						815							
Ile	Asp	Phe																		

(2) INFORMATION FOR SEQ ID NO:345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

Tyr	Arg	Arg	Ser	Gly	Arg	Val	Cys	Pro	Arg	Ile	Leu	Arg	Asn	Lys	Arg	
1				5				10						15		
Ser	Tyr	Ala	Asp	Thr	Arg	Leu	Gln	Pro	Arg	Arg	Ala	Val	Arg	Leu	Arg	
			20				25						30			
Ala	Gly	Thr	Arg	Thr	Lys	Met	Lys	Arg	Arg	Phe	Leu	Ser	Leu	Leu	Leu	
			35				40						45			
Leu	Tyr	Ile	Leu	Ser	Ser	Ile	Ser	Leu	Ser	Ala	Gln	Arg	Phe	Pro	Met	
			50				55						60			
Val	Gln	Gly	Ile	Glu	Leu	Asp	Thr	Asp	Ser	Leu	Phe	Ser	Leu	Pro	Lys	
			65				70						75			
Arg	Pro	Trp	Arg	Ala	Ile	Gly	Lys	Thr	Ile	Gly	Val	Asn	Leu	Ala	Val	
			85				90						95			
Trp	Gly	Phe	Asp	His	Phe	Ile	Met	Asn	Glu	Asp	Phe	Ala	Asp	Ile	Ser	

	100		105		110										
Trp	Gln	Thr	Ile	Lys	Ser	Asn	Phe	Gln	Thr	Gly	Phe	Gly	Trp	Asp	Asn
	115						120					125			
Asp	Lys	Phe	Val	Thr	Asn	Leu	Phe	Ala	His	Pro	Tyr	His	Gly	Ser	Leu
	130					135					140				
Tyr	Phe	Asn	Ala	Ala	Arg	Ser	Asn	Gly	Leu	Ser	Phe	Arg	His	Ser	Ala
145					150					155					160
Pro	Phe	Ala	Phe	Phe	Gly	Ser	Leu	Met	Trp	Glu	Leu	Leu	Met	Glu	Asn
			165					170						175	
Glu	Pro	Pro	Ser	Ile	Asn	Asp	Leu	Cys	Ala	Thr	Thr	Ile	Gly	Gly	Ile
			180					185					190		
Ala	Leu	Gly	Glu	Met	Gly	His	Arg	Leu	Ser	Asp	Leu	Leu	Ile	Asp	Asn
	195						200				205				
Arg	Thr	Thr	Gly	Trp	Glu	Arg	Met	Gly	Arg	Glu	Val	Ala	Ile	Ala	Leu
	210					215					220				
Ile	Asn	Pro	Met	Arg	Phe	Leu	Asn	Arg	Leu	Thr	Ala	Gly	Glu	Val	Thr
225					230					235					240
Ser	Val	Gly	Ser	Arg	Ser	Gly	Gln	Ile	Phe	Gln	Ser	Val	Pro	Ile	Asn
			245						250					255	
Ile	Val	Val	Asp	Ala	Gly	Phe	Arg	Phe	Leu	Ala	Asp	Lys	Arg	His	Ala
	260							265					270		
Arg	Thr	Gly	Ala	Thr	Ala	Leu	Thr	Leu	Asn	Leu	Arg	Phe	Asp	Tyr	Gly
	275						280					285			
Asp	Pro	Phe	Arg	Ser	Glu	Thr	Phe	Ser	Pro	Tyr	Asp	Phe	Phe	Gln	Phe
	290				295						300				
Lys	Ala	Gly	Leu	Ser	Phe	Ser	Glu	Ser	Gln	Pro	Leu	Leu	Ser	Gln	Ile
305					310					315					320
Asn	Leu	Ile	Gly	Ile	Leu	Ser	Gly	Cys	Gln	Leu	Leu	Ala	His	Glu	Arg
			325						330					335	
Thr	Val	Leu	Val	Gly	Gly	Leu	Phe	Gln	His	Phe	Asp	Tyr	Tyr	Asn	Ser
	340						345						350		
Glu	Lys	Arg	Ile	Ser	Lys	Asn	Ser	Glu	Glu	Val	Leu	Val	Thr	Pro	Tyr
	355						360					365			
Arg	Ile	Ser	Gln	Val	Ala	Ala	Leu	Gly	Gly	Gly	Leu	Ile	Phe	Gln	His
	370					375					380				
His	Gly	Lys	Phe	Arg	Arg	Arg	Pro	Leu	Glu	Leu	Tyr	Ala	Glu	Thr	Tyr
385					390					395					400
Leu	Asn	Val	Val	Pro	Met	Gly	Ala	Ser	Leu	Ser	Asp	His	Tyr	Asn	Val
			405						410					415	
Asp	Asn	Arg	Asp	Tyr	Asn	Leu	Gly	Ser	Gly	Leu	Ser	Gly	Lys	Leu	Tyr
			420				425						430		
Leu	Gly	Ala	Thr	Tyr	Asn	Asp	Leu	Trp	Ser	Trp	Leu	Leu	Gly	Val	Glu
	435						440					445			
Ser	Tyr	Arg	Leu	Tyr	Thr	Trp	Ile	Gly	Tyr	Glu	Glu	Pro	His	Gln	Lys
	450					455					460				
Asn	Thr	Asp	Val	Ser	Ser	Phe	Met	Val	Gln	Gly	Asp	Glu	Ser	Lys	Ala
465					470					475					480
Arg	Leu	Leu	Val	Thr	Ser	Ser	Glu	Phe	Ala	Phe	His	Pro	Gly	Pro	Trp
			485						490					495	
His	Val	Ala	Ile	Val	Ala	Arg	Arg	Phe	Ile	Arg	Lys	Thr	Ala	Tyr	Gln
		500					505					510			
Phe	Tyr	Pro	Asn	Val	Ser	Phe	Asp	Thr	Gly	Asp	Ile	Gln	Leu	Arg	Val
	515						520					525			
Gly	Phe	His	Phe												
	530														

(2) INFORMATION FOR SEQ ID NO:346

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met

1	5	10	15
Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala			
	20	25	30
Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu			
	35	40	45
Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn			
	50	55	60
Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys			
	65	70	75
Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr			
	85	90	95
Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu			
	100	105	110
Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala			
	115	120	125
Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser			
	130	135	140
Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala			
	145	150	155
Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe			
	165	170	175
Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp			
	180	185	190
Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys			
	195	200	205
Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn			
	210	215	220
Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala			
	225	230	235
Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu			
	245	250	255
Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu			
	260	265	270
Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe			
	275	280	285
Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe			
	290	295	300

(2) INFORMATION FOR SEQ ID NO:347

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg			
1	5	10	15
Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile			
	20	25	30
Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn			
	35	40	45
Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn			
	50	55	60
Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Glu Phe Ala			
	65	70	75
Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met			
	85	90	95
Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His			
	100	105	110
Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp			
	115	120	125
Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val			
	130	135	140
Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp			

145	150	155	160
Ala Phe Gly Asp	Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu		
	165	170	175
Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu			
	180	185	190
His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu			
	195	200	205
Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe			
	210	215	220

(2) INFORMATION FOR SEQ ID NO:348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu			
1	5	10	15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg			
	20	25	30
Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly			
	35	40	45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala			
	50	55	60
Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu			
65	70	75	80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met			
	85	90	95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu			
	100	105	110
Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met			
	115	120	125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly			
	130	135	140
Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr			
145	150	155	160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp			
	165	170	175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile			
	180	185	190
Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly			
	195	200	205
Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr			
	210	215	220
Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe			
225	230	235	240
Phe Val Gly Ile Gly Tyr Arg Phe			
	245		

(2) INFORMATION FOR SEQ ID NO:349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

```
Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Val Val Leu Leu
1      5      10      15
Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
      20      25      30
Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly
      35      40      45
Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
      50      55      60
Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn
      65      70      75      80
Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn
      85      90      95
Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala
      100     105     110
Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp
      115     120     125
Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser
      130     135     140
Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val
      145     150     155     160
Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val
      165     170     175
Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val
      180     185     190
Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser
      195     200     205
Thr His Phe
      210
```

(2) INFORMATION FOR SEQ ID NO:350

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 953 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

```
Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu
1      5      10      15
Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu
      20      25      30
Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala
      35      40      45
Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile
      50      55      60
Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser
      65      70      75      80
Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile
      85      90      95
Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg
      100     105     110
Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu
      115     120     125
Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr
      130     135     140
Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe
      145     150     155     160
Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe
      165     170     175
```

Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu
 180 185 190
 Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met
 195 200 205
 Phe Met Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro
 210 215 220
 His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp
 225 230 235 240
 Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro
 245 250 255
 Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser
 260 265 270
 Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr
 275 280 285
 Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu
 290 295 300
 Ala Leu Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala
 305 310 315 320
 Gln Ser Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala
 325 330 335
 Asn Tyr Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr
 340 345 350
 Ser Lys Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro
 355 360 365
 Lys Ala Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr
 370 375 380
 Gly Ser Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala
 385 390 395 400
 Arg Thr Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe
 405 410 415
 Pro Gly Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn
 420 425 430
 Met Arg Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn
 435 440 445
 Met Ser Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu
 450 455 460
 Arg Trp Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn
 465 470 475 480
 Ser Ile Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg
 485 490 495
 Asp Trp Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val
 500 505 510
 Pro Leu Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu
 515 520 525
 Trp Trp Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys
 530 535 540
 Thr Phe Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp
 545 550 555 560
 Tyr Ser Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys
 565 570 575
 Pro Trp Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His
 580 585 590
 Arg Phe Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys
 595 600 605
 Arg Arg Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly
 610 615 620
 Lys Leu His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly
 625 630 635 640
 Ala Pro Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn
 645 650 655
 Asn Leu Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys
 660 665 670
 Lys Ile Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met
 675 680 685
 Phe Ala Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu
 690 695 700
 Arg Leu Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro
 705 710 715 720
 Tyr Leu Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr
 725 730 735
 Lys Ser Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu
 740 745 750
 Ile Ser Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu
 755 760 765
 Ser Gly Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu
 770 775 780
 Lys Lys Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp

```

785          790          795          800
Ile Leu Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu
      805          810          815
Glu Arg Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala
      820          825          830
Tyr Ser Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala
      835          840          845
Thr Asp Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg
      850          855          860
Val Thr Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn
865          870          875          880
Trp Ser Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile
      885          890          895
Thr Ser Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile
      900          905          910
Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val
      915          920          925
Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser
      930          935          940
Asn Arg Pro Ile Thr Asn Thr Trp Tyr
945          950

```

(2) INFORMATION FOR SEQ ID NO:351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

```

Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro
1      5      10      15
Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile
      20      25      30
Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile
      35      40      45
Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile
      50      55      60
Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn
65      70      75      80
Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp
      85      90      95
Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro
      100     105     110
Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro
      115     120     125
Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro
      130     135     140
Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr
145     150     155     160
Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln
      165     170     175
Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile
      180     185     190
Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala
      195     200     205
Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His
      210     215     220
Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile
225     230     235     240
Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys
      245     250     255
Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile
      260     265     270
Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn

```

275					280					285					
Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys	Thr	Gly	Asn	Ala	Asn	Asp	Pro
290						295					300				
Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile	Asn	Phe	Pro	Thr	Asn	Tyr	Val
305					310					315					320
Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr	Pro	Asn	Tyr	Pro	Thr	His	Ser
				325					330					335	
Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro	Glu	Ser	Lys	Phe	Asp	Tyr	Ser
		340						345					350		
Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp	Gly	Val	Ala	Gly	Ala	Leu	Val
	355						360					365			
Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr	Tyr	Tyr	Tyr	Phe	Pro	Cys	Asn
370					375						380				
Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala	Lys	Asn	Ser	Gly	Tyr	Thr	Ile
385					390					395					400
His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp	Phe	Ala	Leu	Ala	Asn	Asn	Ser
			405						410					415	
Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn	His	Phe	Phe	Thr	Ala	Thr	Pro
		420						425					430		
Ala	Asn	Leu	Ala	Ala	Ala	Phe	Asp	Asn	Ile	Ala	Gln	Thr	Ile	Asn	Ile
		435					440					445			
Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp	Phe	Val	Ala	Pro	Gly	Phe	Ile
450					455						460				
Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp	Val	Thr	His	Leu	Leu	Asn	Val
465					470					475					480
Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val	Ser	Thr	Lys	Lys	Leu	Thr	Trp
				485					490					495	
Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser	Glu	Ala	Thr	Ile	Thr	Tyr	Arg
		500						505					510		
Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln	Asn	Asn	Asp	Ile	Pro	Val	Asn
		515					520					525			
Thr	Thr	Ser	Ala	Ile	Gly	Pro	Asp	Leu	Gly	Gly	Phe	Asp	Thr	Asn	Thr
	530					535					540				
Glu	Ala	Lys	Leu	Thr	Tyr	Thr	Asn	Ser	Asn	Gly	Glu	Pro	Asn	Gln	Gln
545					550					555					560
Leu	Ile	Phe	Pro	Arg	Pro	Thr	Val	Lys	Leu	Gly	Tyr	Gly	Val	Ile	Lys
			565						570					575	
Arg	His	Tyr	Val	Leu	Val	Asn	Lys	Asp	Gly	Gln	Pro	Ile	Gln	Ala	Asn
		580						585					590		
Gly	Thr	Val	Val	Ser	Ser	Leu	Ser	Glu	Ala	His	Val	Leu	Gln	Ser	Gln
		595					600					605			
Asp	Phe	Phe	Leu	Pro	Ser	Gly	Gly	Gly	His	Ile	Val	Pro	Lys	Trp	Ile
	610					615					620				
Lys	Leu	Asp	Lys	Thr	Thr	Glu	Ala	Leu	Gln	Tyr	Tyr	Ser	Val	Pro	Pro
625					630					635					640
Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp	Gly	Lys	Arg	Tyr	Arg	Phe	Val
			645						650					655	
Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro	Gly	Gln	Ile	Gly	Ile	Ser	Trp
		660						665					670		
Lys	Lys	Pro	Ala	Gly	Asn	Ala	Tyr	Phe	Ala	Tyr	Lys	Leu	Leu	Asn	Tyr
		675					680					685			
Trp	Met	Gly	Gly	Thr	Thr	Asp	Gln	Ser	Glu	Trp	Asp	Val	Thr	Ser	
	690					695				700					
Asn	Trp	Thr	Gly	Ala	Gln	Val	Pro	Leu	Thr	Gly	Glu	Asp	Val	Glu	Phe
705					710					715					720
Ala	Thr	Thr	Glu	Asn	Phe	Gly	Ser	Pro	Ala	Val	Ala	Asp	Leu	His	Val
				725					730					735	
Pro	Thr	Thr	Asn	Pro	Lys	Ile	Ile	Gly	Asn	Leu	Ile	Asn	Asn	Ser	Asp
		740						745					750		
Lys	Asp	Leu	Val	Val	Thr	Thr	Ser	Ser	Gln	Leu	Thr	Ile	Asn	Gly	Val
		755					760					765			
Val	Glu	Asp	Asn	Asn	Pro	Asn	Val	Gly	Thr	Ile	Val	Val	Lys	Ser	Ser
	770					775					780				
Lys	Asp	Asn	Pro	Thr	Gly	Thr	Leu	Leu	Phe	Ala	Asn	Pro	Gly	Tyr	Asn
785					790					795					800
Gln	Asn	Val	Gly	Gly	Thr	Val	Glu	Phe	Tyr	Asn	Gln	Gly	Tyr	Asp	Cys
			805						810					815	
Ala	Asp	Cys	Gly	Met	Tyr	Arg	Arg	Ser	Trp	Gln	Tyr	Phe	Gly	Ile	Pro
			820					825					830		
Val	Asn	Glu	Ser	Gly	Phe	Pro	Ile	Asn	Asp	Val	Gly	Gly	Asn	Glu	Thr
		835						840				845			
Val	Asn	Gln	Trp	Val	Glu	Pro	Phe	Asn	Gly	Asp	Lys	Trp	Arg	Pro	Ala
	850					855					860				
Pro	Tyr	Ala	Pro	Asp	Thr	Glu	Leu	Gln	Lys	Phe	Lys	Gly	Tyr	Gln	Ile
865					870					875					880
Thr	Asn	Asp	Val	Gln	Ala	Gln	Pro	Thr	Gly	Val	Tyr	Ser	Phe	Lys	Gly
			885					890						895	

Met Ile Cys Val Cys Asp Ala Phe Leu Asn Leu Thr Arg Thr Ser Gly
900 905 910
Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly Asn Ser Tyr Thr Gly Ala
915 920 925
Ile Asp Ile Lys Gln Gly Ile Val Phe Pro Pro Glu Val Glu Gln Thr
930 935 940
Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp Gln Trp Arg Lys Leu Asn
945 950 955 960
Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly Gln Tyr Leu Ser Val Pro
965 970 975
Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met
980 985 990
His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk
995 1000 1005
Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn
1010 1015 1020
Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met
1025 1030 1035 1040
Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu
1045 1050 1055
Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp
1060 1065 1070
Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr Ala Met
1075 1080 1085
Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu
1090 1095 1100
Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr
1105 1110 1115 1120
Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu
1125 1130 1135
His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser
1140 1145 1150
Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu
1155 1160 1165
Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr
1170 1175 1180
Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr
1185 1190 1195 1200
Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val
1205 1210 1215
Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr
1220 1225 1230
Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu
1235 1240 1245
Val Glu Tyr
1250

(2) INFORMATION FOR SEQ ID NO:352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp
1 5 10 15
Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu
20 25 30
Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr
35 40 45
His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr
50 55 60
Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala
65 70 75 80

Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly
 85 90 95
 Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly
 100 105 110
 Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val
 115 120 125
 Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala
 130 135 140
 Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser
 145 150 155 160
 Val Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe
 165 170 175
 Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe
 180 185 190
 Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu
 195 200 205
 Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg
 210 215 220
 Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His
 225 230 235 240
 Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr
 245 250 255
 Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly
 260 265 270
 Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala
 275 280 285
 Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu
 290 295 300
 Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro
 305 310 315 320
 Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg
 325 330 335
 Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu
 340 345 350
 Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe
 355 360 365
 Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala
 370 375 380
 Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp
 385 390 395 400
 Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser
 405 410 415
 Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe
 420 425

(2) INFORMATION FOR SEQ ID NO:353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

Tyr Gly Lys Arg Arg Lys Leu Gly Thr Ser Val Arg Pro Ser Val Leu
 1 5 10 15
 Thr Gln Ile Arg Phe Ile Leu Asp Leu His Leu Ile Thr Asp Phe Phe
 20 25 30
 Glu Gly Leu Arg Val Asn Pro Ile Gly Ala Ala Ala Ile Val Ala Phe
 35 40 45
 Ile Ile Asp Leu Leu Leu Leu Cys Ser Ala Phe Met Ser Ser Cys
 50 55 60
 Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu Gln Asn Ile Arg
 65 70 75 80
 Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn Leu Leu Asp Asn
 85 90 95


```

Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn Asn Val Ile Asn
      100      105      110
Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu Gln Thr Phe Val
      115      120      125
Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr Ile Leu Leu Thr
      130      135      140
Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys Val Tyr Ala Arg
      145      150      155      160
Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala Ala Met Ser Val
      165      170      175
Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu Val Lys Ser Thr
      180      185      190
Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr Asp Met Ser Val
      195      200      205
Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr Glu Gly Glu Pro
      210      215      220
Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe Tyr Asn Lys Thr
      225      230      235      240
Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val Asp Val Asp Leu
      245      250      255
Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val Ser Ser Gly Tyr
      260      265      270
Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn Ile Lys Gly Val
      275      280      285
Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys Gly Asp Glu Phe
      290      295      300
Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val Pro Glu Asn Lys
      305      310      315      320
Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn Lys Val His Val
      325      330      335
Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly Leu Ile Thr Met
      340      345      350
Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr Asp Glu Tyr Asp
      355      360      365
Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly Ser Tyr Leu Phe
      370      375      380
Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr Leu Asp Leu Pro
      385      390      395      400
Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp Thr Leu Ser Gly
      405      410      415
Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val Gly Asp Thr Ala
      420      425      430
Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met Asp Lys Arg Arg
      435      440      445
Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr Trp Glu Val Glu
      450      455      460

```

(2) INFORMATION FOR SEQ ID NO:354

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

```

Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val
1      5      10      15
Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn
      20      25      30
Leu Thr Met Asn Ile Asp Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu
      35      40      45
Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys
      50      55      60
Asn Thr Ala Asn Leu Asn Leu Leu Ile Lys His Gly Gln Val Ile Asn
65      70      75      80

```

```

Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val
      85          90          95
Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val
      100        105        110
Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly
      115        120        125
Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val
      130        135        140
Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu
      145        150        155        160
Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr
      165        170        175
Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His
      180        185        190
Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly
      195        200        205
Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp
      210        215        220
Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg
      225        230        235        240
Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn
      245        250        255
Thr Val Asp Val Gly Ile Asp Ile Ser Phe
      260        265

```

(2) INFORMATION FOR SEQ ID NO:355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

```

Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu
1          5          10          15
Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu
      20        25        30
Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe
      35        40        45
Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile
      50        55        60
His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser
      65        70        75        80
Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn
      85        90        95
Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly
      100       105       110
Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp
      115       120       125
Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val
      130       135       140
Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val
      145       150       155       160
Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His
      165       170       175
Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu
      180       185       190
Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile
      195       200       205
Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn
      210       215       220
Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly
      225       230       235       240
Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu
      245       250       255

```

Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe
 260 265 270
 Arg Ser Ile Pro Ala His Thr Ile Lys Arg Val Glu Val Ile Thr Asp
 275 280 285
 Pro Gly Val Lys Tyr Asp Ala Glu Gly Thr Ser Ala Ile Leu Asp Ile
 290 295 300
 Val Thr Glu Glu Gly Lys Lys Leu Glu Gly Tyr Ser Gly Ser Ile Thr
 305 310 315 320
 Ala Ser Val Ser Asn Asn Pro Thr Ala Asn Gly Ser Ile Phe Leu Thr
 325 330 335
 Ala Lys Ser Gly Lys Val Gly Leu Thr Thr Asn Tyr Asn Tyr Tyr Gly
 340 345 350
 Gly Lys Asn Lys Gly Ser Arg Tyr Phe Thr Glu Arg Thr Thr Ser Met
 355 360 365
 Leu Gln Thr Ile Glu Glu Gly Lys Gly Gln Glu Thr Phe Gly Gly His
 370 375 380
 Phe Gly Asn Ala Leu Leu Ser Phe Glu Ile Asp Ser Leu Asn Leu Phe
 385 390 395 400
 Thr Val Gly Gly Asn Val Arg Leu Trp Glu Met Thr Thr Asp Arg Asn
 405 410 415
 Ser Val Glu Lys Ser Phe Ala Gly Ser Asn Leu Met Ser Tyr Ile Asp
 420 425 430
 Arg Lys Leu Lys Thr Gln Met Asp Ala Gly Ser Tyr Glu Leu Asn Ala
 435 440 445
 Asp Tyr Gln His Ser Thr Arg Leu Pro Gly Glu Leu Leu Thr Val Ser
 450 455 460
 Tyr Arg Phe Thr His Asn Pro Asn Asn Ser Glu Thr Phe Ile Asp Gln
 465 470 475 480
 Trp Lys Arg Asp Pro Leu Asn Thr Ala Asn Thr Ile Gln Tyr Ala Gly
 485 490 495
 Gln His Ser Lys Ser Asp Ala Gly Met Asp Glu His Thr Ala Gln Val
 500 505 510
 Asp Tyr Thr Arg Pro Leu Gly Gln Ala His Ser Leu Glu Ala Gly Leu
 515 520 525
 Lys Tyr Ile Tyr Arg His Ala Thr Ser Asp Pro Leu Tyr Glu Ile Arg
 530 535 540
 Pro Ser Glu Asp Ala Pro Trp Gln Pro Gly Ser Leu Tyr Ala Gln Asn
 545 550 555 560
 Pro Ser Asn Gly Lys Phe Arg His Asp Gln Tyr Ile Gly Ala Ala Tyr
 565 570 575
 Ala Gly Tyr Asn Tyr Arg Lys Asp Gln Tyr Ser Leu Gln Thr Gly Leu
 580 585 590
 Arg Val Glu Ser Ser Arg Leu Lys Ala Leu Phe Pro Glu Asn Ala Ala
 595 600 605
 Ala Asp Phe Ser His Asn Ser Phe Asp Trp Val Pro Gln Leu Thr Leu
 610 615 620
 Gly Tyr Thr Pro Ser Pro Met Lys Gln Leu Lys Leu Ala Tyr Asn Phe
 625 630 635 640
 Arg Ile Gln Arg Pro Ala Ile Gly Gln Leu Asn Pro Tyr Arg Leu Gln
 645 650 655
 Thr Asn Asp Tyr Gln Val Gln Tyr Gly Asn Pro Asp Leu Lys Ser Glu
 660 665 670
 Lys Arg His His Val Gly Leu Ser Tyr Asn Gln Tyr Gly Ala Lys Val
 675 680 685
 Met Leu Thr Ala Ser Leu Asp Tyr Asp Phe Cys Asn Asn Ala Ile Gln
 690 695 700
 Asn Tyr Thr Phe Ser Asp Pro Ala Asn Pro Asn Leu Phe His Gln Thr
 705 710 715 720
 Tyr Gly Asn Ile Gly Arg Glu His Ser Phe Ser Leu Asn Thr Tyr Ala
 725 730 735
 Met Tyr Thr Pro Ala Val Trp Val Arg Ile Met Leu Asn Gly Asn Ile
 740 745 750
 Asp Arg Thr Phe Gln Lys Ser Glu Ala Leu Gly Ile Asp Val Asn Ser
 755 760 765
 Trp Ser Gly Met Val Tyr Ser Gly Leu Met Phe Thr Leu Pro Lys Asp
 770 775 780
 Trp Thr Val Asn Leu Phe Gly Gly Tyr Tyr His Gly Gly Arg Ser Tyr
 785 790 795 800
 Gln Thr Lys Tyr Asp Gly Asn Val Phe Asn Asn Ile Gly Ile Ala Lys
 805 810 815
 Gln Leu Phe Asp Lys Lys Leu Arg Val Ser Leu Ser Ala Asn Asn Ile
 820 825 830
 His Ala Lys Tyr Ser Thr Trp Lys Ser Arg Thr Ile Gly Asn Gly Phe
 835 840 845
 Thr Ile Tyr Ser Glu Asn Ala Gly Ile Gln Arg Ser Val Ser Leu Ser
 850 855 860
 Leu Thr Tyr Ser Phe Gly Lys Met Asn Thr Gln Val Arg Lys Val Glu

865	870	875	880
Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln			
	885	890	895
Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn			
900	905		

(2) INFORMATION FOR SEQ ID NO:356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

Trp	Cys	Gln	Ser	Asp	Pro	Ile	Pro	His	Cys	His	Ala	Val	Tyr	Arg	Asn
1			5					10						15	
Ala	Gln	Gly	His	Gln	Gln	Gly	Arg	Ser	Asp	Gln	Asp	Arg	Leu	Pro	Pro
		20					25						30		
Val	Arg	Gly	Tyr	Arg	Tyr	Ala	Arg	Cys	Leu	Gly	Arg	Tyr	Glu	Gly	Phe
		35					40					45			
Gly	Glu	Arg	Met	Arg	Leu	Ser	Ala	Ile	Leu	Ile	Ala	Leu	Ile	Val	Met
	50				55				60						
Leu	Pro	Ala	Val	Leu	Ser	Gly	Gln	His	Tyr	Tyr	Ser	Met	Ala	Gly	Glu
65				70					75					80	
Arg	Leu	Glu	Thr	Asp	Ser	Ile	Arg	Pro	Asn	Glu	Leu	Ser	Ala	Ser	Ile
			85					90						95	
Arg	Ser	Ala	Leu	Phe	Phe	Arg	Asn	Asn	Glu	Tyr	Asn	Ala	Arg	Ser	Val
		100					105						110		
Lys	Gly	Tyr	Thr	Leu	Pro	Gly	Ala	Arg	Val	Ser	Ala	Phe	Ala	Ser	Tyr
		115				120						125			
Ser	Leu	Pro	Ala	Ala	His	Gly	Val	Lys	Leu	Ser	Leu	Gly	Val	Ser	Thr
	130					135					140				
Leu	Asn	Tyr	Trp	Gly	Ala	Ser	Arg	Tyr	Pro	Ala	Gly	Ile	Ala	Tyr	Ser
145				150					155					160	
Asp	Leu	Pro	Tyr	Trp	Thr	Asp	Tyr	Asn	Asp	Tyr	Val	Arg	Leu	Arg	Ile
			165					170					175		
Leu	Pro	Tyr	Val	Gln	Ala	Met	Leu	Lys	Pro	Thr	Ala	Thr	Thr	Ala	Leu
		180					185					190			
Met	Leu	Gly	Asn	Ile	Ala	Gly	Gly	Thr	Ala	His	Gly	Leu	Ile	Glu	Pro
	195						200				205				
Ile	Tyr	Asn	Pro	Glu	Leu	Asp	Leu	Thr	Ala	Asp	Pro	Glu	Ala	Gly	Val
	210				215						220				
Gln	Phe	Arg	Gly	Asp	Trp	Thr	Arg	Phe	Arg	Met	Asp	Val	Trp	Val	Asn
225				230						235				240	
Trp	Met	Ser	Met	Ile	Phe	Lys	Asn	Asp	Asn	His	Gln	Glu	Ser	Phe	Val
			245					250						255	
Phe	Gly	Leu	Ser	Thr	Thr	Ser	Lys	Leu	Ser	Gly	Glu	Gly	Lys	Trp	
		260					265					270			
Arg	Leu	Glu	Leu	Pro	Leu	Gln	Ala	Ile	Ala	Thr	His	Arg	Gly	Gly	Glu
		275				280					285				
Tyr	Asn	Trp	Ala	Gln	Gln	Asp	Thr	Val	His	Thr	Trp	Val	Asn	Gly	Ala
	290				295						300				
Val	Gly	Leu	Lys	Leu	Ser	Tyr	Arg	Pro	Arg	Thr	Asp	Lys	Pro	Met	Gln
305				310						315				320	
Ile	Trp	Gly	Ser	Ala	Tyr	Gly	Val	Ala	Ala	Leu	Ser	Ser	Gly	Gly	Tyr
			325					330						335	
Phe	Pro	Tyr	Glu	Arg	Gly	Trp	Gly	Gly	Tyr	Leu	Ser	Leu	Gly	Met	Asp
		340					345					350			
Leu	Glu	His	Phe	Ala	Phe	Arg	Thr	Asp	Tyr	Trp	Tyr	Gly	Arg	His	Tyr
	355					360						365			
Val	Ser	Pro	Phe	Ala	Ala	Pro	Phe	Ala	Asn	Ser	Leu	Thr	Tyr	Asp	Lys
	370				375						380				
Gln	Pro	Leu	Thr	Asn	Gly	Trp	Gly	Asp	Tyr	Ile	Arg	Leu	Tyr	Ala	Asp
385				390						395				400	
Tyr	Ser	Trp	Arg	Met	Ala	Arg	Ser	Val	Ser	Leu	Ala	Ala	Val	Ala	Arg

```

          405          410          415
Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu
          420          425          430
Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly
          435          440          445
Asn His
          450

```

(2) INFORMATION FOR SEQ ID NO:357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

```

Pro Phe Ser Pro Pro Trp Val Cys Ala Gly Ala Ala Ser Ser Val Arg
1          5          10          15
Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg
          20          25          30
Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro
          35          40          45
Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln
          50          55          60
Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly
65          70          75          80
Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu
          85          90          95
Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys
          100          105          110
Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val
          115          120          125
Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met
          130          135          140
Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln
          145          150          155          160
Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser
          165          170          175
Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val
          180          185          190
Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr
          195          200          205
Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr
          210          215          220
Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro
          225          230          235          240
Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe
          245          250          255
Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr
          260          265          270
Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala
          275          280          285
Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg
          290          295          300
Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg
          305          310          315          320
Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp
          325          330          335
Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp
          340          345          350
Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp
          355          360          365
Gln Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro
          370          375          380
Ala Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met

```

385		390		395		400									
Gly	Gly	Val	Glu	Tyr	Pro	Thr	Glu	Thr	Asn	Phe	Arg	Leu	Phe	Val	
			405					410					415		
Thr	Tyr	Ile	Gly	Arg	His	Tyr	Arg	Tyr	Ser	Ala	Thr	Glu	Thr	Glu	Ser
			420					425					430		
Thr	Asn	Ala	Leu	Arg	Ala	Gly	Leu	Ile	Tyr	Gln	Ile	Pro	Phe	Leu	
		435					440						445		

(2) INFORMATION FOR SEQ ID NO:358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

Tyr	Lys	Gln	Ala	Ile	Met	Lys	His	Leu	Phe	Lys	Ser	Thr	Leu	Val	Leu
1				5					10					15	
Leu	Cys	Ala	Leu	Ser	Phe	Ser	Gly	Thr	Tyr	Thr	Phe	Ala	Gln	Glu	Asn
			20					25					30		
Asn	Thr	Glu	Lys	Ser	Arg	Phe	Asp	Phe	Ser	Val	Arg	Leu	Gly	Gln	Gly
			35				40					45			
Tyr	Ile	Ala	Gly	Ser	Thr	Thr	Asn	Leu	Met	Tyr	Gly	Tyr	Thr	Ser	Ala
	50					55				60					
Asn	Asp	Arg	Leu	Leu	Ser	Gly	Ala	Ile	Tyr	Leu	Gly	Leu	Thr	Pro	Ser
65					70				75					80	
Lys	Lys	Glu	Asn	Ala	Thr	Gly	Val	Ala	Phe	Arg	Phe	Leu	Ser	Pro	Ser
			85					90					95		
Pro	Gly	Tyr	Tyr	Val	Asp	Ile	Ser	Gly	Lys	Glu	Asn	Thr	Leu	Asn	Tyr
			100					105					110		
Ala	Phe	Tyr	Val	Val	Gly	Ala	Tyr	Asn	Arg	Ile	Ala	Ile	Pro	Ile	Arg
			115					120				125			
Pro	Ile	Lys	Asn	Phe	Asn	Phe	Ile	Phe	Ser	Thr	Glu	Val	Gly	Met	Ala
	130					135					140				
Trp	Met	Ser	Arg	His	Glu	Gln	Ile	Tyr	Asn	Ser	Thr	Ser	Gln	Thr	Trp
145					150				155					160	
Asp	Lys	Gln	Arg	Lys	Ser	Arg	Ser	Gly	Leu	Asp	Phe	Gly	Leu	Gly	Met
			165					170					175		
His	Leu	Gln	Unk	His	Ile	Asn	Lys	Thr	Val	Tyr	Phe	Met	Ala	Gly	Thr
			180					185					190		
Asp	Leu	Thr	Ser	Cys	Met	Phe	Gly	Lys	Arg	Ile	Asn	Asp	Tyr	Gln	Gln
			195				200				205				
Lys	Asp	Arg	Thr	Phe	Ile	Ala	Leu	Ile	Asp	Asn	Ser	Ile	Gly	Ile	Gly
	210					215					220				
Leu	Asn	Leu													
225															

(2) INFORMATION FOR SEQ ID NO:359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met
1 5 10 15
Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu
20 25 30
Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val
35 40 45
Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala
50 55 60
Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser
65 70 75 80
Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly
85 90 95
Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile
100 105 110
Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn
115 120 125
Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu
130 135 140
Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu
145 150 155 160
Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser
165 170 175
Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn
180 185 190
Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly
195 200 205
Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser
210 215 220
Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly
225 230 235 240
Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly
245 250 255
Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu
260 265 270
Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp
275 280 285
Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser
290 295 300
Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys
305 310 315 320
Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr
325 330 335
Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr
340 345 350
Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn
355 360 365
Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn
370 375 380
Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly
385 390 395 400
Leu Arg Asn Leu Phe His
405

(2) INFORMATION FOR SEQ ID NO:360

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

Leu Ile Ile Glu Lys Glu Met Lys Thr Thr Val Gln Gln Ile Ile Leu
1 5 10 15

Cys Leu Ala Leu Met Met Ser Gly Val Leu Gly Gly Asn Ala Gln Ser
 20 25 30
 Phe Trp Glu Glu Ile Ala Pro Pro Phe Ile Ser Asn Glu Pro Asn Val
 35 40 45
 Lys Tyr Ile Ile Pro Asn Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr
 50 55 60
 Val Thr Val Thr Lys Arg Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu
 65 70 75 80
 Gln Leu Gly Met Tyr Tyr Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp
 85 90 95
 Lys His Asp Pro Tyr Phe Asp Asp Lys Ile Val Ala Asp Ile Gln Thr
 100 105 110
 Asp Ala Tyr Gly Arg Val Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln
 115 120 125
 Glu Tyr Gln Leu Tyr Ile Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe
 130 135 140
 Lys Thr Ser Val Ser Thr Tyr Glu His Gly Met Ala Val Phe Arg Ser
 145 150 155 160
 Ser Thr Gly Val Thr Tyr Ile Gly Thr Arg His His Ile Phe Ala Ser
 165 170 175
 Gly Val Asn Asp Phe Glu Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro
 180 185 190
 Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu
 195 200 205
 Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln
 210 215 220
 Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile
 225 230 235 240
 Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val
 245 250 255
 Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala
 260 265 270
 Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile
 275 280 285
 Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val
 290 295 300
 Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser
 305 310 315 320
 Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly
 325 330 335
 Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu
 340 345 350
 Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile
 355 360 365
 Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr
 370 375 380
 Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val
 385 390 395 400
 Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp
 405 410 415
 Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly
 420 425 430
 Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His
 435 440 445
 Lys Val Gln Val
 450

(2) INFORMATION FOR SEQ ID NO:361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly
 1 5 10 15
 Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg
 20 25 30
 Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser
 35 40 45
 Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val
 50 55 60
 Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His
 65 70 75 80
 Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe
 85 90 95
 Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His
 100 105 110
 Arg Ser Ser Leu Gln Leu Asn Glu Glu Leu Asn Phe Ala Ala Glu Arg
 115 120 125
 Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val
 130 135 140
 Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn
 145 150 155 160
 Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly
 165 170 175
 Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His
 180 185 190
 Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala
 195 200 205
 Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr
 210 215 220
 Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg
 225 230 235 240
 Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val
 245 250 255
 Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser
 260 265 270
 Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly
 275 280 285
 Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly
 290 295 300
 Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr
 305 310 315 320
 Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:362

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...329
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys
 1 5 10 15
 Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly
 20 25 30
 Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe
 35 40 45
 Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr
 50 55 60
 Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile Thr Arg
 65 70 75 80
 Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu
 85 90 95
 Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Trp Met
 100 105 110

```

Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala
115 120 125
Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala
130 135 140
Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn
145 150 155 160
Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile
165 170 175
Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr
180 185 190
Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr
195 200 205
Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile
210 215 220
Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu
225 230 235 240
Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe
245 250 255
Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe
260 265 270
Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu
275 280 285
Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe
290 295 300
Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly
305 310 315 320
Arg Arg Thr Ser Leu Tyr Tyr His Asp
325

```

(2) INFORMATION FOR SEQ ID NO:363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

```

Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val
1 5 10 15
Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His
20 25 30
Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val
35 40 45
Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val
50 55 60
Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys
65 70 75 80
Asp Thr Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg
85 90 95
Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His
100 105 110
Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly
115 120 125
Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg
130 135 140
Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile
145 150 155 160
Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys
165 170 175
Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys
180 185 190
Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly
195 200 205
Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp
210 215 220

```

```

Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr
225          230          235          240
Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln
          245          250          255
Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala
          260          265          270
Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr
          275          280          285
Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala
          290          295          300
Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
305          310          315

```

(2) INFORMATION FOR SEQ ID NO:364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

```

Pro Tyr Asn Val Gln Ser Ile Ser Asn Lys Thr Ile Lys Lys Gln Met
1          5          10          15
Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu Glu
          20          25          30
Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln Glu
          35          40          45
Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val Val
          50          55          60
Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
65          70          75          80
Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
          85          90          95
Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
          100          105          110
Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
          115          120          125
Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile
          130          135          140
Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Gly Met Ile Val Asp
145          150          155          160
Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val Arg
          165          170          175
Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe Lys
          180          185          190
Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His Lys
          195          200          205
Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile Gly
          210          215          220
Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile Thr
225          230          235          240
Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile His
          245          250          255
Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile Val
          260          265          270
Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu Asp
          275          280          285
Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro Trp
          290          295          300
Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly Lys
305          310          315          320
Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln Gly
          325          330          335
Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His Leu
          340          345          350

```

```

Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala Val
355 360 365
Ile Leu Thr Leu Asp Arg Glu Arg Lys Met Ser Leu Gly Leu Lys
370 375 380
Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro Val
385 390 395 400
Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly Val
405 410 415
Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser Asp
420 425 430
Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu Val
435 440 445
Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn Arg
450 455 460
Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp Val
465 470 475 480
Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val Ile
485 490 495
Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val Glu
500 505 510
Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln Ala
515 520 525
Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys Asp
530 535 540
Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu Gln
545 550 555 560
Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala Lys
565 570 575
Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln Ala
580 585 590
Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu Lys
595 600 605
Glu Lys Leu Ser Glu Asn
610

```

(2) INFORMATION FOR SEQ ID NO:365

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

```

Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu
1 5 10 15
Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly
20 25 30
His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr
35 40 45
Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile
50 55 60
Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile
65 70 75 80
Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu
85 90 95
Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu
100 105 110
Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe
115 120 125
Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr
130 135 140
Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu
145 150 155 160
Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro
165 170 175

```

```

Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser
      180      185      190
Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys
      195      200      205
Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe
      210      215      220
Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp
      225      230      235      240
Thr Phe Asn

```

(2) INFORMATION FOR SEQ ID NO:366

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

```

Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile
1      5      10      15
Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu
      20      25      30
Tyr Glu Ile Gly Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala
      35      40      45
Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Glu Leu Val Gly
      50      55      60
Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp
      65      70      75      80
Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp
      85      90      95
Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg
      100      105      110
Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly
      115      120      125
Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe
      130      135      140
Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly
      145      150      155      160
Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu
      165      170      175
Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp
      180      185      190
Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val
      195      200      205
Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp
      210      215      220
Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln
      225      230      235

```

(2) INFORMATION FOR SEQ ID NO:367

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

```
Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp
1      5      10      15
Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala
20      25      30
Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly
35      40      45
Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu
50      55      60
Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala
65      70      75      80
Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala
85      90      95
Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg
100      105      110
Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys
115      120      125
Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr
130      135      140
Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr
145      150      155      160
Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile
165      170      175
Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser
180      185      190
Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu
195      200      205
Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala
210      215      220
Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg
225      230      235      240
Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser
245      250      255
Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu
260      265      270
Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro
275      280      285
His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu
290      295      300
Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr
305      310      315      320
Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly
325      330      335
Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg
340      345      350
Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr
355      360      365
Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly
370      375      380
Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu
385      390      395      400
Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala
405      410      415
Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys
420      425      430
Leu Lys Leu Asn
435
```

(2) INFORMATION FOR SEQ ID NO:368

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 945 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

Asn	Thr	Ile	Ser	Glu	Asn	Gly	Asn	Asp	Ser	Thr	Tyr	Phe	Ser	Phe	Gln	1	5	10	15
Thr	Phe	Leu	Met	Arg	Ser	Ile	Tyr	Gln	Leu	Leu	Leu	Ser	Ile	Leu	Leu	20	25	30	
Ala	Ser	Leu	Gly	Phe	Val	Gly	Leu	Glu	Ala	Gln	Gln	Ala	Gly	Val	Ala	35	40	45	
Gly	Arg	Val	Leu	Asp	Glu	Glu	Gly	Asn	Pro	Met	Ile	Gln	Ala	Asn	Val	50	55	60	
Gln	Leu	Val	Gln	Ser	Thr	Gly	Gln	Val	Ala	Val	Ala	Ala	Gly	Ala	Thr	65	70	75	80
Asn	Glu	Lys	Gly	Leu	Phe	Ser	Leu	Lys	Thr	Ser	Gln	Glu	Gly	Asp	Tyr	85	90	95	
Ile	Leu	Arg	Val	Ser	Tyr	Val	Gly	Tyr	Thr	Thr	His	Asp	Glu	Lys	Ile	100	105	110	
Ser	Leu	Arg	Asn	Gly	Gln	Thr	Ile	Thr	Leu	Lys	Asp	Ile	Ser	Met	Asn	115	120	125	
Glu	Asp	Ala	Arg	Leu	Leu	Gln	Ser	Val	Thr	Val	Gln	Ala	Lys	Ala	Ala	130	135	140	
Glu	Val	Val	Val	Arg	Asn	Asp	Thr	Leu	Glu	Phe	Asn	Ala	Gly	Ser	Tyr	145	150	155	160
Thr	Val	Ala	Gln	Gly	Ala	Ser	Ile	Glu	Glu	Leu	Ile	Lys	Lys	Leu	Pro	165	170	175	
Gly	Ala	Glu	Ile	Gly	Ser	Asp	Gly	Lys	Ile	Thr	Ile	Asn	Gly	Lys	Asp	180	185	190	
Ile	Ser	Lys	Ile	Leu	Val	Asp	Gly	Lys	Glu	Phe	Phe	Ser	Lys	Asp	Pro	195	200	205	
Gln	Val	Ala	Ile	Lys	Asn	Leu	Pro	Ala	Asp	Met	Val	Asn	Lys	Val	Gln	210	215	220	
Val	Leu	Asn	Lys	Leu	Ser	Glu	Leu	Ser	Arg	Met	Ser	Gly	Phe	Asp	Asp	225	230	235	240
Gly	Glu	Glu	Glu	Thr	Val	Ile	Asn	Leu	Thr	Val	Lys	Pro	Glu	Lys	Lys	245	250	255	
Lys	Gly	Leu	Phe	Gly	Thr	Leu	Gln	Ala	Gly	Tyr	Gly	Thr	Asp	Gln	Arg	260	265	270	
Tyr	Met	Ala	Gly	Gly	Asn	Val	Asn	Arg	Phe	Asp	Gly	Asn	Lys	Gln	Trp	275	280	285	
Thr	Leu	Ile	Gly	Ser	Ala	Asn	Asn	Thr	Asn	Asn	Met	Gly	Phe	Ser	Glu	290	295	300	
Met	Asp	Ser	Glu	Met	Gly	Ser	Met	Thr	Phe	Phe	Ser	Pro	Gln	Gly	Gly	305	310	315	320
Gly	Arg	Arg	Gly	Phe	Gly	Asn	Ser	Gly	Gly	Val	Thr	Ser	Ser	Ser	Met	325	330	335	
Leu	Gly	Gly	Asn	Phe	Ser	Val	Glu	Phe	Ser	Ser	Ala	Leu	Asn	Thr	Gly	340	345	350	
Gly	Asp	Ala	Arg	Tyr	Gly	Tyr	Asn	Asp	Lys	Ala	Ile	Glu	Thr	Thr	Lys	355	360	365	
Arg	Val	Glu	Asn	Ile	Leu	Ala	Glu	Gly	Asn	Thr	Tyr	Met	Asp	Glu	Asn	370	375	380	
Ile	Leu	Glu	Arg	Ser	Phe	Ser	His	Asn	Gly	Gln	Ala	Arg	Phe	Arg	Met	385	390	395	400
Gln	Trp	Lys	Pro	Ser	Glu	Arg	Thr	Glu	Val	Val	Phe	Glu	Pro	Asp	Leu	405	410	415	
Ser	Ile	Ser	Lys	Ile	Asp	Gly	Phe	Phe	Asn	Asp	Thr	Tyr	Glu	Thr	Lys	420	425	430	
Asp	Ala	Thr	Gly	Ile	Ser	Ile	Asn	Lys	Gly	Ser	Ile	His	Gln	Thr	Thr	435	440	445	
Gln	Gly	Asn	Asn	Phe	Arg	Leu	Asn	Gly	Glu	Leu	Asp	Ile	Ser	His	Lys	450	455	460	
Leu	Asn	Asp	Glu	Gly	Arg	Thr	Ile	Ser	Ala	Ser	Val	Ser	Gly	Gly	Leu	465	470	475	480
Thr	Asp	Glu	Asp	Gly	Asp	Gly	Ile	Tyr	Gln	Ala	Val	Leu	Gln	Ser	Val	485	490	495	
Glu	Thr	Asn	Gln	Lys	Gln	Phe	Asn	Asp	Asn	Ser	Asn	Leu	Gln	Tyr	Arg	500	505	510	
Leu	Arg	Leu	Ser	Tyr	Val	Glu	Pro	Leu	Gly	Lys	Asn	Tyr	Phe	Ala	Gln	515	520	525	
Ala	Ile	Leu	Asn	Arg	Arg	Phe	Ser	Arg	Arg	Asn	Ser	Asp	Arg	Glu	Val	530	535	540	
Tyr	Arg	Leu	Gly	Asp	Asp	Gly	Gln	Tyr	Ser	Ile	Leu	Asp	Ser	Gln	Tyr	545	550	555	560
Gly	Leu	Ser	Tyr	Ser	Asn	Glu	Phe	Thr	Gln	Tyr	Arg	Ile	Gly	Leu	Asn	565	570	575	

Leu Lys Lys Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val
 580 585 590
 Asp Pro Asn Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln
 595 600 605
 Asp Lys Leu Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile
 610 615 620
 Asn Tyr Lys Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly
 625 630 635 640
 Arg Thr Thr Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile
 645 650 655
 Thr Asn Pro Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser
 660 665 670
 Tyr Ser Asn Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser
 675 680 685
 Gln Arg Ala Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp
 690 695 700
 Ile Val Pro Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr
 705 710 715 720
 Arg Tyr Glu Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr
 725 730 735
 Leu Ser Leu Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu
 740 745 750
 Phe Asn Arg Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Lys Asn
 755 760 765
 Lys Ala Leu Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg
 770 775 780
 Asn Asn Trp Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met
 785 790 795 800
 Ala Asn Asn Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe
 805 810 815
 Gly Gly Asn Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile
 820 825 830
 Asp Ser Asp Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe
 835 840 845
 Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu
 850 855 860
 Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly
 865 870 875 880
 Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu
 885 890 895
 Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr
 900 905 910
 Arg Phe Asn Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg
 915 920 925
 Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro
 930 935 940
 Ser
 945

(2) INFORMATION FOR SEQ ID NO:369

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys
 1 5 10 15
 Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu Ile Thr
 20 25 30
 Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr
 35 40 45
 Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp Trp Gln
 50 55 60


```

Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val Ala Ser
65      70      75      80
Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser Tyr Asp
85      90      95
Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg Ser Ser
100     105     110
Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys Pro Asn
115     120     125
Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp Asp Gly
130     135     140
Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser Ser Val
145     150     155     160
Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr Thr Ser
165     170     175
Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn Tyr Pro
180     185     190
Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr Pro Gly
195     200     205
Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn Pro Tyr
210     215     220
Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser Tyr Tyr
225     230     235     240
Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His Tyr Pro
245     250     255
Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr Ser Tyr
260     265     270
Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys Leu Gly
275     280     285
Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys Asn Lys
290     295     300
Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn Val Lys
305     310     315     320
Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu Thr Val
325     330     335
Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn
340     345     350
Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg
355     360     365
Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn
370     375     380
Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met
385     390     395     400
Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
405     410

```

(2) INFORMATION FOR SEQ ID NO:370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

```

Ser Asn Ser Ser Ser His Lys Trp Leu Ile Tyr Tyr His Ile Glu Lys
1      5      10      15
Thr Lys Ser Ile Met Ile Arg Lys Leu Ile Leu Leu Ala Leu Met
20     25     30
Pro Val Ala Ser Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser
35     40     45
Lys Asp Asn Arg Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg
50     55     60
Asp Asp Ala Pro Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile
65     70     75     80
Gln Ser Asp Met Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp
85     90     95

```

Phe Gly Asn Ser Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu
100 105 110
Phe Gly Ala Arg Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu
115 120 125
Pro Glu Met Gly Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr
130 135 140
His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser
145 150 155 160
Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn
165 170 175
Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg
180 185 190
Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly
195 200 205
Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu
210 215 220
Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His
225 230 235 240
Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp
245 250 255
Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu
260 265 270
Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu
275 280 285
Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp
290 295 300
Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser
305 310 315 320
Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu
325 330 335
Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met
340 345 350
Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala
355 360 365
Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln
370 375 380
Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg
385 390 395 400
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp
405 410 415
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly
420 425 430
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile
435 440 445
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu
450 455 460
Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala
465 470 475 480
Gly Glu Lys Pro Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly
485 490 495
Lys Tyr Lys Leu Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr
500 505 510
Leu His Thr Lys Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu
515 520 525
Leu Ser Ile Leu Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn
530 535 540
Ile Gly Glu Thr Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr
545 550 555 560
His Gly Ala His Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly
565 570 575
Met Asn Cys Ser Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly
580 585 590
Phe Tyr Leu Ser Tyr Ser Thr Asn Leu
595 600

(2) INFORMATION FOR SEQ ID NO:371

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

```
Arg Gly Ser Ser Ser Gly Ile Ser Ala Arg Gly Arg Asp Met Arg Ser
1      5      10      15
Leu Phe Leu Ser Ala Leu Arg Ser Ser Leu His Gly Ser Glu Arg
20      25      30
Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg Gln Lys Ile
35      40      45
Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp His Leu Ile
50      55      60
Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp Thr Asp Glu
65      70      75      80
Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr His Thr Gly
85      90      95
Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg Tyr Leu Val
100     105     110
Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser Arg Pro Asp
115     120     125
Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala Phe His Ser
130     135     140
Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val Cys His Asp
145     150     155     160
Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys Asp Asn Gln
165     170     175
Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val Ala Cys Phe
180     185     190
Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr His Thr Ala
195     200     205
Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg Thr Leu Ser
210     215     220
Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe Glu Phe Gly
225     230     235     240
Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
245     250
```

(2) INFORMATION FOR SEQ ID NO:372

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

```
Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser
1      5      10      15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
20      25      30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
35      40      45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
50      55      60
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
65      70      75      80
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
85      90      95
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
100     105     110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
115     120     125
```

Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
 130 135 140
 Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
 145 150 155 160
 Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
 165 170 175
 Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
 180 185 190
 Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
 195 200 205
 Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
 210 215 220
 Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
 225 230 235 240
 Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
 245 250 255
 Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
 260 265 270
 Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn
 275 280 285
 Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly
 290 295 300
 Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly
 305 310 315 320
 Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu
 325 330 335
 Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val
 340 345 350
 His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr
 355 360 365
 Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn
 370 375 380
 Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn
 385 390 395 400
 Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His
 405 410 415
 Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala
 420 425 430
 Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly
 435 440 445
 Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly
 450 455 460
 Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp
 465 470 475 480
 Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn
 485 490 495
 Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala
 500 505 510
 Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe
 515 520 525
 Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe
 530 535 540
 Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly
 545 550 555 560
 Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu
 565 570 575
 Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser
 580 585 590
 Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val
 595 600 605
 Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala
 610 615 620
 His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala
 625 630 635 640
 Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg
 645 650 655
 Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly
 660 665 670
 Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val
 675 680 685
 Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys
 690 695 700
 Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro
 705 710 715 720
 Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly
 725 730 735
 Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser

	740		745		750										
Ala	Ser	Ile	Gln	Trp	Met	Met	Asp	Thr	Lys	Pro	Asn	Tyr	Asn	Arg	Gly
	755						760					765			
Met	Lys	Glu	Ser	Asp	Arg	Pro	Tyr	Ser	Phe	Ser	Thr	Glu	Gln	Gln	Arg
	770					775					780				
Arg	Ala	Asn	His	Ser	Asn										
785					790										

(2) INFORMATION FOR SEQ ID NO:373

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...286
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

Ile	Cys	Gly	Ser	Lys	Met	Asn	Leu	Ser	Gly	Leu	Gln	Ser	Phe	Thr	Met
1				5					10					15	
Met	Lys	Ser	Met	Arg	Ser	Val	Leu	Leu	Leu	Phe	Pro	Leu	Ser	Leu	
			20				25					30			
Ile	Thr	Ala	Leu	Gly	Cys	Ser	Asn	Asn	Lys	Ala	Ala	Glu	Ser	Lys	Ser
			35				40					45			
Val	Ser	Phe	Asp	Ser	Ala	Tyr	Leu	Glu	Arg	Tyr	Ile	Pro	Leu	Arg	Ala
	50				55					60					
Asp	Ile	Asp	Thr	Pro	Ser	Leu	His	Val	Met	Ile	Ser	Tyr	Val	Tyr	Pro
65				70					75					80	
Ser	Gly	Asp	Asp	Met	Leu	Thr	Glu	Ile	Phe	Asn	Gly	Leu	Leu	Phe	Gly
			85					90					95		
Asp	Ser	Leu	Met	Asp	Ser	Ser	Ser	Pro	Glu	Asn	Ala	Met	Glu	Gly	Tyr
		100					105					110			
Ala	Gln	Met	Leu	Gly	Glu	Asp	Tyr	Arg	Ser	Asn	Asn	Ala	Glu	Ala	Asn
	115					120					125				
Leu	Gln	Gly	Leu	Pro	Ser	Asp	Leu	Leu	Asp	Tyr	Ile	Tyr	Lys	Gln	Glu
	130					135					140				
Asn	Thr	Ile	Ala	Tyr	Cys	Asp	Thr	Gly	Leu	Ile	Ser	Thr	Arg	Ile	Asn
145			150						155					160	
Thr	Tyr	Thr	Tyr	Glu	Gly	Gly	Ala	His	Thr	Glu	Asn	Thr	Val	Arg	Phe
			165					170					175		
Ala	Asn	Ile	Leu	Arg	Thr	Thr	Gly	Lys	Val	Leu	Glu	Glu	Arg	Asp	Ile
	180						185						190		
Phe	Lys	Ile	Asp	Tyr	Ala	Glu	Arg	Leu	Ser	Ala	Leu	Ile	Ile	Gly	Gln
	195					200					205				
Leu	Val	His	Asp	Phe	Gly	Lys	Thr	Thr	Pro	Ala	Glu	Leu	Asp	Ala	Ile
	210				215				220						
Gly	Phe	Phe	Asn	Ala	Glu	Glu	Ile	Gln	Pro	Asn	Gly	Asn	Phe	Met	Ile
225				230					235					240	
Asp	Asp	Lys	Gly	Leu	Thr	Tyr	Cys	Phe	Asn	Glu	Tyr	Gln	Ile	Ala	Ala
			245					250					255		
Tyr	Ala	Arg	Gly	Ala	Val	Tyr	Val	Arg	Leu	Gly	Tyr	Asp	Val	Leu	Ala
	260						265					270			
Pro	Leu	Leu	Arg	Asp	Asp	Ser	Pro	Leu	Lys	Arg	Tyr	Leu	Pro		
	275					280						285			

(2) INFORMATION FOR SEQ ID NO:374

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

```
Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly
1      5      10      15
Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His
20     25     30
Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala
35     40     45
Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser
50     55     60
Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu
65     70     75     80
Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu
85     90     95
Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp
100    105    110
Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser
115    120    125
Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser
130    135    140
Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala
145    150    155    160
Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser
165    170    175
Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe
180    185    190
Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser
195    200    205
Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu
210    215    220
Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala
225    230    235    240
Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu
245    250    255
Gly Ala Tyr Trp Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro
260    265    270
Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser
275    280    285
Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe
290    295    300
Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile
305    310    315    320
Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr
325    330    335
Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys
340    345    350
Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly
355    360    365
Phe Asn Phe Thr Val Gly Leu Trp Thr Asn
370    375
```

(2) INFORMATION FOR SEQ ID NO:375

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1269 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

Val Lys Cys Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu
1 5 10 15
Phe Pro Phe Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu
20 25 30
Cys Ala Ser Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp
35 40 45
Leu Glu Lys Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu
50 55 60
Gly Ile Ser Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly
65 70 75 80
Ala Val Val Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr
85 90 95
Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn
100 105 110
Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys
115 120 125
Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser
130 135 140
Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys
145 150 155 160
Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu
165 170 175
Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu
180 185 190
Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu
195 200 205
Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile
210 215 220
Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg
225 230 235 240
Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr
245 250 255
Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu
260 265 270
Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn
275 280 285
Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys
290 295 300
Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg
305 310 315 320
Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys
325 330 335
Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu
340 345 350
Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu
355 360 365
Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu
370 375 380
Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile
385 390 395 400
Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr
405 410 415
Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala
420 425 430
Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu
435 440 445
Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn
450 455 460
Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu
465 470 475 480
Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser
485 490 495
Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys
500 505 510
Ala Leu Leu Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu
515 520 525
Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser Ser Gly
530 535 540
Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys
545 550 555 560
Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile
565 570 575
Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala
580 585 590
Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys
595 600 605
Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn

610		615		620	
Phe Asn Arg Pro Tyr Trp	Leu Gly Gln Ile	Ala Tyr Ala Cys Asn Arg			
625	630	635		640	
Cys Met Ser Val Gly Gly	Asn Pro Asp Gly	Lys Asp Thr Pro Gln Thr			
	645	650		655	
Thr Asp Asp Thr Ile Ile	Ile Gln Thr His	Ala Asp Glu Thr Gly Ala			
	660	665		670	
Lys Gln Gln Thr Leu Gly	Cys Ala Ala Glu	Asn Gly Val Leu Glu Glu			
	675	680		685	
Ile Tyr Val Ser Leu Glu	Pro Lys Ala Asn	Ser Ala Val His Ala Leu			
	690	695		700	
Asn Tyr Leu Asn Glu Arg	Val Arg Glu Val	Val Ala Ser Arg Ser Lys			
705	710	715		720	
Ser Ile Gln Ile Thr Glu	Lys Asp Lys Gly	Leu Tyr Glu Ala Leu Pro			
	725	730		735	
Thr Ile Ala Gly Asp	Asn Lys His Ile	Pro Ile Ser Leu Glu Ala Leu			
	740	745		750	
Ala Ala Gln Leu Asn Lys	Gly Arg Ala Glu	Asn Asp Leu Tyr Thr Ile			
	755	760		765	
Glu Tyr Leu Gln Thr Glu	Leu Asn Gln Leu	Ser Leu Arg Gly Glu Val			
	770	775		780	
Leu Tyr Tyr Arg Glu	Asn Glu Lys Leu	Asn Asn Tyr Val Trp Leu Asp			
785	790	795		800	
Pro Ala Ala Phe Val Gln	Met Ile His Gly	Glu Ile Leu Gln Lys Asp			
	805	810		815	
Asn Ile Asn Arg Gly Thr	Val Pro Lys Asp	Ile Phe Glu Cys Lys Leu			
	820	825		830	
His Asn Leu Ser Ser Gly	Ser Ile Phe Glu	Glu Asp Gly Gln Asn Gly			
	835	840		845	
Asn Met Ile Leu Gln Leu	Leu Leu Glu Glu	Leu Ile Val Tyr Glu Asp			
	850	855		860	
Lys Asp Cys Tyr Val Ile	Pro Gly Tyr Leu	Pro Leu His Ser Asp Asp			
865	870	875		880	
Glu Ala Tyr Lys Trp Leu	Thr Leu Gly Phe	Glu Arg Pro Asn Phe Val			
	885	890		895	
Leu Lys Phe Glu Arg Phe	Ile Pro Phe Gly	Leu Ile Asn Gln Ile Ile			
	900	905		910	
Ala Tyr Tyr Gly Arg Glu	Glu Gly Ala Leu	Lys Arg Tyr Trp Arg Asp			
	915	920		925	
Gln Val Ile Phe Thr Ala	Gly Arg Glu Met	Asp Arg Gln Thr Leu Glu			
	930	935		940	
Gln Glu Glu Glu Lys Glu	Gly Leu Pro Lys Thr	Asn Ala Glu Asp Tyr			
945	950	955		960	
Gln Ile Trp Ile Lys Leu	Asp Phe Thr Asp	Leu Ala Ile Ser Val Phe			
	965	970		975	
Ile Lys Glu Gln Arg Lys	Thr Ser Ala Lys	Asp Met Gln Arg Lys Glu			
	980	985		990	
Ala Thr Ile Leu Ser Asp	Met Leu Asp Met	Tyr Trp Asn Asn Ile Pro			
	995	1000		1005	
Pro Arg Glu Gln Ile Gly	Asp Lys Asp Thr	Glu Gln Thr Arg Ser Thr			
	1010	1015		1020	
Ile Arg Glu Thr Asn Arg	Lys Lys Arg Pro	Ile Gln Asp Leu Tyr Leu			
1025	1030	1035		1040	
Ser Cys Ala Gln Ala Asp	Lys Asp Leu Thr	Glu Ser His Tyr Ile His			
	1045	1050		1055	
Leu Gly Thr Leu Asp Asp	Glu Ser Lys Thr	Thr Ala Arg Ile Ala Ala			
	1060	1065		1070	
Tyr Pro Leu Lys Asn Gly	Val Ile Asp Lys	Glu Arg Val Arg Glu Val			
	1075	1080		1085	
Ser Thr Arg Pro Tyr Lys	His Leu Ser Val	Asn Lys Asn Leu Ala Thr			
	1090	1095		1100	
Ala Lys Gln Ile Phe Ile	Ser Tyr Ser Lys	Glu Asp Gln Thr Glu Leu			
1105	1110	1115		1120	
Glu Thr Cys Leu Gln Phe	Lys Pro Leu Glu	Lys Asn Gly Gln Ile			
	1125	1130		1135	
Glu Ile Tyr Tyr Asp Lys	Leu Thr Lys Phe	Glu Thr Pro Ile His Pro			
	1140	1145		1150	
Glu Ile Arg Lys Arg Ile	Val Glu Ala Asp	Cys Ile Ile Ala Leu Ile			
	1155	1160		1165	
Ser Gln Arg Tyr Leu Ala	Thr Asp Tyr Ile	Leu Asp His Glu Leu Pro			
	1170	1175		1180	
Val Phe Arg Glu Tyr Asn	Lys Thr Ile Val	Pro Ile Leu Ile Lys Pro			
1185	1190	1195		1200	
Cys Thr Phe Glu Asp Asp	Glu Phe Leu Arg	Glu Lys Tyr Phe Ala Gln			
	1205	1210		1215	
Lys Ala Gln Ile Ile Asn	Leu Gly Lys Glu	Gly Lys Thr Ile Lys Ala			
	1220	1225		1230	

Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala
1235 1240 1245
Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu
1250 1255 1260
Val Asn Thr Asp Glu
1265

(2) INFORMATION FOR SEQ ID NO:376

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...231
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu
1 5 10 15
Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg
20 25 30
Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val
35 40 45
Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly
50 55 60
Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly
65 70 75 80
Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn
85 90 95
Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly
100 105 110
Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys
115 120 125
Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu
130 135 140
Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro
145 150 155 160
Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp
165 170 175
Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys
180 185 190
Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln
195 200 205
Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala
210 215 220
Gln Thr Val Ser Gln Gln Lys
225 230

(2) INFORMATION FOR SEQ ID NO:377

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 563 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

Ser	Leu	Ile	Asn	Asn	Ser	Arg	Asp	Trp	Arg	Ala	Pro	Val	Arg	Leu	Ser
1			5						10					15	
Leu	Lys	Lys	Lys	Thr	Lys	Thr	Met	Lys	Thr	Lys	Val	Leu	Arg	Lys	Phe
		20					25						30		
Val	Val	Ala	Ala	Phe	Ala	Val	Ala	Thr	Leu	Cys	Pro	Leu	Ala	Gln	Ala
		35				40					45				
Gln	Thr	Met	Gly	Gly	Asp	Asp	Val	Lys	Val	Val	Gln	Tyr	Asn	Gln	Glu
	50				55					60					
Lys	Leu	Val	Gln	Thr	Arg	Met	Ser	Val	Ala	Asp	Asn	Gly	Trp	Ile	Tyr
65				70					75					80	
Val	Met	Thr	His	Ser	Gly	Tyr	Asp	Thr	Gly	Asn	Ser	Asn	Val	Lys	Ile
			85					90					95		
Phe	Arg	Ser	Lys	Asp	Gln	Gly	Ala	Thr	Tyr	Gln	Lys	Leu	Arg	Asp	Trp
		100					105						110		
Asp	Pro	Ser	Asp	Asp	Tyr	Gln	Phe	Gln	Asp	Phe	Asp	Ile	Val	Val	Thr
		115				120					125				
Gly	Lys	Asn	Glu	Ser	Asp	Ile	Lys	Ile	Trp	Ser	Val	Glu	Leu	Met	Asn
	130				135					140					
Lys	Pro	Gly	Gly	Tyr	Lys	Ser	Arg	Val	Ala	Val	Phe	Ser	Arg	Asp	Ala
145				150					155					160	
Asn	Ala	Gln	Asn	Ala	Lys	Leu	Val	Tyr	Lys	Glu	Asp	Phe	Ser	Asn	Val
			165					170					175		
Gln	Leu	Tyr	Asp	Val	Asp	Ile	Ala	Ser	Asn	Tyr	Arg	Ser	Pro	Ser	Ser
		180					185						190		
Leu	Asn	Asn	Gly	Gly	Asn	Pro	Phe	Ala	Leu	Ala	Phe	Ala	Tyr	Thr	Gly
	195				200						205				
Phe	Asn	Asn	Thr	His	Lys	Ile	Ser	Phe	Val	Asp	Tyr	Val	Phe	Ser	Leu
	210				215					220					
Asn	Gly	Gly	Gln	Asn	Phe	Asn	Lys	Asn	Leu	Leu	Phe	Ser	Gln	Asp	Gly
225				230					235					240	
Glu	Lys	Lys	Ile	Asp	Lys	Val	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Glu
			245					250					255		
Ser	Met	Gly	His	Asn	Ala	Trp	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met
	260					265							270		
Asn	Lys	Gln	Gly	Gly	Lys	Ser	Asp	Ile	Gly	Phe	Leu	Ser	Asn	Phe	Val
	275					280					285				
Asp	Asn	Asp	Pro	Glu	Phe	Gln	Trp	Ser	Gly	Pro	Ile	Lys	Val	Ser	Glu
	290					295				300					
Ser	Asp	Met	Ser	Phe	Ser	Pro	Lys	Ile	Gln	Met	Leu	Leu	Asp	Glu	Asp
305				310					315					320	
Asn	Asn	Thr	Ile	Asn	Gly	Glu	Ser	Cys	His	Asn	Phe	Met	Ile	Thr	Tyr
			325					330					335		
Ser	Asp	Tyr	Asp	Ser	Glu	Tyr	Ser	Asp	Trp	Asp	Ile	Arg	Tyr	Val	Tyr
		340					345					350			
Pro	Lys	Lys	Ser	Phe	Lys	Tyr	Glu	Lys	Gly	Lys	Thr	Pro	Thr	Met	Asp
	355						360					365			
Asp	Leu	Val	Glu	Ala	Phe	Leu	Thr	Ala	Ser	Tyr	Gln	Ser	Glu	Thr	Asn
	370				375						380				
Ser	Gly	Leu	Gly	Tyr	Asp	Lys	Asn	Ala	Asn	His	Tyr	Leu	Ile	Thr	Tyr
385				390					395					400	
Ala	Lys	Lys	Glu	Glu	Asn	Gly	Thr	Asn	Thr	Leu	Lys	Tyr	Arg	Trp	Ala
			405					410					415		
Asn	Tyr	Asp	Lys	Ile	His	Asn	Lys	Asp	Leu	Trp	Ser	Asp	Thr	Phe	Thr
		420					425						430		
Tyr	Thr	Ser	Ser	Ala	Asn	Ala	Leu	Tyr	Thr	Pro	Gln	Val	Asp	Ile	Asn
		435					440					445			
Pro	Thr	Lys	Gly	Leu	Val	Cys	Trp	Ser	Trp	Val	Glu	Tyr	Leu	Pro	Gly
	450				455					460					
Lys	Arg	Ile	Val	Trp	Ser	Asp	Thr	Gln	Trp	Thr	His	Ala	Asn	Gly	Val
465				470					475					480	
Glu	Asp	Ile	Val	Met	Gln	Glu	Gly	Ser	Met	Lys	Leu	Tyr	Pro	Asn	Pro
			485					490					495		
Ala	Gln	Glu	Tyr	Ala	Val	Ile	Ser	Leu	Pro	Thr	Ala	Ala	Asn	Cys	Lys
		500					505					510			
Ala	Val	Val	Tyr	Asp	Met	Gln	Gly	Arg	Val	Val	Ala	Glu	Ala	Ser	Phe
		515					520					525			
Ser	Gly	Asn	Glu	Tyr	Arg	Leu	Asn	Val	Gln	His	Leu	Ala	Lys	Gly	Thr
	530					535					540				
Tyr	Ile	Leu	Lys	Val	Val	Ser	Asp	Thr	Glu	Arg	Phe	Val	Glu	Lys	Leu
545				550					555					560	
Ile	Val	Glu													

(2) INFORMATION FOR SEQ ID NO:378

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 786 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

```
Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met
1      5      10      15
Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala
20      25      30
Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr
35      40      45
Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn
50      55      60
Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn
65      70      75      80
Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp
85      90      95
Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His
100      105      110
Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu
115      120      125
Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly Ser
130      135      140
Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu
145      150      155      160
Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala
165      170      175
Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn
180      185      190
Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu
195      200      205
Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr
210      215      220
Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser Arg
225      230      235      240
Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr Val
245      250      255
Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp Gly
260      265      270
Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser Phe
275      280      285
Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser Phe
290      295      300
Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu Glu
305      310      315      320
Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala Ile
325      330      335
Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val Glu
340      345      350
Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala Leu
355      360      365
Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly Glu
370      375      380
Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp Arg
385      390      395      400
Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro Leu
405      410      415
Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr Leu
420      425      430
Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu Tyr
435      440      445
Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val Ile
450      455      460
Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr Ala
465      470      475      480
```

Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His Pro
 485 490 495
 Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro Leu
 500 505 510
 Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr Leu
 515 520 525
 Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys Glu
 530 535 540
 Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr Tyr
 545 550 555 560
 Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser Phe
 565 570 575
 Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn Pro
 580 585 590
 Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro His
 595 600 605
 Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe Ser
 610 615 620
 Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Asp Pro Thr Asn
 625 630 635 640
 Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu
 645 650 655
 Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe
 660 665 670
 Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met
 675 680 685
 Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro
 690 695 700
 Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val Arg
 705 710 715 720
 Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile Thr
 725 730 735
 Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr Val
 740 745 750
 Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser His
 755 760 765
 Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn Arg
 770 775 780
 Pro Arg
 785

(2) INFORMATION FOR SEQ ID NO:379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly
 1 5 10 15
 Arg Arg Asn Gln Lys Ser Asn Gln Ser Ser Cys Phe Gly Gly Gly Thr
 20 25 30
 Ala Pro Arg Phe Phe Ile Met Cys Lys Ile Arg Phe Ser Leu Leu Gln
 35 40 45
 Ala Leu Val Val Cys Leu Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln
 50 55 60
 Glu Glu Gly Ile Trp Asn Thr Leu Leu Ala Ile His Lys Thr Glu Lys
 65 70 75 80
 Ala Val Glu Thr Pro Lys Lys Val Phe Ala Val Ala Asn Gly Val Leu
 85 90 95
 Tyr Ser Val Gly Lys Glu Ala Pro His Glu Ala Lys Ile Phe Asp Arg
 100 105 110
 Ile Ser Gly Leu Ser Asp Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu
 115 120 125

Gln Leu Lys Ser Leu Val Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile
 130 135 140
 Leu Asp Glu Ala Gly Arg Val Thr Asn Val Pro Ala Leu Lys Asp Asn
 145 150 155 160
 Ile Asp Leu Ile Asp Lys Thr Leu Asn Arg Leu Leu Ile Val Gly Asn
 165 170 175
 Arg Ala Tyr Leu Ala Gly Gly Phe Gly Leu Ser Val Leu Asp Val Ala
 180 185 190
 Glu Ala Arg Ile Pro Ala Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp
 195 200 205
 Val Ala Lys Leu Asp Asn Asp Arg Leu Leu Met Leu Lys Glu Gly Gln
 210 215 220
 Leu Phe Ile Gly Lys Glu Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp
 225 230 235 240
 Thr Ala Leu Ser Leu Asn Leu Pro Met Gly Ser Val Thr Gly Leu Gly
 245 250 255
 Ile Val Gly Glu Asp Ile Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr
 260 265 270
 Val Ala Ala Asn Gln Ser Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser
 275 280 285
 Ala Asp Ser Arg Leu Tyr Val Thr Asp Arg Gly Leu Phe Ile Cys Ala
 290 295 300
 Glu Asn Arg Ile Tyr Phe Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe
 305 310 315 320
 Pro Ile Ala Asp Val Leu Gly Val Gly Ala Met Asn Glu Ser Asn Thr
 325 330 335
 Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Ala
 340 345 350
 Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly
 355 360 365
 Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala
 370 375 380
 Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val
 385 390 395 400
 Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val
 405 410 415
 Gln Glu Gln Leu Gly Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile
 420 425 430
 Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly
 435 440 445
 Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser
 450 455 460
 Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val
 465 470 475 480
 Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly
 485 490 495
 Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp
 500 505 510
 His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn
 515 520 525
 Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg
 530 535 540
 Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly
 545 550 555 560
 Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe
 565 570 575
 Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met
 580 585 590
 Ala Val Asp His Asn Gly Ser Val Trp Met Gly Ser Asp Ile Gly Ile
 595 600 605
 Phe Gly Val Tyr Asn Ala Ala Gly Val Leu Ser Ser Thr Ser Thr Pro
 610 615 620
 Ile Ala Val Arg Pro Val Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val
 625 630 635 640
 Leu Asp Lys Val Thr Val Thr Asp Ile Val Val Asp Lys Leu Asn His
 645 650 655
 Lys Trp Val Ala Thr Gln Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp
 660 665 670
 Cys Ser Lys Ile Leu Ala Gln Phe Thr Val Glu Asn Ser Pro Leu Leu
 675 680 685
 Ser Asn Asn Ile Leu Ser Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu
 690 695 700
 Tyr Ile Gly Thr Ala Asp Gly Leu Met Thr Phe Gln Thr Gly Thr Gly
 705 710 715 720
 Ser Gly Ser Ala Ser Glu Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro
 725 730 735
 Leu Arg Pro Glu Tyr Pro Asp Gly Val Thr Ile Ala Gly Leu Gln Ala

370	375	380
Val Asp Leu Ser Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro		
385	390	395
Asn Gln Asn Leu His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser		400
	405	410
Thr Gln Ala Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg		415
	420	425
Glu Lys Asn Gly Leu Lys Val Leu Val Val Leu Gln Glu Gln Val Phe		430
	435	440
Asn Glu Phe Ser Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe		445
	450	455
Ala Lys Met Phe Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu		460
	465	470
Thr Phe Pro Met Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn		475
	485	490
Arg Lys Val Ser Val Ala Trp Gln Lys Pro Tyr Leu Gln Gln Thr Glu		495
	500	505
Phe Leu Leu Thr Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr		510
	515	520
Val Thr Asp Asp Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val		525
	530	535
Asn Ile Gly Trp Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val		540
	545	550
Arg Thr Pro Ala Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr		555
	565	570
Glu Glu Asp Arg Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala		575
	580	585
Ala Asp Asn Gly Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp		590
	595	600
Thr Val Lys Arg Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln		605
	610	615
Asp Val Tyr Pro His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly		620
	625	630
Ala Lys Lys Lys Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu		635
	645	650
Asn Tyr Ala Gly His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu		655
	660	665
Leu Thr Leu Asn Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile		670
	675	680
Trp Ile Thr Ala Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr		685
	690	695
Ser Ala Gly Glu Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile		700
	705	710
Met Phe Ser Thr Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile		715
	725	730
Asn Gly Phe Met Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg		735
	740	745
Tyr Arg Thr Met Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu		750
	755	760
Ser Thr Val Phe Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met		765
	770	775
Gly Asp Pro Ser Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu		780
	785	790
Thr Ala Ile Asn Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met		795
	805	810
Leu Lys Ser Leu Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu		815
	820	825
Lys Gly Thr Phe Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val		830
	835	840
Phe Asp Gly Arg Lys Lys Met Thr Ala Leu Glu Glu Glu Gly Asn Asp		845
	850	855
Leu Ser Leu Val Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile		860
	865	870
Ala Glu Val Lys Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys		875
	885	890
Asp Val Asn Tyr Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr		895
	900	905
Asn Glu Ser Thr Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg		910
	915	920
Val Gln Pro Gly Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro		925
	930	935
Glu Ile Ile Ser Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp		940
	945	950
Glu Val Asn Pro Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn		955
	965	970
Gly Ile Asn Ile Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys		975
	980	985
		990

```

Ile Asp Gly Arg Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr
  995          1000          1005
Ser Ser Ala Thr Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro
 1010          1015          1020
Ala Leu Ala Glu Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile
 1025          1030          1035          1040
Phe Asn Asn Ala Val His His Asp Phe Ser Phe Arg Val Val Asp Gly
      1045          1050          1055
Ile Ala Pro Asp Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg
      1060          1065          1070
Glu Ser Ala Thr Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu
      1075          1080          1085
Asn Val Ala Val Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser
      1090          1095          1100
Leu Pro Val Lys Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile
      1105          1110          1115          1120
Lys Trp Asp Leu Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe
      1125          1130          1135
Tyr Leu Tyr Arg Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser
      1140          1145          1150
Met Ala Lys Lys Met Ile Val Val Gly Gln
      1155          1160

```

(2) INFORMATION FOR SEQ ID NO:381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

```

Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu
1          5          10          15
Phe Pro Leu Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys
      20          25          30
Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu Lys Lys Arg Ile
      35          40          45
Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln
      50          55          60
Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu
      65          70          75          80
Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr
      85          90          95
Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu
      100          105          110
Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp
      115          120          125
Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys
      130          135          140
Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala
      145          150          155          160
Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu
      165          170          175
Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu
      180          185          190
Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr
      195          200          205
Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala
      210          215          220
Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn Met Ala Glu Asn
      225          230          235          240
Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu
      245          250          255
Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr
      260          265          270

```


Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys
 275 280 285
 Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr
 290 295 300
 Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser
 305 310 315 320
 Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu
 325 330 335
 Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys
 340 345 350
 Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln
 355 360 365
 Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu
 370 375 380
 Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile
 385 390 395 400
 Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser
 405 410 415
 Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His Asn Lys Leu Ile
 420 425 430
 Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr Gly Ile Thr His
 435 440 445
 Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu Asn Glu Lys Met
 450 455 460
 Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr Glu Leu His Lys
 465 470 475 480
 Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu Val Asn Gln Leu
 485 490 495
 Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr Pro Glu Trp Arg
 500 505 510
 Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile Asp Ser Phe Ala
 515 520 525
 Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu Gln Pro Glu Ser
 530 535 540
 Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu Gln Lys Ile Ile
 545 550 555 560
 Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu Ala Gly Gly Arg
 565 570 575
 Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys Asn Leu Ile Ile
 580 585 590
 Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr Asp Gln Ala His
 595 600 605
 Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr Glu Lys His Gly
 610 615 620
 Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val Glu Asn Leu Arg
 625 630 635 640
 Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly Ser Ala Phe Thr
 645 650 655
 Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala Glu Ile Leu Pro
 660 665 670
 Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val His Ile Ala Pro
 675 680 685
 Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu Asn His Arg Phe
 690 695 700
 Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp Asn Lys Asp Ile
 705 710 715 720
 Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr Asn Val Leu Ser
 725 730 735
 Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr Glu His Ile Pro
 740 745 750
 Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met Asp Gly Ile Glu
 755 760 765
 Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys His Ile Pro Ile
 770 775 780
 Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg Leu Glu Gly Ile
 785 790 795 800
 Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe Ser Pro Glu Glu
 805 810 815
 Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg Glu Leu Leu Lys
 820 825 830
 Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys Pro Glu Glu Glu
 835 840 845
 Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu Leu Ala Ala Lys
 850 855 860
 Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp Phe Ser Ala Gln
 865 870 875 880
 Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln Leu Asn Arg Lys

Leu	Thr	Ser	Val	Val	Gly	Cys	Ser	Thr	Ile	Gly	Tyr	Ile	Gln	Gln	Ile
900								905				910			
Lys	Ile	Lys	Leu	Ala	Cys	Lys	Leu	Leu	Ala	Asp	Glu	Ser	Lys	Asn	Ile
915								920				925			
Ser	Asp	Ile	Ser	Ile	Glu	Ala	Gly	Phe	Ser	Asp	Pro	Ala	Tyr	Phe	Ser
930								935				940			
Arg	Thr	Phe	Lys	Arg	Tyr	Met	Asn	Cys	Ser	Pro	Ser	Gln	Tyr	Arg	Gln
945								950				955			
Lys	Leu	Leu	Ala	Met	Pro	Gly	Ser	Asp	Lys	Glu	Thr	Val			
965								970							

355	360	365
Leu Tyr Ile Lys His Tyr Pro Ile Leu Gly Glu Gln Ala Gly Pro Asp		
370	375	380
Tyr Lys Ile Glu Ala Asp Val Val Ser Cys Ala Asn Ala Thr Ile Ser		
385	390	395
Pro Val Gln Cys Tyr Tyr Arg Ile Asn Gly Ser Gly Ser Phe Lys Ala		400
	405	410
Ala Asp Met Thr Met Glu Ser Thr Gly His Tyr Thr Tyr Ser Phe Thr		415
	420	425
Gly Leu Asn Lys Asn Asp Lys Val Glu Tyr Tyr Ile Ser Ala Ala Asp		430
	435	440
Asn Ser Gly Arg Lys Glu Thr Tyr Pro Phe Ile Gly Glu Pro Asp Pro		445
	450	455
Phe Lys Phe Thr Cys Met Asn Glu Thr Asn Thr Cys Thr Val Thr Gly		460
465	470	475
Ala Ala Lys Ala Leu Arg Ala Trp Phe Asn Ala Gly Arg Ser Glu Leu		480
	485	490
Ala Val Ser Val Ser Leu Asn Ile Ala Gly Thr Tyr Arg Ile Lys Leu		495
	500	505
Tyr Asn Thr Ala Gly Glu Glu Val Ala Ala Met Thr Lys Glu Leu Val		510
	515	520
Ala Gly Thr Ser Val Phe Ser Met Asp Val Tyr Ser Gln Ala Pro Gly		525
	530	535
Thr Tyr Val Leu Val Val Glu Gly Asn Gly Ile Arg Glu Thr Met Lys		540
545	550	555
Ile Leu Lys		560

(2) INFORMATION FOR SEQ ID NO:383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

Thr Thr Asn Arg Lys Pro Asn Thr Asn Met Lys Leu Ser Ser Lys Lys	
1	5 10 15
Ile Leu Ala Ile Ile Ala Leu Leu Thr Met Gly His Ala Val Gln Ala	
	20 25 30
Gln Phe Val Pro Ala Pro Thr Thr Gly Ile Arg Met Ser Val Thr Thr	
	35 40 45
Thr Lys Ala Val Gly Glu Lys Ile Glu Leu Leu Val His Ser Ile Glu	
	50 55 60
Lys Lys Gly Ile Trp Ile Asp Leu Asn Gly Asp Ala Thr Tyr Gln Gln	
65	70 75 80
Gly Glu Glu Ile Thr Val Phe Asp Glu Ala Tyr His Glu Tyr Thr Ile	
	85 90 95
Gly Thr Gln Thr Leu Thr Ile Tyr Gly Asn Thr Thr Arg Leu Gly Cys	
	100 105 110
Arg Ser Thr Gly Ala Thr Ala Val Asp Val Thr Lys Asn Pro Asn Leu	
	115 120 125
Thr Tyr Leu Ala Cys Pro Lys Asn Asn Leu Lys Ser Leu Asp Leu Thr	
	130 135 140
Gln Asn Pro Lys Leu Leu Arg Val Trp Cys Asp Ser Asn Glu Ile Glu	
145	150 155 160
Ser Leu Asp Leu Ser Gly Asn Pro Ala Leu Ile Ile Leu Gly Cys Asp	
	165 170 175
Arg Asn Lys Leu Thr Glu Leu Lys Thr Asp Asn Asn Pro Lys Leu Ala	
	180 185 190
Ser Leu Trp Cys Ser Asp Asn Asn Leu Thr Glu Leu Glu Leu Ser Ala	
	195 200 205
Asn Pro Arg Leu Asn Asp Leu Trp Cys Phe Gly Asn Arg Ile Thr Lys	
210	215 220
Leu Asp Leu Ser Ala Asn Pro Leu Leu Val Thr Leu Trp Cys Ser Asp	

225		230		235		240									
Asn	Glu	Leu	Ser	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Asp	Val	Ala	Tyr
				245					250						255
Leu	Trp	Cys	Ser	Ser	Asn	Lys	Leu	Thr	Ser	Leu	Asn	Leu	Ser	Gly	Val
				260					265						270
Lys	Gly	Leu	Ser	Val	Leu	Val	Cys	His	Ser	Asn	Gln	Ile	Ala	Gly	Glu
				275					280						285
Glu	Met	Thr	Lys	Val	Val	Asn	Ala	Leu	Pro	Thr	Leu	Ser	Pro	Gly	Ala
				290					295						300
Gly	Ala	Gln	Ser	Lys	Phe	Val	Val	Val	Asp	Leu	Lys	Asp	Thr	Asp	Glu
					310					315					320
Lys	Asn	Ile	Cys	Thr	Val	Lys	Asp	Val	Glu	Lys	Ala	Lys	Ser	Lys	Asn
				325					330						335
Trp	Arg	Val	Phe	Asp	Phe	Asn	Gly	Asp	Ser	Asp	Asn	Met	Leu	Pro	Tyr
				340					345						350
Glu	Gly	Ser	Pro	Thr	Ser	Asn	Leu	Ala	Val	Asp	Ala	Pro	Thr	Val	Arg
				355					360						365
Ile	Tyr	Pro	Asn	Pro	Val	Gly	Arg	Tyr	Ala	Leu	Val	Glu	Ile	Pro	Glu
				370					375						380
Ser	Leu	Leu	Gly	Gln	Glu	Ala	Ala	Leu	Tyr	Asp	Met	Asn	Gly	Val	Lys
					390					395					400
Val	Tyr	Ser	Phe	Ala	Val	Glu	Ser	Leu	Arg	Gln	Asn	Ile	Asp	Leu	Thr
				405					410						415
His	Leu	Pro	Asp	Gly	Thr	Tyr	Phe	Phe	Arg	Leu	Asp	Asn	Tyr	Thr	Thr
				420					425						430
Lys	Leu	Ile	Lys	Gln											
				435											

(2) INFORMATION FOR SEQ ID NO:384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

Asn	His	Leu	Lys	Thr	Asn	Ile	Lys	Met	Arg	Lys	Thr	Ile	Ile	Phe	Cys
1				5					10					15	
Leu	Leu	Leu	Ala	Leu	Phe	Gly	Cys	Ser	Trp	Ala	Gln	Glu	Arg	Val	Asp
			20					25					30		
Glu	Lys	Val	Phe	Ser	Ala	Gly	Thr	Ser	Ile	Phe	Arg	Gly	Ile	Leu	Glu
			35				40					45			
Lys	Val	Lys	Ala	Pro	Leu	Met	Tyr	Gly	Asp	Arg	Glu	Val	Trp	Gly	Met
			50			55				60					
Ala	Arg	Ala	Ser	Glu	Asp	Phe	Phe	Phe	Ile	Leu	Pro	Val	Thr	Asp	Asp
				70					75					80	
Leu	Thr	Pro	Val	Leu	Phe	Tyr	Asn	Arg	Leu	Thr	Asn	Glu	Pro	Cys	Phe
			85					90					95		
Val	Ser	Asp	Gln	Gly	Ile	Thr	Glu	Tyr	Phe	Lys	Phe	Ala	Gln	Glu	Gly
			100				105					110			
Asp	Tyr	Ile	Glu	Val	Glu	Gly	Ser	Ser	Val	Phe	Met	Ala	Asn	Leu	Leu
			115				120				125				
Tyr	Tyr	Arg	Phe	Phe	Pro	Thr	Arg	Ile	Thr	Ser	Tyr	Asn	Ala	Pro	Ile
			130			135				140					
Glu	Gly	Val	Val	Ser	Lys	Thr	Gly	Asn	Pro	Ala	Phe	Thr	Ile	Pro	Met
			145		150				155					160	
Leu	Pro	Gly	Val	Ser	Asp	Cys	Ile	Glu	Ile	Ser	Asn	Asn	Arg	Lys	Val
			165				170						175		
Phe	Leu	Thr	Asn	Gln	Leu	Gly	Val	Val	Asn	Ile	Thr	Asp	Gly	Met	Glu
			180			185					190				
Pro	Pro	Ile	Ile	Ala	Gly	Val	Ser	Ala	Ser	Tyr	Gly	Ser	Ser	Val	Arg
			195			200				205					
Val	Tyr	Gly	His	Val	Ser	Gln	Arg	Trp	Asp	Ile	Ile	Gly	His	Cys	Tyr
			210			215				220					
Leu	Asp	Ile	Tyr	Pro	Thr	Asn	Cys	Tyr	Pro	Leu	Ser	Thr	Lys	Pro	Val

```

225          230          235          240
Ala Gly Asp Asp Glu Val Phe Val Lys Gln Gln Gly Arg Gln Ile Glu
          245          250          255
Ile Asp Ser Asn Ser Pro Ile Val Gln Val Val Val Tyr Asp Leu Glu
          260          265          270
Gly Lys Ser Val Phe Arg Lys Arg Met Thr Glu Asn Ala Tyr Thr Leu
          275          280          285
Ser Phe Arg Ala Pro Met Leu Gly Phe Met Thr Ile Met Ile Glu Thr
          290          295          300
Gln Asn Ser Ile Ile Asn Lys Lys Leu Asn Val Thr Gln Leu
305          310          315

```

(2) INFORMATION FOR SEQ ID NO:385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

```

Arg Arg Ala Val Lys Ile Arg Ser Pro Pro His Ile His Ser Leu Phe
1          5          10          15
Val Arg Lys Cys Leu Phe Ser Asp Phe Lys Tyr Leu Tyr Leu Ser Arg
          20          25          30
Lys Ile Thr Gln Glu Arg Leu Gly Arg Leu Ser Ile Arg Leu Lys Ser
          35          40          45
Tyr Asn Pro Ile Ile Ile Ile Glu Met Lys Lys Thr Thr Ile Ile Ser
          50          55          60
Leu Ile Val Phe Gly Ala Phe Phe Ala Ala Val Gly Gln Thr Lys Asp
65          70          75          80
Asn Ser Ser Tyr Lys Pro Phe Ser Lys Glu Asp Ile Ala Gly Gly Val
          85          90          95
Tyr Ser Leu Pro Thr Gln Asn Arg Ala Gln Lys Asp Asn Ala Glu Trp
          100          105          110
Leu Leu Thr Ala Thr Val Ser Thr Asn Gln Ser Ala Asp Thr His Phe
          115          120          125
Ile Phe Asp Glu Asn Asn Arg Tyr Ile Ala Arg Asp Ile Lys Ala Asn
          130          135          140
Gly Val Arg Lys Ser Thr Asp Ser Ile Tyr Tyr Asp Ala Asn Gly Arg
          145          150          155          160
Ile Ser His Val Asp Leu Tyr Ile Ser Phe Ser Gly Gly Glu Pro Ala
          165          170          175
Leu Asp Thr Arg Phe Lys Tyr Thr Tyr Asp Asp Glu Gly Lys Met Thr
          180          185          190
Val Arg Glu Val Phe Met Leu Val Met Asp Pro Asn Thr Pro Ile Ser
          195          200          205
Arg Leu Glu Tyr His Tyr Asp Ala Gln Gly Arg Leu Thr His Trp Ile
          210          215          220
Ser Phe Ala Phe Gly Ala Glu Ser Gln Lys Asn Thr Tyr His Tyr Asn
          225          230          235          240
Glu Lys Gly Leu Leu Val Ser Glu Val Leu Ser Asn Ala Met Gly Thr
          245          250          255
Thr Tyr Ser Asp Thr Gly Lys Thr Glu Tyr Ser Tyr Asp Asp Ala Asp
          260          265          270
Asn Met Val Lys Ala Glu Tyr Phe Val Val Gln Gln Gly Lys Ala Trp
          275          280          285
Gln Val Leu Lys Arg Glu Glu Tyr Thr Tyr Glu Asp Asn Ile Cys Ile
          290          295          300
Gln Tyr Leu Ala Ile Asn Gly Thr Asp Thr Lys Val Tyr Lys Arg Asp
          305          310          315          320
Ile Glu Ser Asp Lys Ser Ile Ser Ala Asn Val Ile Asp Ile Pro Ser
          325          330          335
Met Pro Glu Gln Thr Trp Pro Asn Met Tyr Gly Phe Asn Ala Lys Arg
          340          345          350
Leu Lys Glu Thr Tyr Ser Ser Tyr Glu Gly Asp Val Ala Thr Pro Ile

```

355	360	365
Phe Asp Tyr Ile Tyr Thr Tyr Lys Ala Leu Thr Ser Met Ala Thr Pro		
370	375	380
Ser Thr Glu Ala Gln Val Ala Val Tyr Leu Asn Pro Ser Thr Asp Arg		
385	390	395
Leu Val Ile Leu Ala Asn Gly Ile Thr His Leu Ser Met Tyr Asp Leu		
405	410	415
Gln Gly Lys Leu Ile Arg Asp Cys Ala Leu Ser Gly Asp Lys Val Glu		
420	425	430
Met Gly Val Gly Ser Leu Thr Lys Gly Thr Tyr Leu Leu Lys Val Asn		
435	440	445
Thr Asp Gln Gly Ala Phe Val Arg Lys Val Val Ile Arg		
450	455	460

(2) INFORMATION FOR SEQ ID NO:386

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

```

Met Ala Lys Val Ile Lys Thr Lys Lys Gly Leu Ala Leu Asn Leu Lys
1      5      10      15
Gly Lys Pro Leu Pro Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr
20      25      30
Tyr Ala Val Val Pro Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr
35      40      45
Ala Arg Pro Gly Asp Lys Val Arg Ala Gly Ser Ala Leu Met His His
50      55      60
Lys Ala Tyr Pro Glu Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val
65      70      75      80
Ile Ala Val Asn Arg Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val
85      90      95
Lys Pro Asp Gly Leu Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro
100     105     110
Ser Ala Leu Ser Ala Glu Gln Ile Lys Glu Leu Leu Leu Ser Ser Gly
115     120     125
Met Trp Gly Phe Ile Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro
130     135     140
Asp Ile Ala Pro Arg Asp Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro
145     150     155     160
Leu Ala Pro Asp Phe Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu
165     170     175
Gln Thr Ala Ile Asp Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr
180     185     190
Val Gly Leu Lys Pro Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile
195     200     205
Val Glu Val His Gly Pro His Pro Ala Gly Asn Val Gly Val Leu Ile
210     215     220
Asn His Thr Lys Pro Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys
225     230     235     240
Ala Thr Asp Leu Ile Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala
245     250     255
Asp Phe Thr Arg Met Ile Ala Met Thr Gly Ser Asp Ala Ala His
260     265     270
Gly Tyr Val Arg Ile Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro
275     280     285
Gly Arg Leu Thr Ile Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn
290     295     300
Val Leu Thr Gly Lys Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala
305     310     315     320
Arg Cys Asp Gln Ile Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu
325     330     335
Leu Phe Gly Trp Ala Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg

```

	340		345		350										
Ala	Tyr	Phe	Ser	Trp	Leu	Gln	Gly	Lys	Asn	Lys	Glu	Tyr	Val	Leu	Asp
	355					360						365			
Ala	Arg	Ile	Lys	Gly	Gly	Glu	Arg	Ala	Met	Ile	Met	Ser	Asn	Glu	Tyr
	370					375						380			
Asp	Arg	Val	Phe	Pro	Met	Asp	Ile	Tyr	Pro	Glu	Tyr	Leu	Leu	Lys	Ala
	385				390				395					400	
Ile	Ile	Ala	Phe	Asp	Ile	Asp	Lys	Met	Glu	Asp	Leu	Gly	Ile	Tyr	Glu
		405							410				415		
Val	Ala	Pro	Glu	Asp	Phe	Ala	Thr	Cys	Glu	Phe	Val	Asp	Thr	Ser	Lys
		420						425					430		
Ile	Glu	Leu	Gln	Arg	Ile	Val	Arg	Glu	Gly	Leu	Asp	Met	Leu	Tyr	Lys
		435				440						445			
Glu	Met	Asn													
	450														

(2) INFORMATION FOR SEQ ID NO:387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

Met	Asp	Lys	Val	Ser	Tyr	Ala	Leu	Gly	Leu	Ser	Ile	Gly	Asn	Asn	Phe
1			5						10				15		
Lys	Ser	Ser	Gly	Ile	Asp	Ser	Val	Val	Met	Asp	Asp	Phe	Met	Gln	Gly
		20					25						30		
Leu	Ser	Asp	Val	Leu	Glu	Glu	Lys	Ala	Pro	Gln	Leu	Ser	Tyr	Asp	Glu
		35					40					45			
Ala	Lys	Arg	Glu	Ile	Glu	Ala	Tyr	Phe	Met	Asp	Leu	Gln	Gln	Lys	Ala
	50					55				60					
Val	Lys	Leu	Asn	Lys	Glu	Ala	Gly	Glu	Glu	Phe	Leu	Lys	Ile	Asn	Ala
	65				70					75				80	
His	Lys	Glu	Gly	Val	Thr	Thr	Leu	Pro	Ser	Gly	Leu	Gln	Tyr	Glu	Val
		85						90					95		
Ile	Lys	Met	Gly	Glu	Gly	Pro	Lys	Pro	Thr	Leu	Ser	Asp	Thr	Val	Thr
		100					105						110		
Cys	His	Tyr	His	Gly	Thr	Leu	Ile	Asn	Gly	Ile	Val	Phe	Asp	Ser	Ser
		115				120					125				
Met	Asp	Arg	Gly	Glu	Pro	Ala	Ser	Phe	Pro	Leu	Arg	Gly	Val	Ile	Ala
	130					135				140					
Gly	Trp	Thr	Glu	Ile	Leu	Gln	Leu	Met	Pro	Val	Gly	Ser	Lys	Trp	Lys
	145				150					155				160	
Val	Thr	Ile	Pro	Ser	Asp	Leu	Ala	Tyr	Gly	Asp	Arg	Gly	Ala	Gly	Glu
		165							170				175		
His	Ile	Lys	Pro	Gly	Ser	Thr	Leu	Ile	Phe	Ile	Ile	Glu	Leu	Leu	Ser
		180					185						190		
Ile	Asn	Lys													
	195														

(2) INFORMATION FOR SEQ ID NO:388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

```
Met Lys Lys Ala Leu Leu Ile Gly Ala Ala Leu Leu Gly Ala Val Ser
1      5      10      15
Phe Ala Ser Ala Gln Ser Leu Ser Thr Ile Lys Val Gln Asn Asn Ser
      20      25      30
Val Gln Gln Pro Arg Glu Glu Ala Thr Ile Gln Val Cys Gly Glu Leu
      35      40      45
Ala Glu Gln Val Asp Cys Ile Gly Thr Gly Asn Ser Ala Ile Ile Ala
      50      55      60
Ala Ala Ala Lys Phe Glu Ser Asp Asp Leu Glu Ser Tyr Val Gly Trp
65      70      75      80
Glu Ile Met Ser Val Asp Phe Phe Pro Gly Tyr Lys Ala Cys Lys Tyr
      85      90      95
Thr Ser Ala Val Trp Ala Asp Asp Met Thr Ile Leu Gly Gln Ser Glu
      100      105      110
Asp Ser Asp Pro Glu Met Gln Thr Ile Asn Asn Leu Ala Leu Lys Thr
      115      120      125
Ser Val Lys Ile Glu Ala Gly Lys Asn Tyr Ile Val Gly Tyr Ile Ala
130      135      140
Asn Thr Ala Gly Gly His Pro Ile Gly Cys Asp Gln Gly Pro Ala Val
145      150      155      160
Asp Gly Tyr Gly Asp Leu Val Ser Ile Ser Glu Asp Gly Gly Ala Thr
      165      170      175
Phe Pro Pro Phe Glu Ser Leu His Gln Ala Val Pro Thr Leu Asn Tyr
      180      185      190
Asn Ile Tyr Val Val Val His Leu Lys Lys Gly Glu Gly Val Glu Ala
195      200      205
Val Leu Thr Asn Asp Lys Ala Asn Ala Tyr Val Gln Asn Gly Val Ile
210      215      220
Tyr Val Ala Gly Ala Asn Gly Arg Gln Val Ser Leu Phe Asp Met Asn
225      230      235      240
Gly Lys Val Val Tyr Thr Gly Val Ser Glu Thr Ile Ala Ala Pro Gln
      245      250      255
Lys Gly Met Tyr Ile Leu Arg Val Gly Ala Lys Ser Ile Lys Leu Ala
260      265      270
Ile
```

(2) INFORMATION FOR SEQ ID NO:389

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 554 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

```
Met Pro Arg Ile Met Lys Leu Lys Ile Ala Leu Arg Leu Leu Leu Ala
1      5      10      15
Thr Phe Ala Ile Val Leu Phe Ser Pro Leu Ala Lys Ala Gln Met Asp
      20      25      30
Ile Gly Gly Asp Asp Val Leu Ile Glu Thr Met Ser Thr Leu Ser Gly
      35      40      45
Tyr Ser Glu Asp Phe Tyr Tyr Lys Met Ala Val Ala Asp Asn Gly Trp
50      55      60
Ile Tyr Val Met Leu Asp Phe Ser Arg Ile Tyr Phe Asp Asp Val Arg
65      70      75      80
Leu Tyr Arg Ser Lys Asp Gly Gly Ala Thr Tyr Gln Lys Leu Gly Ser
      85      90      95
Leu Gly Ser Leu Val Pro Tyr Asp Phe Asp Val Ser His Cys Asp Phe
100      105      110
```



```

Ile Val Thr Gly Lys Asp Glu Asp Asp Ile Asn Val Trp Thr Val Met
115 120 125
Thr Ala Phe Glu Tyr Val Gly Gly Thr Ile Gly Asn Gly Val Leu Leu
130 135 140
Met His Arg His Asp Ala Asp Ile Asn Asn Thr Glu Cys Val Tyr Lys
145 150 155 160
Lys Asp Phe Pro Asn Asn Arg Leu Met Gly Val Ala Ile Ala Ser Asn
165 170 175
Tyr Arg Ala Pro Ser Pro Tyr Gly Leu Gly Gly Asp Pro Phe Ala Leu
180 185 190
Ala Val Ala Val Ser Gly Ser Gly Ser Asp His Ser Phe Leu Asp Tyr
195 200 205
Ile Phe Ser Leu Asp Gly Gly Val His Phe Glu Gln Lys Arg Ile Tyr
210 215 220
Thr Arg Pro Gln Lys Leu Thr Ile Asn Arg Val Asp Leu Ser Leu Gly
225 230 235 240
Ser Thr Ser Pro Ser Leu Gly Phe Asn Thr Trp Pro Leu Met Gly Val
245 250 255
Val Phe Glu Met Asn Lys Asn Leu Asp Gly Phe Asp Ile Gly Phe Ile
260 265 270
Ser Asn Phe Val Asp Tyr Asp Pro Arg Tyr Ala Trp Ser Glu Pro Ile
275 280 285
Ile Ile Glu Glu Asp Cys Gly Trp Thr Asp Phe Asn Pro Leu Gly Ala
290 295 300
Leu Ser Ile Glu Ile Gln Met Met Leu Asp Asp Asn Ser Asp Asn Thr
305 310 315 320
Val Gly Gly Glu Arg Ser His Asn Phe Leu Ile Thr Tyr Pro Gly His
325 330 335
Tyr Val Tyr Pro Lys Gln Ser Phe Asn Tyr Ser Pro Gly His Thr Pro
340 345 350
Thr Lys Lys Asp Leu Val Phe Lys His Cys Ile Gly Ile Pro Ala Leu
355 360 365
Ala Tyr Asp Lys Glu Gly Asp Arg Tyr Leu Thr Thr Phe Gln Asp His
370 375 380
Asn Leu Met Arg Tyr Arg Trp Ile Lys Tyr Asp Asp Ile Asn Ser Phe
385 390 395 400
Tyr Gly Trp Ser Trp Pro Tyr Val Tyr Ala Lys Glu Ala Lys Asp Lys
405 410 415
Lys Arg Arg Arg Pro Gln Val Ala Leu Asn Pro Thr Asn Gly Lys Ala
420 425 430
Cys Trp Val Trp His Thr Arg Lys Ser Pro Tyr Asp Glu Thr Lys Pro
435 440 445
His Pro Thr Pro Val Ile Ile Lys His Phe Leu Trp Ser Asp Thr Glu
450 455 460
Trp Val His Ala Leu Asp Val Gly Asp Val Leu Gln Lys Glu Gly Ser
465 470 475 480
Met Lys Leu Tyr Pro Asn Pro Ala Lys Glu Tyr Val Leu Ile Asn Leu
485 490 495
Pro Lys Glu Gly Gly His Glu Ala Val Val Tyr Asp Met Gln Gly Arg
500 505 510
Ile Val Glu Lys Val Ser Phe Ser Gly Lys Glu Tyr Lys Leu Asn Val
515 520 525
Gln Tyr Leu Ser Lys Gly Thr Tyr Met Leu Lys Val Val Ala Asp Thr
530 535 540
Glu Tyr Phe Val Glu Lys Ile Ile Val Glu
545 550

```

(2) INFORMATION FOR SEQ ID NO:390

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...550
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

Met	Lys	Leu	Lys	Ile	Ala	Leu	Arg	Leu	Leu	Leu	Ala	Thr	Phe	Ala	Ile
1				5					10					15	
Val	Leu	Phe	Ser	Pro	Leu	Ala	Lys	Ala	Gln	Met	Asp	Ile	Gly	Gly	Asp
			20					25					30		
Asp	Val	Leu	Ile	Glu	Thr	Met	Ser	Thr	Leu	Ser	Gly	Tyr	Ser	Glu	Asp
		35					40					45			
Phe	Tyr	Tyr	Lys	Met	Ala	Val	Ala	Asp	Asn	Gly	Trp	Ile	Tyr	Val	Met
	50					55				60					
Leu	Asp	Phe	Ser	Arg	Ile	Tyr	Phe	Asp	Asp	Val	Arg	Leu	Tyr	Arg	Ser
65					70					75					80
Lys	Asp	Gly	Gly	Ala	Thr	Tyr	Gln	Lys	Leu	Gly	Ser	Leu	Gly	Ser	Leu
				85				90					95		
Val	Pro	Tyr	Asp	Phe	Asp	Val	Ser	His	Cys	Asp	Phe	Ile	Val	Thr	Gly
			100					105					110		
Lys	Asp	Glu	Asp	Asp	Ile	Asn	Val	Trp	Thr	Val	Met	Thr	Ala	Phe	Glu
		115				120						125			
Tyr	Val	Gly	Gly	Thr	Ile	Gly	Asn	Gly	Val	Leu	Leu	Met	His	Arg	His
	130					135						140			
Asp	Ala	Asp	Ile	Asn	Asn	Thr	Glu	Cys	Val	Tyr	Lys	Lys	Asp	Phe	Pro
145					150					155					160
Asn	Asn	Arg	Leu	Met	Gly	Val	Ala	Ile	Ala	Ser	Asn	Tyr	Arg	Ala	Pro
			165						170					175	
Ser	Pro	Tyr	Gly	Leu	Gly	Gly	Asp	Pro	Phe	Ala	Leu	Ala	Val	Ala	Val
		180						185					190		
Ser	Gly	Ser	Gly	Ser	Asp	His	Ser	Phe	Leu	Asp	Tyr	Ile	Phe	Ser	Leu
		195				200						205			
Asp	Gly	Gly	Val	His	Phe	Glu	Gln	Lys	Arg	Ile	Tyr	Thr	Arg	Pro	Gln
	210					215						220			
Lys	Leu	Thr	Ile	Asn	Arg	Val	Asp	Leu	Ser	Leu	Gly	Ser	Thr	Ser	Pro
225					230					235					240
Ser	Leu	Gly	Phe	Asn	Thr	Trp	Pro	Leu	Met	Gly	Val	Val	Phe	Glu	Met
			245						250					255	
Asn	Lys	Asn	Leu	Asp	Gly	Phe	Asp	Ile	Gly	Phe	Ile	Ser	Asn	Phe	Val
		260						265					270		
Asp	Tyr	Asp	Pro	Arg	Tyr	Ala	Trp	Ser	Glu	Pro	Ile	Ile	Ile	Glu	Glu
	275					280						285			
Asp	Cys	Gly	Trp	Thr	Asp	Phe	Asn	Pro	Leu	Gly	Ala	Leu	Ser	Ile	Glu
	290					295					300				
Ile	Gln	Met	Met	Leu	Asp	Asn	Ser	Asp	Asn	Thr	Val	Gly	Gly	Glu	
305				310					315					320	
Arg	Ser	His	Asn	Phe	Leu	Ile	Thr	Tyr	Pro	Gly	His	Tyr	Val	Tyr	Pro
			325						330					335	
Lys	Gln	Ser	Phe	Asn	Tyr	Ser	Pro	Gly	His	Thr	Pro	Thr	Lys	Lys	Asp
		340						345					350		
Leu	Val	Phe	Lys	His	Cys	Ile	Gly	Ile	Pro	Ala	Leu	Ala	Tyr	Asp	Lys
		355					360					365			
Glu	Gly	Asp	Arg	Tyr	Leu	Thr	Thr	Phe	Gln	Asp	His	Asn	Leu	Met	Arg
	370					375					380				
Tyr	Arg	Trp	Ile	Lys	Tyr	Asp	Asp	Ile	Asn	Ser	Phe	Tyr	Gly	Trp	Ser
385					390					395					400
Trp	Pro	Tyr	Val	Tyr	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Lys	Arg	Arg	Arg
			405						410					415	
Pro	Gln	Val	Ala	Leu	Asn	Pro	Thr	Asn	Gly	Lys	Ala	Cys	Trp	Val	Trp
		420						425					430		
His	Thr	Arg	Lys	Ser	Pro	Tyr	Asp	Glu	Thr	Lys	Pro	His	Pro	Thr	Pro
	435					440						445			
Val	Ile	Ile	Lys	His	Phe	Leu	Trp	Ser	Asp	Thr	Glu	Trp	Val	His	Ala
	450					455						460			
Leu	Asp	Val	Gly	Asp	Val	Leu	Gln	Lys	Glu	Gly	Ser	Met	Lys	Leu	Tyr
465					470					475					480
Pro	Asn	Pro	Ala	Lys	Glu	Tyr	Val	Leu	Ile	Asn	Leu	Pro	Lys	Glu	Gly
			485						490					495	
Gly	His	Glu	Ala	Val	Val	Tyr	Asp	Met	Gln	Gly	Arg	Ile	Val	Glu	Lys
		500						505					510		
Val	Ser	Phe	Ser	Gly	Lys	Glu	Tyr	Lys	Leu	Asn	Val	Gln	Tyr	Leu	Ser
	515						520					525			
Lys	Gly	Thr	Tyr	Met	Leu	Lys	Val	Val	Ala	Asp	Thr	Glu	Tyr	Phe	Val
	530					535						540			
Glu	Lys	Ile	Ile	Val	Glu										
545					550										

(2) INFORMATION FOR SEQ ID NO:391

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391

```
Met Lys Arg Leu Leu Pro Phe Leu Leu Leu Ala Gly Leu Val Ala Val
1          5          10          15
Gly Asn Val Ser Ala Gln Ser Pro Arg Ile Pro Gln Val Asp Val His
20          25          30
Thr Arg Ile Ala Arg Asn Ala Arg Tyr Arg Leu Asp Lys Ile Ser Val
35          40          45
Pro Asp Ser Arg Gln Ile Phe Asp Tyr Phe Tyr Lys Glu Glu Thr Ile
50          55          60
Pro Thr Lys Ile Gln Thr Thr Thr Gly Gly Ala Ile Thr Ser Ile Asp
65          70          75          80
Ser Leu Phe Tyr Glu Asp Asp Arg Leu Val Gln Val Arg Tyr Phe Asp
85          90          95
Asn Asn Leu Glu Leu Lys Gln Ala Glu Lys Tyr Val Tyr Asp Gly Ser
100          105          110
Lys Leu Val Leu Arg Glu Ile Arg Lys Ser Pro Thr Asp Glu Thr Pro
115          120          125
Ile Lys Lys Val Ser Tyr His Tyr Leu Cys Gly Ser Asp Met Pro Phe
130          135          140
Glu Ile Thr Thr Glu Met Ser Asp Gly Tyr Phe Glu Ser His Thr Leu
145          150          155          160
Asn Tyr Leu Asn Gly Lys Ile Ala Arg Ile Asp Ile Met Thr Gln Gln
165          170          175
Asn Pro Ser Ala Glu Leu Ile Glu Thr Gly Arg Met Val Tyr Glu Phe
180          185          190
Asp Ala Asn Asn Asp Ala Val Leu Leu Arg Asp Ser Val Phe Leu Pro
195          200          205
Leu Gln Asn Lys Trp Val Glu Met Phe Thr His Arg Tyr Thr Tyr Asp
210          215          220
Asn Lys His Asn Cys Ile Arg Trp Glu Gln Asp Glu Phe Gly Thr Leu
225          230          235          240
Thr Leu Ala Asn Asn Phe Glu Tyr Asp Thr Thr Ile Pro Leu Ser Ser
245          250          255
Val Leu Phe Pro Thr His Glu Glu Phe Phe Arg Pro Leu Leu Pro Asn
260          265          270
Phe Met Lys His Met Arg Thr Lys Gln Thr Tyr Phe Asn Asn Ser Gly
275          280          285
Glu Gly Leu Ser Glu Val Cys Asp Tyr Asn Tyr Phe Tyr Thr Asp Met
290          295          300
Gln Gly Asn Ala Leu Thr Asp Val Ala Val Asn Glu Ser Ile Lys Ile
305          310          315          320
Tyr Pro Arg Pro Ala Thr Asp Phe Leu Arg Ile Glu Gly Ser Gln Leu
325          330          335
Leu Arg Leu Ser Leu Phe Asp Met Asn Gly Lys Leu Ile Arg Ala Thr
340          345          350
Glu Leu Thr Gly Asp Leu Ala Ile Ile Gly Val Ala Ser Leu Pro Arg
355          360          365
Gly Thr Tyr Ile Ala Glu Ile Thr Ala Ala Asn Ser Lys Thr Ile Arg
370          375          380
Ala Lys Val Ser Leu Arg
385          390
```

(2) INFORMATION FOR SEQ ID NO:392

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

```
Met Arg Gln His Leu Ser Leu Phe Pro Phe Ile Leu Phe Leu Leu Leu
1      5      10      15
Ala Phe Ser Tyr Val Gly Cys Arg Thr Val Arg Gln Thr Pro Lys Gln
20      25      30
Ser Glu Arg Tyr Val Val Val Leu Ser Leu Asp Gly Phe Arg Pro Asp
35      40      45
Tyr Thr Asp Arg Ala Arg Thr Pro Ala Leu Asp Arg Met Ala Gln Glu
50      55      60
Gly Leu Ser Gly Ser Leu Gln Pro Cys Phe Pro Ser Leu Thr Phe Pro
65      70      75      80
Asn His Tyr Ser Met Ala Thr Gly Leu Tyr Pro Asp His His Gly Ile
85      90      95
Val Ala Asn Glu Phe Val Asp Ser Leu Leu Gly Ile Phe Arg Ile Ser
100     105     110
Asp Arg Lys Ala Val Glu Thr Pro Gly Phe Trp Gly Gly Glu Pro Val
115     120     125
Trp Asn Thr Ala Ala Arg Gln Gly Ile Arg Thr Gly Val Tyr Phe Trp
130     135     140
Val Gly Ser Glu Thr Ala Val Asn Gly Asn Arg Pro Trp Arg Trp Lys
145     150     155     160
Lys Phe Ser Ser Thr Val Pro Phe Arg Asp Arg Ala Asp Ser Val Ile
165     170     175
Ala Trp Leu Gly Leu Pro Glu Lys Glu Arg Pro Arg Leu Leu Met Trp
180     185     190
Tyr Ile Glu Glu Pro Asp Met Ile Gly His Ser Gln Thr Pro Glu Ser
195     200     205
Pro Leu Thr Leu Ala Met Val Glu Arg Leu Asp Ser Val Val Gly Tyr
210     215     220
Phe Arg Lys Arg Leu Asp Ser Leu Pro Ile Ala Ala Gln Thr Asp Phe
225     230     235     240
Ile Ile Val Ser Asp His Gly Met Ala Thr Tyr Glu Asn Glu Lys Cys
245     250     255
Val Asn Leu Ser His Tyr Leu Pro Ala Asp Ser Phe Leu Tyr Met Ala
260     265     270
Thr Gly Ala Phe Thr His Leu Tyr Pro Lys Pro Ser Tyr Thr Glu Arg
275     280     285
Ala Tyr Glu Ile Leu Arg Ala Ile Pro His Ile Ser Val Tyr Arg Lys
290     295     300
Gly Glu Val Pro Lys Arg Leu Arg Cys Gly Thr Asn Pro Arg Leu Gly
305     310     315     320
Glu Leu Val Val Ile Pro Asp Ile Gly Ser Thr Val Phe Phe Ala Ile
325     330     335
Asn Glu Asp Val Arg Pro Gly Ala Ala His Gly Tyr Asp Asn Gln Ala
340     345     350
Pro Glu Met Arg Ala Leu Leu Arg Ala Val Gly Pro Asp Phe Arg Pro
355     360     365
Gly Ser Arg Val Glu Asn Leu Pro Asn Ile Thr Ile Tyr Pro Leu Ile
370     375     380
Cys Arg Leu Leu Gly Ile Glu Pro Ala Pro Asn Asp Ala Asp Glu Thr
385     390     395     400
Leu Leu Asn Gly Leu Ile Arg Asp Lys Arg Pro
405     410
```

(2) INFORMATION FOR SEQ ID NO:393

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

```
Met Lys Val Gly Leu Phe Ile Pro Cys Tyr Val Asn Ala Val Tyr Pro
1      5      10      15
Glu Val Gly Ile Ala Thr Tyr Lys Leu Leu Lys Ser Leu Asp Ile Asp
      20      25      30
Val Asp Tyr Pro Met Asp Gln Thr Cys Cys Gly Gln Pro Met Ala Asn
      35      40      45
Ala Gly Phe Glu Gln Lys Ala Gln Lys Leu Ala Leu Arg Phe Glu Glu
      50      55      60
Leu Phe Glu Ser Tyr Asp Val Val Val Gly Pro Ser Ala Ser Cys Val
      65      70      75      80
Ala Phe Val Lys Glu Asn Tyr Asp His Ile Leu Arg Pro Thr Gly His
      85      90      95
Val Cys Lys Ser Ala Ala Lys Val Arg Asp Ile Cys Glu Phe Leu His
      100      105      110
Asp Asp Leu Lys Ile Thr Ser Leu Pro Ser Arg Phe Ala His Lys Val
      115      120      125
Ser Leu His Asn Ser Cys His Gly Val Arg Glu Leu His Leu Ser Thr
      130      135      140
Pro Ser Glu Val His Arg Pro Tyr His Asn Lys Val Arg Arg Leu Leu
      145      150      155      160
Glu Met Val Gln Gly Ile Glu Val Phe Glu Pro Lys Arg Ile Asp Glu
      165      170      175
Cys Cys Gly Phe Gly Gly Met Tyr Ser Val Glu Glu Pro Glu Val Ser
      180      185      190
Thr Cys Met Gly His Asp Lys Val Leu Asp His Ile Ser Thr Gly Ala
      195      200      205
Glu Tyr Ile Thr Gly Pro Asp Ser Ser Cys Leu Met His Met Gln Gly
      210      215      220
Val Ile Asp Arg Glu Lys Leu Pro Ile Lys Thr Ile His Ala Val Glu
      225      230      235      240
Ile Leu Ala Ala Asn Leu
      245
```

(2) INFORMATION FOR SEQ ID NO:394

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

```
Met Asp Ile Val Ser Met Ala Asp Lys Ala Leu Val Val Glu Met Arg
1      5      10      15
Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn
      20      25      30
Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly
      35      40      45
Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile
      50      55      60
Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys
      65      70      75      80
Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln
      85      90      95
Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe
      100      105      110
Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg
      115      120      125
Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys
      130      135      140
Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala
```

```

145          150          155          160
Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr
          165          170          175
Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr
          180          185          190
Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His Asn Ser
          195          200          205
Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn
          210          215          220
Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg
225          230          235          240
Lys Asn Thr Glu Ile Asp

```

(2) INFORMATION FOR SEQ ID NO:395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

```

Met Ala Asp Lys Ala Leu Val Val Glu Met Arg Asp Val Thr Leu Cys
1          5          10          15
Gln Glu Glu Asn Val Ile Phe Gln Asn Leu Asn Leu Thr Leu Ser Ala
          20          25          30
Gly Asp Phe Val Tyr Leu Ile Gly Ser Val Gly Ser Gly Lys Ser Thr
          35          40          45
Leu Leu Lys Ala Leu Tyr Ala Glu Val Pro Ile Ser Ala Gly Tyr Ala
          50          55          60
Arg Val Ile Asp Tyr Asp Leu Ala Lys Leu Lys Arg Lys Gln Leu Pro
65          70          75          80
Tyr Leu Arg Arg Asn Leu Gly Ile Val Phe Gln Asp Phe Gln Leu Leu
          85          90          95
Asn Gly Arg Thr Val Ala Glu Asn Leu Asp Phe Val Leu Arg Ala Thr
          100          105          110
Asp Trp Lys Asn Arg Ala Asp Arg Glu Gln Arg Ile Glu Glu Val Leu
          115          120          125
Thr Arg Val Gly Met Ser Arg Lys Ala Tyr Lys Arg Pro His Glu Leu
          130          135          140
Ser Gly Gly Glu Gln Gln Arg Val Gly Ile Ala Arg Ala Leu Leu Ala
145          150          155          160
Lys Pro Ala Leu Ile Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Ser
          165          170          175
Val Thr Gly Leu Gln Ile Ala Ser Leu Leu Tyr Glu Ile Ser Lys Gln
          180          185          190
Gly Thr Ala Val Leu Met Ser Thr His Asn Ser Ser Leu Leu Ser His
          195          200          205
Leu Pro Ala Arg Thr Leu Ala Val Arg Lys Asn Gly Asp Ala Ser Ser
          210          215          220
Leu Val Glu Leu Ser Ala Asp Ala Val Ser Arg Lys Asn Thr Glu Ile
225          230          235
Asp

```

(2) INFORMATION FOR SEQ ID NO:396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

```
Met Arg Asp Val Thr Leu Cys Gln Glu Glu Asn Val Ile Phe Gln Asn
1      5      10      15
Leu Asn Leu Thr Leu Ser Ala Gly Asp Phe Val Tyr Leu Ile Gly Ser
      20      25      30
Val Gly Ser Gly Lys Ser Thr Leu Leu Lys Ala Leu Tyr Ala Glu Val
      35      40      45
Pro Ile Ser Ala Gly Tyr Ala Arg Val Ile Asp Tyr Asp Leu Ala Lys
      50      55      60
Leu Lys Arg Lys Gln Leu Pro Tyr Leu Arg Arg Asn Leu Gly Ile Val
      65      70      75      80
Phe Gln Asp Phe Gln Leu Leu Asn Gly Arg Thr Val Ala Glu Asn Leu
      85      90      95
Asp Phe Val Leu Arg Ala Thr Asp Trp Lys Asn Arg Ala Asp Arg Glu
      100     105     110
Gln Arg Ile Glu Glu Val Leu Thr Arg Val Gly Met Ser Arg Lys Ala
      115     120     125
Tyr Lys Arg Pro His Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Gly
      130     135     140
Ile Ala Arg Ala Leu Leu Ala Lys Pro Ala Leu Ile Leu Ala Asp Glu
145      150      155      160
Pro Thr Gly Asn Leu Asp Ser Val Thr Gly Leu Gln Ile Ala Ser Leu
      165     170     175
Leu Tyr Glu Ile Ser Lys Gln Gly Thr Ala Val Leu Met Ser Thr His
      180     185     190
Asn Ser Ser Leu Leu Ser His Leu Pro Ala Arg Thr Leu Ala Val Arg
      195     200     205
Lys Asn Gly Asp Ala Ser Ser Leu Val Glu Leu Ser Ala Asp Ala Val
      210     215     220
Ser Arg Lys Asn Thr Glu Ile Asp
225      230
```

(2) INFORMATION FOR SEQ ID NO:397

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

```
Met Ile Glu Ile Ser Asn Leu Thr Lys Val Phe Arg Thr Glu Glu Ile
1      5      10      15
Glu Thr Val Ala Leu Asp Gly Val Ser Leu Lys Val Asp Lys Gly Glu
      20      25      30
Phe Ile Ala Ile Met Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu
      35      40      45
Asn Ile Leu Gly Leu Leu Asp Asn Pro Thr Ser Gly Ile Tyr Lys Leu
      50      55      60
Asp Gly Ala Glu Val Gly Asn Leu Arg Glu Lys Asp Arg Thr Ala Val
      65      70      75      80
Arg Lys Gly Asn Ile Gly Phe Val Phe Gln Ser Phe Asn Leu Ile Glu
      85      90      95
Glu Met Thr Val Ser Glu Asn Val Glu Leu Pro Leu Val Tyr Leu Gly
      100     105     110
Val Lys Ala Ser Glu Arg Lys Glu Arg Val Glu Glu Ala Leu Arg Lys
      115     120     125
```

Met	Ser	Ile	Ser	His	Arg	Ala	Gly	His	Phe	Pro	Asn	Gln	Leu	Ser	Gly
130						135				140					
Gly	Gln	Gln	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Val	Val	Ala	Asn	Pro
145					150					155					160
Lys	Leu	Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Asn	Leu	Asp	Ser	Lys	Asn
				165					170					175	
Gly	Ala	Asp	Val	Met	Glu	Leu	Leu	Arg	Gly	Leu	Asn	Arg	Glu	Gly	Ala
			180					185					190		
Thr	Ile	Val	Met	Val	Thr	His	Ser	Glu	His	Asp	Ala	Arg	Ser	Ala	Gly
	195						200					205			
Arg	Ile	Ile	Asn	Leu	Phe	Asp	Gly	Lys	Ile	Arg					
210						215									

(2) INFORMATION FOR SEQ ID NO:398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

Met	Lys	Glu	Phe	Phe	Lys	Met	Phe	Phe	Ala	Ser	Ile	Leu	Gly	Val	Ile
1			5						10					15	
Thr	Ala	Gly	Ile	Ile	Leu	Phe	Cys	Ile	Phe	Leu	Phe	Ile	Phe	Phe	Gly
			20					25					30		
Ile	Val	Ala	Gly	Ile	Ala	Ser	Lys	Ala	Thr	Gly	Gly	Thr	Ile	Pro	Lys
		35					40					45			
Ile	Glu	Ala	Asn	Ser	Ile	Leu	His	Ile	Unk	Asn	Ser	Ser	Phe	Pro	Glu
	50					55				60					
Ile	Val	Ser	Ala	Asn	Pro	Trp	Ser	Met	Leu	Thr	Gly	Lys	Asp	Glu	Ser
65				70					75					80	
Val	Ser	Leu	Ser	Gln	Ala	Val	Glu	Ala	Ile	Gly	Gln	Ala	Lys	Asn	Asn
				85				90						95	
Pro	Asn	Ile	Thr	Gly	Ile	Phe	Leu	Asp	Leu	Asp	Asn	Leu	Ser	Val	Gly
			100				105						110		
Met	Ala	Ser	Ala	Glu	Glu	Leu	Arg	Arg	Ala	Leu	Gln	Asp	Phe	Lys	Met
		115					120					125			
Ser	Gly	Lys	Phe	Val	Val	Ser	Tyr	Ala	Asp	Arg	Tyr	Thr	Gln	Lys	Gly
	130					135				140					
Tyr	Tyr	Leu	Ser	Ser	Ile	Ala	Asp	Lys	Leu	Tyr	Leu	Asn	Pro	Lys	Gly
145					150					155					160
Met	Leu	Gly	Leu	Ile	Gly	Ile	Ala	Thr	Gln	Thr	Met	Phe	Tyr	Lys	Asp
			165					170						175	
Ala	Leu	Asp	Lys	Phe	Gly	Val	Lys	Met	Glu	Ile	Phe	Lys	Val	Gly	Thr
		180					185						190		
Tyr	Lys	Ala	Ala	Val	Glu	Pro	Phe	Met	Leu	Asn	Arg	Met	Ser	Asp	Ala
	195					200					205				
Asn	Arg	Glu	Gln	Ile	Thr	Thr	Tyr	Ile	Asn	Gly	Leu	Trp	Asp	Lys	Ile
	210					215				220					
Thr	Ser	Asp	Ile	Ala	Glu	Ser	Arg	Lys	Thr	Ala	Met	Asp	Ser	Val	Lys
225					230					235				240	
Met	Phe	Ala	Asp	Lys	Gly	Glu	Met	Phe	Gly	Leu	Ala	Glu	Lys	Ala	Val
			245					250						255	
Glu	Met	Lys	Leu	Val	Asp	Glu	Leu	Ala	Tyr	Arg	Thr	Asp	Val	Glu	Lys
		260					265					270			
Glu	Leu	Lys	Lys	Met	Ser	Gln	Arg	Gly	Glu	Lys	Asp	Glu	Leu	Arg	Phe
	275					280					285				
Val	Ser	Leu	Ser	Gln	Val	Leu	Ala	Asn	Gly	Pro	Met	Asn	Lys	Thr	Lys
	290					295				300					
Gly	Ser	Arg	Ile	Ala	Val	Leu	Phe	Ala	Glu	Gly	Glu	Ile	Thr	Glu	Glu
305					310					315					320
Ile	Ile	Lys	Lys	Pro	Phe	Asp	Thr	Asp	Gly	Ser	Ser	Ile	Thr	Gln	Glu
			325					330						335	
Leu	Ala	Lys	Glu	Ile	Lys	Ala	Ala	Ala	Asp	Asp	Asp	Asp	Ile	Lys	Ala
	340						345						350		

Val Val Leu Arg Val Asn Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu
 355 360 365
 Gln Ile Trp Lys Gln Val Ala Asp Leu Lys Ala Lys Lys Pro Ile Val
 370 375 380
 Val Ser Met Gly Asp Val Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys
 385 390 395 400
 Ala Ala Asn Ser Ile Val Ala Glu His Thr Leu Thr Gly Ser Ile
 405 410 415
 Gly Ile Phe Gly Met Phe Pro Asn Phe Ala Gly Val Ala Lys Lys Ile
 420 425 430
 Gly Val Asn Met Asp Val Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly
 435 440 445
 Asn Thr Phe Ala Pro Met Thr Val Glu Asp Arg Ala Leu Ile Gln Arg
 450 455 460
 Tyr Ile Glu Gln Gly Tyr Asp Leu Phe Leu Thr Arg Val Ser Glu Gly
 465 470 475 480
 Arg Asn Arg Thr Lys Ala Gln Ile Asp Ser Ile Ala Gln Gly Arg Val
 485 490 495
 Trp Leu Gly Asp Lys Ala Leu Ala Leu Gly Leu Val Asp Glu Leu Gly
 500 505 510
 Gly Leu Asp Thr Ala Ile Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly
 515 520 525
 Gly Asn Tyr Ser Ile Glu Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu
 530 535 540
 Glu Leu Leu Ser Ser Ser Ala Ala Asp Met Lys Ser Ala Ile Leu Ser
 545 550 555 560
 Thr Ile Leu Ser Asp Pro Glu Ile Glu Val Leu Arg Glu Leu Arg Ser
 565 570 575
 Met Pro Pro Arg Pro Ser Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe
 580 585 590
 Met Pro Tyr
 595

(2) INFORMATION FOR SEQ ID NO:399

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

Met Phe Phe Ala Ser Ile Leu Gly Val Ile Thr Ala Gly Ile Ile Leu
 1 5 10 15
 Phe Cys Ile Phe Leu Phe Ile Phe Phe Gly Ile Val Ala Gly Ile Ala
 20 25 30
 Ser Lys Ala Thr Gly Gly Thr Ile Pro Lys Ile Glu Ala Asn Ser Ile
 35 40 45
 Leu His Ile Unk Asn Ser Ser Phe Pro Glu Ile Val Ser Ala Asn Pro
 50 55 60
 Trp Ser Met Leu Thr Gly Lys Asp Glu Ser Val Ser Leu Ser Gln Ala
 65 70 75 80
 Val Glu Ala Ile Gly Gln Ala Lys Asn Asn Pro Asn Ile Thr Gly Ile
 85 90 95
 Phe Leu Asp Leu Asp Asn Leu Ser Val Gly Met Ala Ser Ala Glu Glu
 100 105 110
 Leu Arg Arg Ala Leu Gln Asp Phe Lys Met Ser Gly Lys Phe Val Val
 115 120 125
 Ser Tyr Ala Asp Arg Tyr Thr Gln Lys Gly Tyr Tyr Leu Ser Ser Ile
 130 135 140
 Ala Asp Lys Leu Tyr Leu Asn Pro Lys Gly Met Leu Gly Leu Ile Gly
 145 150 155 160
 Ile Ala Thr Gln Thr Met Phe Tyr Lys Asp Ala Leu Asp Lys Phe Gly
 165 170 175
 Val Lys Met Glu Ile Phe Lys Val Gly Thr Tyr Lys Ala Ala Val Glu
 180 185 190

```

Pro Phe Met Leu Asn Arg Met Ser Asp Ala Asn Arg Glu Gln Ile Thr
195 200 205
Thr Tyr Ile Asn Gly Leu Trp Asp Lys Ile Thr Ser Asp Ile Ala Glu
210 215 220
Ser Arg Lys Thr Ala Met Asp Ser Val Lys Met Phe Ala Asp Lys Gly
225 230 235 240
Glu Met Phe Gly Leu Ala Glu Lys Ala Val Glu Met Lys Leu Val Asp
245 250 255
Glu Leu Ala Tyr Arg Thr Asp Val Glu Lys Glu Leu Lys Lys Met Ser
260 265 270
Gln Arg Gly Glu Lys Asp Glu Leu Arg Phe Val Ser Leu Ser Gln Val
275 280 285
Leu Ala Asn Gly Pro Met Asn Lys Thr Lys Gly Ser Arg Ile Ala Val
290 295 300
Leu Phe Ala Glu Gly Glu Ile Thr Glu Glu Ile Ile Lys Lys Pro Phe
305 310 315 320
Asp Thr Asp Gly Ser Ser Ile Thr Gln Glu Leu Ala Lys Glu Ile Lys
325 330 335
Ala Ala Ala Asp Asp Asp Ile Lys Ala Val Val Leu Arg Val Asn
340 345 350
Ser Pro Gly Gly Ser Ala Phe Thr Ser Glu Gln Ile Trp Lys Gln Val
355 360 365
Ala Asp Leu Lys Ala Lys Lys Pro Ile Val Val Ser Met Gly Asp Val
370 375 380
Ala Ala Ser Gly Gly Tyr Tyr Ile Ala Cys Ala Ala Asn Ser Ile Val
385 390 395 400
Ala Glu His Thr Thr Leu Thr Gly Ser Ile Gly Ile Phe Gly Met Phe
405 410 415
Pro Asn Phe Ala Gly Val Ala Lys Lys Ile Gly Val Asn Met Asp Val
420 425 430
Val Gln Thr Ser Lys Tyr Ala Asp Leu Gly Asn Thr Phe Ala Pro Met
435 440 445
Thr Val Glu Asp Arg Ala Leu Ile Gln Arg Tyr Ile Glu Gln Gly Tyr
450 455 460
Asp Leu Phe Leu Thr Arg Val Ser Glu Gly Arg Asn Arg Thr Lys Ala
465 470 475 480
Gln Ile Asp Ser Ile Ala Gln Gly Arg Val Trp Leu Gly Asp Lys Ala
485 490 495
Leu Ala Leu Gly Leu Val Asp Glu Leu Gly Gly Leu Asp Thr Ala Ile
500 505 510
Lys Arg Ala Ala Lys Leu Ala Gln Leu Gly Gly Asn Tyr Ser Ile Glu
515 520 525
Tyr Gly Lys Thr Lys Arg Asn Phe Phe Glu Glu Leu Leu Ser Ser Ser
530 535 540
Ala Ala Asp Met Lys Ser Ala Ile Leu Ser Thr Ile Leu Ser Asp Pro
545 550 555 560
Glu Ile Glu Val Leu Arg Glu Leu Arg Ser Met Pro Pro Arg Pro Ser
565 570 575
Gly Ile Gln Ala Arg Leu Pro Tyr Tyr Phe Met Pro Tyr
580 585

```

(2) INFORMATION FOR SEQ ID NO:400

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...313
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

```

Met Arg Ala Asn Ile Trp Gln Ile Leu Ser Val Ser Val Leu Phe Phe
1 5 10 15
Phe Gly Thr Ala Ile Gly Gln Ala Gln Ser Arg Asn Arg Thr Tyr Glu
20 25 30
Ala Tyr Val Lys Gln Tyr Ala Asp Glu Ala Ile Arg Gln Met Ser Arg
35 40 45

```

```

Tyr Asn Ile Pro Ala Ser Ile Thr Ile Ala Gln Ala Leu Val Glu Thr
50          55          60
Gly Ala Gly Ala Ser Thr Leu Ala Ser Val His Asn Asn His Phe Gly
65          70          75          80
Ile Lys Cys His Lys Ser Trp Thr Gly Lys Arg Thr Tyr Arg Thr Asp
85          90          95
Asp Ala Pro Asn Glu Cys Phe Arg Ser Tyr Ser Ala Ala Arg Glu Ser
100         105         110
Tyr Glu Asp His Ser Arg Phe Leu Leu Gln Pro Arg Tyr Arg Pro Leu
115         120         125
Phe Lys Leu Asp Arg Glu Asp Tyr Arg Gly Trp Ala Thr Gly Leu Gln
130         135         140
Arg Cys Gly Tyr Ala Thr Asn Arg Gly Tyr Ala Asn Leu Leu Ile Lys
145         150         155         160
Met Val Glu Leu Tyr Glu Leu Tyr Ala Leu Asp Arg Glu Lys Tyr Pro
165         170         175
Ser Trp Phe His Lys Ser Tyr Pro Gly Ser Asn Lys Lys Ser His Gln
180         185         190
Thr Thr Lys Gln Lys Gln Ser Gly Leu Lys His Glu Ala Tyr Phe Ser
195         200         205
Tyr Gly Leu Leu Tyr Ile Ile Ala Lys Gln Gly Asp Thr Phe Asp Ser
210         215         220
Leu Ala Glu Glu Phe Asp Met Arg Ala Ser Lys Leu Ala Lys Tyr Asn
225         230         235         240
Asp Ala Pro Val Asp Phe Pro Ile Glu Lys Gly Asp Val Ile Tyr Leu
245         250         255
Glu Lys Lys His Ala Cys Ser Ile Ser Lys His Thr Gln His Val Val
260         265         270
Arg Val Gly Asp Ser Met His Ser Ile Ser Gln Arg Tyr Gly Ile Arg
275         280         285
Met Lys Asn Leu Tyr Lys Leu Asn Asp Lys Asp Gly Glu Tyr Ile Pro
290         295         300
Gln Glu Gly Asp Ile Leu Arg Leu Arg
305         310

```

(2) INFORMATION FOR SEQ ID NO:401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

```

Met Asp Gly Arg Arg Tyr Ser Asp Gly Leu His Gln Ala Ile Glu Ala
1          5          10          15
Lys Glu His Val Lys Val Glu Ala Ala Thr Gln Thr Phe Ala Thr Ile
20         25         30
Thr Leu Gln Asn Tyr Phe Arg Met Tyr His Lys Leu Ala Gly Met Thr
35         40         45
Gly Thr Ala Glu Thr Glu Ala Gly Glu Leu Trp Asp Ile Tyr Lys Leu
50         55         60
Asp Val Val Val Ile Pro Thr Asn Lys Pro Ile Ala Arg Lys Asp Met
65         70         75         80
Asn Asp Arg Ile Tyr Lys Thr Ala Arg Glu Lys Tyr Ala Ala Val Ile
85         90         95
Glu Glu Ile Val Arg Leu Val Glu Glu Gly Arg Pro Val Leu Val Gly
100        105        110
Thr Thr Ser Val Glu Ile Ser Glu Leu Leu Ser Arg Met Leu Arg Leu
115        120        125
Arg Gly Ile Gln His Asn Val Leu Asn Ala Lys Leu His Gln Lys Glu
130        135        140
Ala Glu Ile Val Ala Gln Ala Gly Gln Lys Gly Thr Val Thr Ile Ala
145        150        155        160
Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Ser Ala Glu Val
165        170        175

```

Lys Lys Ala Gly Gly Leu Ala Ile Ile Gly Thr Glu Arg His Glu Ser
 180 185 190
 Arg Arg Val Asp Arg Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp
 195 200 205
 Pro Gly Ser Ser Ile Phe Tyr Val Ser Leu Glu Asp His Leu Met Arg
 210 215 220
 Leu Phe Ala Thr Glu Lys Ile Ala Ser Leu Met Asp Arg Leu Gly Phe
 225 230 235 240
 Lys Glu Gly Glu Val Leu Glu Asn Asn Met Leu Ser Lys Ser Val Glu
 245 250 255
 Arg Ala Gln Lys Lys Val Glu Glu Asn Asn Phe Gly Ile Arg Lys His
 260 265 270
 Leu Leu Glu Tyr Asp Asp Val Met Asn Ser Gln Arg Glu Val Ile Tyr
 275 280 285
 Thr Arg Arg Arg His Ala Leu Met Gly Glu Arg Ile Gly Met Asp Val
 290 295 300
 Leu Asn Thr Ile Tyr Asp Val Cys Lys Ala Leu Ile Asp Asn Tyr Ala
 305 310 315 320
 Glu Ala Asn Asp Phe Glu Gly Phe Lys Glu Asp Leu Met Arg Ala Leu
 325 330 335
 Ala Ile Glu Ser Pro Ile Thr Gln Glu Ile Phe Arg Gly Lys Lys Ala
 340 345 350
 Glu Glu Leu Thr Asp Met Leu Phe Asp Glu Ala Tyr Lys Ser Phe Gln
 355 360 365
 Arg Lys Met Asp Leu Ile Ala Glu Val Ala His Pro Val Val His Gln
 370 375 380
 Val Phe Glu Thr Gln Ala Ala Val Tyr Glu Arg Ile Leu Ile Pro Ile
 385 390 395 400
 Thr Asp Gly Lys Arg Val Tyr Asn Ile Gly Cys Asn Leu Arg Glu Ala
 405 410 415
 Asp Glu Thr Gln Gly Lys Ser Ile Ile Lys Glu Phe Glu Lys Ala Ile
 420 425 430
 Val Leu His Thr Ile Asp Glu Ser Trp Lys Glu His Leu Arg Glu Met
 435 440 445
 Asp Glu Leu Arg Asn Ser Val Gln Asn Ala Ser Tyr Glu Asn Lys Asp
 450 455 460
 Pro Leu Leu Ile Tyr Lys Leu Glu Ser Tyr Glu Leu Phe Arg Lys Met
 465 470 475 480
 Val Glu Ala Met Asn Arg Lys Thr Val Ala Ile Leu Met Arg Ala Arg
 485 490 495
 Ile Pro Val Pro Glu Ala Pro Ser Gln Glu Glu Leu Glu His Arg Arg
 500 505 510
 Gln Ile Glu Ile Arg His Ala Thr Gln Gln Arg
 515 520

(2) INFORMATION FOR SEQ ID NO:402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

Met Asn Phe Leu Lys Lys Glu Pro Phe Lys Ile Phe Ser Met Ile Tyr
 1 5 10 15
 Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu Arg Ala Val
 20 25 30
 Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg Val Ser Leu
 35 40 45
 Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln Val Glu Lys
 50 55 60
 Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly Asn Ala Leu
 65 70 75 80
 Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile Lys Ala Leu
 85 90 95

```

Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn Ile Phe Ile
    100                      105                      110
Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile Phe Thr Ile
    115                      120                      125
Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile Thr Lys Arg
    130                      135                      140
Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val Ala Leu Thr
    145                      150                      155                      160
Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly Arg Ser Lys
    165                      170                      175
Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val Gln Arg Asp
    180                      185                      190
Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu Thr Tyr Gln
    195                      200                      205
Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val Leu Arg Glu
    210                      215                      220
Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu Asn Glu Ser
    225                      230                      235                      240
Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser Gln Ile Glu
    245                      250                      255
Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu Ser Ser Ala
    260                      265                      270
Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met Val Leu Leu
    275                      280                      285
Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp Cys Pro Thr
    290                      295                      300
Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe Leu Val Pro
    305                      310                      315                      320
Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu Leu Met Asp
    325                      330                      335
Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu Leu Met Val
    340                      345                      350
Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys Lys Leu Phe
    355                      360                      365
Val Glu Ile Gly Tyr Met Asn
    370                      375

```

(2) INFORMATION FOR SEQ ID NO:403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

```

Met Ile Tyr Leu Leu Leu Asp Thr Ile Thr Asn Arg Ala Gly Thr Glu
1      5      10      15
Arg Ala Val Ile Asn Leu Ala Asn Asn Leu His Ala Asn Gly His Arg
    20      25      30
Val Ser Leu Val Ser Val Cys Thr Lys Glu Gly Glu Pro Ser Phe Gln
    35      40      45
Val Glu Lys Gly Ile Glu Val His His Leu Gly Ile Arg Leu Tyr Gly
    50      55      60
Asn Ala Leu Ala Arg Lys Thr Val Tyr Phe Lys Ala Tyr Arg Arg Ile
65      70      75      80
Lys Ala Leu Tyr Lys Lys Arg Glu Pro Val Leu Leu Ile Gly Thr Asn
    85      90      95
Ile Phe Ile Asn Thr Ile Leu Ser Gln Ile Ser Asn Arg Gly Arg Ile
    100     105     110
Phe Thr Ile Gly Cys Glu His Ile Ser Tyr Asp Ile Ala Arg Pro Ile
    115     120     125
Thr Lys Arg Ile Arg Gly Phe Leu Tyr Ser Gly Leu Asp Ala Val Val
    130     135     140
Ala Leu Thr Lys Arg Asp Gln Gln Ser Phe Glu Ala Ile Leu Arg Gly
145     150     155     160

```

```

Arg Ser Lys Ala Tyr Val Ile Pro Asn Gln Val Ser Phe Thr Thr Val
      165      170      175
Gln Arg Asp Ala Thr Thr His Lys Gln Met Leu Ala Ile Gly Arg Leu
      180      185      190
Thr Tyr Gln Lys Gly Phe Glu Phe Met Ile Glu Asp Ala Ser Arg Val
      195      200      205
Leu Arg Glu Arg Pro Asp Trp Lys Leu Ile Ile Val Gly Asp Gly Glu
      210      215      220
Asn Glu Ser Met Leu Arg Lys Glu Ile Ala Ser Arg Asn Met Glu Ser
      225      230      235      240
Gln Ile Glu Ile His Pro Ser Thr Pro Glu Ile Arg Lys Tyr Tyr Glu
      245      250      255
Ser Ser Ala Ile Tyr Leu Met Thr Ser Arg Phe Glu Gly Leu Pro Met
      260      265      270
Val Leu Leu Glu Ala Glu Ala Tyr Ala Leu Pro Ile Ile Ser Tyr Asp
      275      280      285
Cys Pro Thr Gly Pro Arg Glu Leu Ile Glu Asn Gly Arg Asn Gly Phe
      290      295      300
Leu Val Pro Met Glu Ala His Glu Asp Phe Ala Asp Lys Leu Arg Leu
      305      310      315      320
Leu Met Asp Asp Glu Thr Leu Arg Lys Lys Met Gly Gln Glu Ser Glu
      325      330      335
Leu Met Val Lys Ser Tyr Ser Pro Ala Asn Ile Tyr Glu Cys Trp Lys
      340      345      350
Lys Leu Phe Val Glu Ile Gly Tyr Met Asn
      355      360

```

(2) INFORMATION FOR SEQ ID NO:404

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

```

Met Gly Lys Ile Ile Gly Ile Asp Leu Gly Thr Thr Asn Ser Cys Val
1      5      10      15
Ser Val Leu Glu Gly Asn Glu Pro Ile Val Ile Thr Asn Ser Glu Gly
      20      25      30
Lys Arg Thr Thr Pro Ser Val Val Ala Phe Val Asp Gly Gly Glu Arg
      35      40      45
Lys Val Gly Asp Pro Ala Lys Arg Gln Ala Ile Thr Asn Pro Thr Lys
      50      55      60
Thr Ile Tyr Ser Ile Lys Arg Phe Met Gly Glu Thr Tyr Asp Gln Val
      65      70      75      80
Ser Arg Glu Val Glu Arg Val Pro Phe Lys Val Val Arg Gly Asp Asn
      85      90      95
Asn Thr Pro Arg Val Asp Ile Asp Gly Arg Leu Tyr Thr Pro Gln Glu
      100      105      110
Ile Ser Ala Met Ile Leu Gln Lys Met Lys Lys Thr Ala Glu Asp Tyr
      115      120      125
Leu Gly Gln Glu Val Thr Glu Ala Val Ile Thr Val Pro Ala Tyr Phe
      130      135      140
Asn Asp Ala Gln Arg Gln Ala Thr Lys Glu Ala Gly Glu Ile Ala Gly
      145      150      155      160
Leu Lys Val Arg Arg Ile Val Asn Glu Pro Thr Ala Ala Ser Leu Ala
      165      170      175
Tyr Gly Leu Asp Lys Ser Asn Lys Asp Met Lys Ile Ala Val Phe Asp
      180      185      190
Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Leu Gly Asp Gly
      195      200      205
Val Phe Glu Val Lys Ser Thr Asn Gly Asp Thr His Leu Gly Gly Asp
      210      215      220
Asp Phe Asp His Val Ile Asp Trp Leu Ala Glu Phe Lys Ser
      225      230      235      240

```

Gln Glu Gly Val Asp Leu Arg Gln Asp Pro Met Ala Met Gln Arg Leu
 245 250 255
 Lys Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu Ser Ser Thr Ser Ser
 260 265 270
 Thr Glu Ile Asn Leu Pro Tyr Ile Met Pro Val Asn Gly Ile Pro Lys
 275 280 285
 His Leu Val Met Thr Leu Thr Arg Ala Lys Phe Glu Gln Leu Ala Asp
 290 295 300
 Arg Leu Ile Gln Ala Cys Val Ala Pro Cys Glu Thr Ala Leu Lys Asp
 305 310 315 320
 Ala Gly Met Ser Arg Gly Asp Ile Asp Glu Val Ile Leu Val Gly Gly
 325 330 335
 Ser Thr Arg Ile Pro Ala Ile Gln Glu Ile Val Glu Lys Ile Phe Gly
 340 345 350
 Lys Ala Pro Ser Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly
 355 360 365
 Ala Ala Ile Gln Gly Gly Val Leu Thr Gly Glu Val Lys Asp Val Leu
 370 375 380
 Leu Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Met Gly Gly
 385 390 395 400
 Val Met Thr Arg Leu Ile Asp Ala Asn Thr Thr Ile Pro Thr Lys Lys
 405 410 415
 Ser Glu Ile Phe Thr Thr Ala Val Asp Asn Gln Pro Ser Val Glu Ile
 420 425 430
 His Val Leu Gln Gly Glu Arg Ser Leu Ala Lys Asp Asn Lys Ser Ile
 435 440 445
 Gly Arg Phe Asn Leu Asp Gly Ile Ala Pro Ala Pro Arg Gln Thr Pro
 450 455 460
 Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val
 465 470 475 480
 Thr Ala His Asp Lys Ala Thr Gly Lys Lys Gln Asn Ile Arg Ile Glu
 485 490 495
 Ala Ser Ser Gly Leu Ser Asp Asp Glu Ile Lys Arg Met Lys Glu Glu
 500 505 510
 Ala Gln Ala Asn Ala Glu Ala Asp Lys Lys Glu Lys Glu Arg Ile Asp
 515 520 525
 Lys Ile Asn Gln Ala Asp Ser Met Ile Phe Gln Thr Glu Lys Gln Leu
 530 535 540
 Lys Glu Leu Gly Asp Lys Phe Pro Ala Asp Lys Lys Ala Pro Ile Asp
 545 550 555 560
 Thr Ala Leu Asp Lys Leu Lys Glu Ala His Lys Ala Gln Asp Val Ala
 565 570 575
 Ala Ile Asp Thr Ala Met Ala Glu Leu Gln Thr Ala Leu Ser Ala Ala
 580 585 590
 Gly Glu Glu Leu Tyr Lys Asn Ala Gly Ala Ala Gln Gly Gly Ala Gln
 595 600 605
 Pro Gly Pro Asp Phe Gly Gly Ala Gln Gly Pro Ser Ala Gly Asp Gln
 610 615 620
 Pro Ser Asp Asp Lys Asn Val Thr Asp Val Asp Phe Glu Glu Val Lys
 625 630 635 640

(2) INFORMATION FOR SEQ ID NO:405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Arg Tyr Asp Leu Ala Ile Ile Gly Gly Gly Pro Ala Gly Tyr Thr
 1 5 10 15
 Ala Ala Glu Arg Ala Ala Lys Gly Gly Leu Lys Thr Leu Leu Ile Glu
 20 25 30
 Lys Asn Ala Leu Gly Gly Val Cys Leu Asn Glu Gly Cys Ile Pro Thr
 35 40 45

Lys Thr Leu Leu Tyr Ser Ala Lys Val Leu His Gln Ile Ala Thr Ala
 50 55 60
 Ser Lys Tyr Ala Val Ser Gly Thr Ala Asp Gly Leu Asp Leu Gly Lys
 65 70 75 80
 Val Ile Ala Arg Lys Gly Lys Ile Ile Arg Lys Leu Thr Ala Gly Ile
 85 90 95
 Arg Ser Arg Leu Thr Glu Ala Gly Val Glu Met Val Thr Ala Glu Ala
 100 105 110
 Thr Val Thr Gly Cys Asp Ala Asp Gly Ile Ile Gly Ile Thr Ala Gly
 115 120 125
 Glu Ala Gln Tyr Lys Ala Ala Asn Leu Leu Leu Cys Thr Gly Ser Glu
 130 135 140
 Thr Phe Ile Pro Pro Ile Pro Gly Val Glu Gln Thr Glu Tyr Trp Thr
 145 150 155 160
 Asn Arg Glu Ala Leu Gln Asn Lys Glu Ile Pro Thr Ser Leu Val Ile
 165 170 175
 Ile Gly Gly Gly Val Ile Gly Met Glu Phe Ala Ser Phe Phe Asn Gly
 180 185 190
 Ile Gly Thr Gln Val His Val Val Glu Met Leu Pro Glu Ile Leu Asn
 195 200 205
 Gly Ile Asp Pro Glu His Ala Ala Met Leu Arg Ala His Tyr Glu Lys
 210 215 220
 Glu Gly Ile Lys Phe Tyr Leu Gly His Lys Val Thr Ser Val Arg Asn
 225 230 235 240
 Gly Ala Val Thr Val Glu Tyr Glu Gly Glu Ser Lys Glu Ile Glu Gly
 245 250 255
 Glu Arg Ile Leu Met Ser Val Gly Arg Arg Pro Val Leu Gln Gly Phe
 260 265 270
 Glu Ser Leu Gly Leu Val Leu Ala Gly Lys Gly Val Lys Thr Asn Glu
 275 280 285
 Arg Met Gln Thr Ser Leu Pro Asn Val Tyr Ala Ala Gly Asp Ile Thr
 290 295 300
 Gly Phe Ser Leu Leu Ala His Thr Ala Val Arg Glu Ala Glu Val Ala
 305 310 315 320
 Val Asp Gln Ile Leu Gly Lys Thr Asp Glu Thr Met Ser Tyr Arg Ala
 325 330 335
 Val Pro Gly Val Val Tyr Thr Asn Pro Glu Val Ala Gly Val Gly Glu
 340 345 350
 Thr Glu Glu Ser Leu Arg Lys Ala Gly Arg Ala Tyr Thr Val Arg Arg
 355 360 365
 Leu Pro Met Ala Phe Ser Gly Arg Phe Val Ala Glu Asn Glu Gln Gly
 370 375 380
 Asn Gly Glu Cys Lys Leu Leu Asp Glu Glu Asn Arg Leu Ile Gly
 385 390 395 400
 Ala His Leu Ile Gly Asn Pro Ala Gly Glu Leu Ile Val Thr Ala Ala
 405 410 415
 Met Ala Ile Glu Thr Gly Met Thr Asp Arg Gln Ile Glu Arg Ile Ile
 420 425 430
 Phe Pro His Pro Thr Val Gly Glu Ile Leu Lys Glu Thr Leu Ala Gly
 435 440 445
 Gly

(2) INFORMATION FOR SEQ ID NO:406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

Met Glu Leu Lys Arg Phe Leu Ser Leu Gly Leu Leu Leu Val Gly Phe
 1 5 10 15
 Ile Pro Met Lys Leu Ser Ala Gln Gln Ala Gln Pro Leu Pro Thr Asp
 20 25 30

Pro Ala Val Arg Val Gly Lys Leu Asp Asn Gly Leu Thr Tyr Phe Ile
 35 40 45
 Arg His Asn Glu Asn Pro Lys Asp Arg Ala Asp Phe Phe Ile Ala Gln
 50 55 60
 Lys Val Gly Ser Ile Leu Glu Glu Asp Ser Gln Ser Gly Leu Ala His
 65 70 75 80
 Phe Leu Glu His Met Ala Phe Asn Gly Thr Lys Asn Phe Pro Gly Lys
 85 90 95
 Asn Leu Ile Asn Tyr Leu Glu Thr Ile Gly Val Arg Phe Gly Gln Asn
 100 105 110
 Leu Asn Ala Ser Thr Gly Phe Asp Lys Thr Glu Tyr Thr Ile Met Asp
 115 120 125
 Val Pro Thr Thr Arg Gln Gly Ile Ile Asp Ser Cys Leu Leu Ile Leu
 130 135 140
 His Asp Trp Ser Asn Asn Ile Thr Leu Asp Gly His Glu Ile Asp Glu
 145 150 155 160
 Glu Arg Gly Val Ile Gln Glu Glu Trp Arg Ala Arg Arg Asp Ala Asn
 165 170 175
 Leu Arg Met Phe Glu Ala Ile Leu Ala Lys Ala Met Pro Gly Asn Lys
 180 185 190
 Tyr Ala Glu Arg Met Pro Ile Gly Leu Met Asp Val Val Leu Asn Phe
 195 200 205
 Lys His Asp Glu Leu Arg Asn Tyr Tyr Lys Lys Trp Tyr Arg Pro Asp
 210 215 220
 Leu Gln Gly Leu Val Ile Val Gly Asp Ile Asp Val Asp Tyr Val Glu
 225 230 235 240
 Asn Lys Ile Lys Glu Leu Phe Lys Asp Val Pro Ala Pro Val Asn Pro
 245 250 255
 Ala Glu Arg Ile Tyr Thr Pro Val Glu Asp Asn Asp Glu Pro Ile Val
 260 265 270
 Ala Ile Ala Thr Asp Ala Glu Ala Thr Thr Thr Gln Leu Ser Ile Ser
 275 280 285
 Phe Lys Ser Asp Pro Thr Pro Gln Glu Val Arg Gly Ser Ile Phe Gly
 290 295 300
 Leu Val Glu Asp Tyr Met Lys Gln Val Ile Thr Thr Ala Val Asn Glu
 305 310 315 320
 Arg Leu Ser Glu Ile Thr His Lys Pro Asn Ala Pro Phe Leu Ser Ala
 325 330 335
 Gly Ala Phe Phe Ser Asn Phe Met Tyr Ile Thr Gln Thr Lys Asp Ala
 340 345 350
 Phe Asn Phe Val Ala Thr Val Arg Glu Gly Glu Ala Glu Lys Ala Met
 355 360 365
 Asn Ala Leu Val Ala Glu Ile Glu Ser Leu Arg Gln Phe Gly Ile Thr
 370 375 380
 Lys Gly Glu Tyr Asp Arg Ala Arg Thr Asn Val Leu Lys Arg Tyr Glu
 385 390 395 400
 Asn Gln Tyr Asn Glu Arg Asp Lys Arg Lys Asn Asn Ala Tyr Ala Asn
 405 410 415
 Glu Tyr Ser Thr Tyr Phe Thr Asp Gly Gly Tyr Ile Pro Gly Ile Glu
 420 425 430
 Val Glu Tyr Gln Thr Val Asn Ala Phe Ala Pro Gln Val Pro Leu Glu
 435 440 445
 Ala Phe Asn Gln Ala Ile Ala Gln Met Ile Asp Pro Val Lys Asn Ala
 450 455 460
 Val Val Thr Leu Thr Gly Pro Ser Lys Ala Glu Ala Lys Ile Pro Ser
 465 470 475 480
 Glu Ala Asp Phe Leu Ala Ala Phe Lys Ala Ala Arg Gln Gln Lys Val
 485 490 495
 Glu Ala Lys Lys Asp Glu Val Ser Asp Gln Lys Leu Met Glu Lys Ala
 500 505 510
 Pro Lys Ala Gly Lys Ile Val Ser Glu Lys Lys Asp Gln Lys Phe Gly
 515 520 525
 Thr Thr Glu Leu Thr Leu Ser Asn Gly Ile Lys Val Tyr Leu Lys Lys
 530 535 540
 Thr Asp Phe Lys Ser Asn Glu Ile Leu Met Ser Ala Leu Ser Pro Gly
 545 550 555 560
 Gly Ile Leu Ser Gly Lys His Ala Pro Asn Gln Ser Val Met Asn Ser
 565 570 575
 Phe Met Asn Val Gly Gly Leu Gly Asn Phe Asp Ala Ile Gln Leu Asp
 580 585 590
 Lys Val Leu Thr Gly Arg Ser Ala Ser Val Ser Pro Ser Leu Ser Leu
 595 600 605
 Leu Ser Glu Gly Leu Ser Gly Lys Thr Thr Val Glu Asp Met Glu Thr
 610 615 620
 Phe Phe Gln Leu Ile Tyr Leu Gln Met Thr Ala Asn Arg Lys Asp Pro
 625 630 635 640
 Glu Ala Phe Lys Ala Thr Gln Glu Lys Leu Tyr Asn Asn Leu Lys Asn

645												650				655						
Gln	Glu	Ala	Asn	Pro	Met	Ala	Ala	Leu	Met	Asp	Ser	Ile	Arg	His	Thr							
660												665				670						
Met	Tyr	Gly	Asp	Asn	Pro	Met	Met	Lys	Pro	Met	Lys	Ala	Ala	Asp	Val							
675												680				685						
Glu	Lys	Val	Asn	Tyr	Asp	Gln	Val	Met	Ala	Phe	Tyr	Asn	Glu	Arg	Phe							
690												695				700						
Ala	Asp	Ala	Gly	Asp	Phe	Met	Phe	Phe	Phe	Ile	Gly	Asn	Leu	Asp	Glu							
705	710												715				720					
Ala	Lys	Met	Lys	Pro	Leu	Ile	Glu	Thr	Tyr	Leu	Ala	Ser	Leu	Pro	Asn							
725												730				735						
Leu	Lys	Arg	Gly	Asp	Lys	Met	Asn	Lys	Ala	Gln	Val	Pro	Ala	Ala	Arg							
740												745				750						
Ser	Gly	Lys	Ile	Asp	Cys	Lys	Phe	Glu	Lys	Glu	Met	Asp	Thr	Pro	Ser							
755												760				765						
Thr	Thr	Ile	Phe	Asp	Val	Val	Ser	Gly	Asn	Val	Glu	Tyr	Thr	Leu	Lys							
770	775												780									
Asn	Ser	Leu	Leu	Leu	Glu	Val	Phe	Ser	Ala	Val	Met	Asp	Gln	Val	Tyr							
785	790												795				800					
Thr	Ala	Thr	Val	Arg	Glu	Lys	Glu	Gly	Gly	Ala	Tyr	Ser	Val	Ala	Ala							
805												810				815						
Phe	Gly	Gly	Leu	Glu	Gln	Tyr	Pro	Gln	Pro	Lys	Ala	Leu	Met	Gln	Ile							
820												825				830						
Tyr	Phe	Pro	Thr	Asp	Pro	Ala	Arg	Ala	Glu	Glu	Met	Asn	Ala	Ile	Val							
835												840				845						
Phe	Ala	Glu	Leu	Glu	Lys	Leu	Ala	Lys	Glu	Gly	Pro	Asn	Val	Glu	Tyr							
850												855				860						
Phe	Lys	Lys	Thr	Ile	Glu	Asn	Leu	Asn	Lys	Gln	His	Lys	Glu	Ser	Leu							
865	870												875				880					
Arg	Glu	Asn	Arg	Phe	Trp	Leu	Glu	Ala	Met	Lys	Ala	Ser	Phe	Phe	Glu							
885												890				895						
Gly	Asn	Asp	Phe	Ile	Thr	Asp	Tyr	Glu	Ser	Val	Leu	Asn	Gly	Leu	Thr							
900												905				910						
Pro	Ala	Glu	Leu	Gln	Lys	Phe	Ala	Ala	Asp	Leu	Leu	Lys	Gln	Gln	Asn							
915												920				925						
Arg	Val	Val	Val	Met	Met	Ala	Pro	Val	Ala	Lys	Ala	Gln										
930												935				940						

(2) INFORMATION FOR SEQ ID NO:407

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

Met	Ser	Lys	Lys	Gly	Thr	Ile	Gly	Val	Thr	Ser	Asp	Asn	Ile	Phe	Pro							
1	5												10				15					
Val	Ile	Lys	Lys	Phe	Leu	Tyr	Ser	Asp	His	Glu	Ile	Phe	Leu	Arg	Glu							
20												25				30						
Ile	Val	Ser	Asn	Ala	Val	Asp	Ala	Thr	Gln	Lys	Leu	Lys	Thr	Leu	Thr							
35												40				45						
Ser	Val	Gly	Glu	Phe	Lys	Gly	Glu	Thr	Gly	Asp	Leu	Arg	Val	Thr	Val							
50												55				60						
Ser	Val	Asp	Glu	Val	Ala	Arg	Thr	Ile	Thr	Val	Ser	Asp	Arg	Gly	Val							
65	70												75				80					
Gly	Met	Thr	Glu	Glu	Glu	Val	Glu	Lys	Tyr	Ile	Asn	Gln	Ile	Ala	Phe							
85												90				95						
Ser	Ser	Ala	Glu	Glu	Phe	Leu	Glu	Lys	Tyr	Lys	Asp	Asp	Lys	Ala	Ala							
100												105				110						
Ile	Ile	Gly	His	Phe	Gly	Leu	Gly	Phe	Tyr	Ser	Ala	Phe	Met	Val	Ser							
115												120				125						
Glu	Arg	Val	Asp	Val	Ile	Thr	Arg	Ser	Phe	Arg	Glu	Asp	Ala	Thr	Ala							
130												135				140						
Val	Lys	Trp	Ser	Cys	Asp	Gly	Ser	Pro	Glu	Tyr	Thr	Leu	Glu	Pro	Ala							

145	150	155	160
Asp Lys Ala Asp Arg Gly Thr Asp Ile Val Met His Ile Asp Glu Glu			
	165	170	175
Asn Ser Glu Phe Leu Lys Lys Glu Lys Ile Glu Gly Leu Leu Gly Lys			
	180	185	190
Tyr Cys Lys Phe Leu Thr Val Pro Ile Ile Phe Gly Lys Lys Gln Glu			
	195	200	205
Trp Lys Asp Gly Lys Met Gln Asp Thr Asp Glu Asp Asn Gln Ile Asn			
	210	215	220
Asp Thr His Pro Ala Trp Thr Lys Lys Pro Ala Asp Leu Lys Asp Glu			
	225	230	235
Asp Tyr Lys Glu Phe Tyr Arg Ser Leu Tyr Pro Met Ser Glu Glu Pro			
	245	250	255
Leu Phe Trp Ile His Leu Asn Val Asp Tyr Pro Phe Asn Leu Thr Gly			
	260	265	270
Ile Leu Tyr Phe Pro Lys Ile Lys Asn Asn Leu Asp Leu Gln Arg Asn			
	275	280	285
Lys Ile Gln Leu Tyr Cys Asn Gln Val Tyr Val Thr Asp Glu Val Gln			
	290	295	300
Gly Ile Val Pro Asp Phe Leu Thr Leu Leu His Gly Val Ile Asp Ser			
	305	310	315
Pro Asp Ile Pro Leu Asn Val Ser Arg Ser Tyr Leu Gln Ser Asp Ala			
	325	330	335
Asn Val Lys Lys Ile Ser Ser His Ile Thr Lys Lys Val Ala Asp Arg			
	340	345	350
Leu Glu Glu Ile Phe Lys Asn Asp Arg Pro Thr Phe Glu Glu Lys Trp			
	355	360	365
Asp Ser Leu Lys Leu Phe Val Glu Tyr Gly Met Leu Thr Asp Glu Lys			
	370	375	380
Phe Tyr Glu Arg Ala Ala Lys Phe Phe Leu Phe Thr Asp Met Asp Gly			
	385	390	395
His Lys Tyr Thr Phe Asp Glu Tyr Arg Thr Leu Val Glu Gly Val Gln			
	405	410	415
Thr Asp Lys Asp Gly Gln Val Val Tyr Leu Tyr Ala Thr Asp Lys His			
	420	425	430
Gly Gln Tyr Ser His Val Lys Arg Ala Ser Asp Lys Gly Tyr Ser Val			
	435	440	445
Met Leu Leu Asp Gly Gln Leu Asp Pro His Ile Val Ser Leu Leu Glu			
	450	455	460
Gln Lys Leu Glu Lys Thr His Phe Val Arg Val Asp Ser Asp Thr Ile			
	465	470	475
Asn Asn Leu Ile Arg Lys Glu Glu Arg Ala Glu Val Lys Leu Ser Asp			
	485	490	495
Thr Glu Arg Ala Thr Leu Val Lys Leu Phe Glu Ala Arg Leu Pro Arg			
	500	505	510
Asp Glu Lys Lys His Phe Asn Val Ala Phe Glu Ser Leu Gly Ala Glu			
	515	520	525
Gly Glu Ala Ile Leu Ile Thr Gln Ala Glu Phe Met Arg Arg Met Arg			
	530	535	540
Asp Met Ala Gln Leu Gln Pro Gly Met Ser Phe Tyr Gly Glu Leu Pro			
	545	550	555
Asp Ser Tyr Asn Leu Val Leu Asn Thr Asp His Pro Leu Ile Asp Arg			
	565	570	575
Val Leu Ser Gly Glu Lys Glu Ser Val Glu Pro Ser Leu Thr Glu Leu			
	580	585	590
Arg Ala Lys Ile Ala Glu Leu Lys Ala Glu Glu Ala Lys Leu Leu Asp			
	595	600	605
Glu Glu Lys Gly Lys Lys Pro Glu Glu Ile Pro Val Ala Thr Lys Glu			
	610	615	620
Ala Lys Glu Asn Asn Ala Val Glu Gln Ala Lys Thr Glu Gly Ser Ile			
	625	630	635
Asn Asp Gln Leu Thr Lys Tyr Ala Gln Asp Asn Glu Leu Ile Gly Gln			
	645	650	655
Leu Ile Asp Leu Ala Leu Leu Gly Ser Gly Leu Leu Thr Gly Glu Ala			
	660	665	670
Leu Ala Glu Phe Ile Arg Arg Ser Gln Arg Leu Leu			
	675	680	

(2) INFORMATION FOR SEQ ID NO:408

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

Met	Glu	Lys	Leu	Ile	Asp	Ile	Leu	Val	Val	Asp	Asp	Asp	Val	Ala	Val
1			5					10					15		
Cys	Ala	Ala	Leu	Arg	Leu	Val	Leu	Lys	Arg	Ala	Gly	Tyr	Asn	Pro	Val
			20					25					30		
Ile	Ala	Asn	Ser	Pro	Asp	Glu	Ala	Leu	Ser	Ile	Met	Arg	Asn	Pro	Asp
		35					40					45			
Gly	Gly	Cys	Lys	Pro	Ala	Val	Ile	Leu	Met	Asp	Met	Asn	Phe	Ser	Leu
	50					55					60				
Ser	Thr	Ser	Gly	Arg	Glu	Gly	Leu	Glu	Leu	Leu	Glu	Lys	Met	Gln	Ile
65				70						75				80	
Phe	Thr	Ser	Cys	Pro	Val	Ile	Leu	Met	Thr	Ala	Trp	Ala	Ser	Ile	Pro
			85					90					95		
Leu	Ala	Val	Glu	Gly	Met	Arg	Leu	Gly	Ala	Phe	Asp	Phe	Ile	Gly	Lys
		100						105					110		
Pro	Trp	Asp	Asn	Asp	Arg	Leu	Leu	Arg	Thr	Ile	Asp	Thr	Ala	Leu	His
	115					120						125			
Leu	Ala	Ala	Pro	Ser	Ala	Val	Ala	Asn	Pro	Ser	Glu	Gln	Ser	Asp	Arg
	130					135					140				
Asp	Thr	Ala	Arg	Gln	Pro	Lys	Ala	Thr	Val	Gln	Glu	Asn	Asp	Pro	Cys
145				150						155				160	
Ala	His	Ile	Ile	Gly	Arg	Ser	Asp	Ala	Ile	Cys	Lys	Ile	Lys	Glu	Arg
			165					170						175	
Ile	Arg	Arg	Ile	Ala	Pro	Thr	His	Ala	Ser	Val	Leu	Ile	Thr	Gly	Glu
	180						185						190		
Ser	Gly	Thr	Gly	Lys	Glu	Leu	Ile	Ala	Glu	Ala	Leu	His	Arg	Gly	Ser
	195					200						205			
Lys	Arg	Ala	Ser	Ala	Pro	Phe	Val	Lys	Val	Asn	Leu	Gly	Gly	Ile	Pro
	210				215						220				
Glu	Ser	Leu	Phe	Glu	Ser	Glu	Leu	Phe	Gly	His	Lys	Lys	Gly	Ala	Phe
225				230					235					240	
Thr	Asn	Ala	Phe	Ser	Asp	Arg	Lys	Gly	Arg	Phe	Glu	Leu	Ala	Asp	Gly
			245					250						255	
Gly	Thr	Ile	Phe	Leu	Asp	Glu	Ile	Gly	Glu	Leu	Pro	Val	Gly	Asn	Gln
		260					265						270		
Val	Lys	Leu	Leu	Arg	Val	Leu	Gln	Glu	Gln	Thr	Phe	Glu	Pro	Leu	Gly
	275					280						285			
Glu	Ser	Val	Ser	His	Arg	Val	Asp	Ile	Arg	Val	Val	Ser	Ala	Thr	Asn
	290					295					300				
Ala	Ser	Leu	Glu	Arg	Met	Val	Ala	Glu	Gly	Arg	Phe	Arg	Glu	Asp	Leu
305				310						315				320	
Tyr	Tyr	Arg	Ile	Asn	Leu	Ile	His	Leu	His	Leu	Pro	Pro	Leu	Arg	Glu
			325					330						335	
Arg	Gln	Glu	Asp	Ile	Gln	Leu	Leu	Val	Glu	Ala	Phe	Ser	Glu	Ala	Phe
		340					345						350		
Ala	Gln	Ser	Asn	Gly	Leu	Pro	His	Ala	Val	Trp	Ser	Ala	Glu	Ala	Met
		355				360					365				
Arg	Arg	Ile	Cys	Ala	Met	Pro	Leu	Pro	Gly	Asn	Val	Arg	Glu	Leu	Lys
	370					375					380				
Asn	Val	Val	Glu	Arg	Thr	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Ile	Ser	
385				390						395				400	
Ala	Arg	Asp	Val	Ala	Asp	Phe	Gly	Ser	Gln	Val	Thr	Ala	Ala	Asp	His
			405						410					415	
Ser	Asp	Glu	Arg	Ala	Leu	Thr	Asp	Met	Glu	Glu	Ala	Ala	Ile	Arg	Glu
		420					425						430		
Thr	Leu	Thr	Lys	Tyr	Asn	Gly	Asn	Val	Ser	Arg	Ala	Ala	Arg	Ala	Leu
	435					440					445				
Gly	Leu	Ser	Arg	Ala	Ala	Leu	Tyr	Arg	Arg	Met	Glu	Lys	Tyr	Gly	Leu
	450				455						460				

(2) INFORMATION FOR SEQ ID NO:409

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```
Met Leu Lys Ile Lys Asn Leu His Ala Thr Val Gln Gly Lys Glu Ile
1      5      10      15
Leu Lys Gly Ile Asn Leu Glu Ile Asn Ala Gly Glu Ile His Ala Ile
20     25     30
Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ser Ser Val Leu Val
35     40     45
Gly His Pro Ser Phe Glu Val Thr Glu Gly Glu Val Thr Phe Asn Gly
50     55     60
Ile Asp Leu Leu Glu Leu Glu Pro Glu Glu Arg Ala His Leu Gly Leu
65     70     75     80
Phe Leu Ser Phe Gln Tyr Pro Val Glu Ile Pro Gly Val Ser Met Val
85     90     95
Asn Phe Met Arg Ala Ala Val Asn Glu His Arg Lys Ala Ile Gly Ala
100    105    110
Glu Pro Val Ser Ala Ser Asp Phe Leu Lys Met Met Arg Glu Lys Arg
115    120    125
Ala Ile Val Glu Leu Asp Asn Lys Leu Ala Ser Arg Ser Val Asn Glu
130    135    140
Gly Phe Ser Gly Gly Glu Lys Lys Arg Asn Glu Ile Phe Gln Met Ala
145    150    155    160
Met Leu Glu Pro Lys Leu Ala Ile Leu Asp Glu Thr Asp Ser Gly Leu
165    170    175
Asp Ile Asp Ala Leu Arg Ile Val Ala Gly Gly Val Asn Arg Leu Arg
180    185    190
Ser Pro Glu Asn Ala Ala Ile Val Ile Thr His Tyr Gln Arg Leu Leu
195    200    205
Glu Tyr Ile Lys Pro Asp Phe Val His Val Leu Tyr Lys Gly Arg Ile
210    215    220
Val Lys Ser Gly Gly Ala Glu Leu Ala Leu Thr Leu Glu Glu Lys Gly
225    230    235    240
Tyr Asp Trp Ile Lys Glu Glu Ile Gly Glu
245    250
```

(2) INFORMATION FOR SEQ ID NO:410

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```
Met Ala Lys Glu Lys Thr Ile Tyr Val Cys Arg Ser Cys Gly Thr Lys
1      5      10      15
Tyr Ala Lys Trp Gln Gly Asn Cys Asn Ala Cys Gly Glu Trp Asn Cys
20     25     30
Ile Asp Glu Glu Lys Val Pro Ala Pro Ala Ser Gly Lys His Ala Ala
35     40     45
Lys Ser Phe Met Pro Arg Glu Gln Asp Asn Arg Pro Arg Leu Leu Gln
50     55     60
Asp Val Glu Ser Gly Asp Glu Glu Arg Ile Arg Leu Gly Asp Glu Glu
65     70     75     80
Phe Asp Arg Val Leu Gly Gly Gly Ile Val Lys Gly Ala Phe Val Leu
```



```

65          70          75          80
Ala Ile Val Thr Asp Ile Asp Glu Thr Ile Leu Asp Asn Thr Pro Asn
      85          90          95
Ser Val Tyr Gln Ala Leu Arg Gly Lys Asp Tyr Asp Glu Glu Thr Trp
      100         105         110
Gly Lys Trp Cys Ala Gln Ala Asp Thr Leu Ala Gly Ala Leu
      115         120         125
Ser Phe Phe Leu His Ala Ala Asn Lys Gly Ile Glu Val Phe Tyr Val
      130         135         140
Thr Asn Arg Arg Asp Asn Leu Arg Glu Ala Thr Leu Gln Asn Leu Gln
      145         150         155         160
Arg Tyr Gly Phe Pro Phe Ala Asp Glu Glu His Leu Leu Thr Thr His
      165         170         175
Gly Pro Ser Asp Lys Glu Pro Arg Arg Leu Lys Ile Gln Glu Gln Tyr
      180         185         190
Glu Ile Val Leu Leu Ile Gly Asp Asn Leu Gly Asp Phe His His Phe
      195         200         205
Phe Asn Thr Lys Glu Glu Ser Gly Arg Lys Gln Ala Leu Gly Leu Thr
      210         215         220
Ala Gly Glu Phe Gly Arg His Phe Ile Met Leu Pro Asn Pro Asn Tyr
      225         230         235         240
Gly Ser Trp Glu Pro Ala Trp Tyr Gly Gly Lys Tyr Pro Pro Leu Pro
      245         250         255
Glu Arg Asp Lys Ala Leu Lys Gln Leu His Ser Gln Asn Ser Arg
      260         265         270

```

(2) INFORMATION FOR SEQ ID NO:412

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

```

Met Ser Thr Asn Ile Asp Val Gln Gln Ile Lys Gln Arg Phe Gly Ile
1          5          10          15
Ile Gly Ser Ser Pro Leu Met Glu His Ala Ile Arg Val Ala Ala Gln
      20         25         30
Val Ala Pro Thr Asp Met Ser Val Leu Val Thr Gly Glu Ser Gly Ser
      35         40         45
Gly Lys Glu Phe Phe Pro Gln Ile Ile His Tyr Tyr Ser Ala Arg Lys
      50         55         60
His His Ser Tyr Ile Ala Val Asn Cys Gly Ala Ile Pro Glu Gly Thr
65         70         75         80
Ile Asp Ser Glu Leu Phe Gly His Arg Lys Gly Ser Phe Thr Gly Ala
      85         90         95
Val Ser Asp Arg Lys Gly Tyr Phe Glu Glu Ala Ser Gly Gly Thr Ile
      100        105        110
Phe Leu Asp Glu Val Gly Glu Leu Pro Leu Pro Thr Gln Ala Arg Leu
      115        120        125
Leu Arg Val Leu Glu Thr Gly Glu Phe Ile Pro Val Gly Ala Ser Gln
      130        135        140
Ser Gln Lys Thr Asp Val Arg Ile Val Ala Ala Thr Asn Val Asn Leu
      145        150        155        160
Lys Glu Ala Val Ala Asn Gly Lys Phe Arg Glu Asp Leu Phe Phe Arg
      165        170        175
Leu Asn Thr Val Pro Ile Glu Val Pro Ala Leu Arg Met Arg Pro Asp
      180        185        190
Asp Val Pro Leu Leu Phe Arg Arg Phe Ala Ala Asp Ser Ala Glu Lys
      195        200        205
Tyr Arg Met Pro Pro Leu Arg Leu Ser Asp Glu Ala Arg Thr Ile Leu
      210        215        220
Met Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Arg Asn Ile Thr
      225        230        235        240
Asp Arg Leu Ser Ile Leu Glu Glu Glu Arg Thr Val Ser Ala Glu Thr

```


	100		105		110										
Pro	Ala	Ile	Val	Lys	Glu	Cys	Asn	Leu	Asp	Ala	Lys	Glu	Ile	Val	Ala
	115						120					125			
Lys	Ile	Ser	Ala	Ala	Gly	Ile	Val	Gly	Leu	Gly	Gly	Ala	Thr	Phe	Pro
	130					135						140			
Thr	His	Val	Lys	Leu	Ser	Pro	Pro	Pro	Gly	Asn	Lys	Ala	Glu	Ile	Leu
	145				150					155					160
Ile	Ile	Asn	Ala	Val	Glu	Cys	Glu	Pro	Tyr	Leu	Thr	Ser	Asp	His	Val
			165						170					175	
Leu	Met	Leu	Glu	His	Gly	Glu	Glu	Ile	Met	Ile	Gly	Val	Ser	Ile	Leu
		180						185					190		
Met	Lys	Ala	Ile	Gln	Val	Asn	Lys	Ala	Val	Ile	Gly	Val	Glu	Asn	Asn
		195					200					205			
Lys	Lys	Asp	Ala	Ile	Ala	His	Leu	Thr	Lys	Leu	Ala	Thr	Ala	Tyr	Pro
	210					215						220			
Gly	Ile	Glu	Val	Met	Pro	Leu	Lys	Val	Gln	Tyr	Pro	Gln	Gly	Gly	Glu
	225				230					235					240
Lys	Gln	Leu	Ile	Asp	Ala	Val	Ile	Arg	Lys	Gln	Val	Lys	Ser	Gly	Ala
			245						250					255	
Leu	Pro	Ile	Ser	Thr	Gly	Ala	Val	Val	Gln	Asn	Val	Gly	Thr	Val	Phe
		260						265						270	
Ala	Val	Tyr	Glu	Ala	Val	Gln	Lys	Asn	Lys	Pro	Leu	Val	Glu	Arg	Ile
	275						280					285			
Val	Thr	Val	Thr	Gly	Lys	Lys	Leu	Ser	Arg	Pro	Ser	Asn	Leu	Leu	Val
	290					295					300				
Arg	Ile	Gly	Thr	Pro	Ile	Ala	Ala	Leu	Ile	Glu	Ala	Ala	Gly	Gly	Leu
	305				310					315					320
Pro	Glu	Asn	Thr	Gly	Lys	Ile	Ile	Gly	Gly	Gly	Pro	Met	Met	Gly	Arg
			325						330					335	
Ala	Leu	Leu	Ser	Pro	Asp	Val	Pro	Val	Thr	Lys	Gly	Ser	Ser	Gly	Val
		340					345							350	
Leu	Ile	Leu	Asp	Arg	Glu	Glu	Ala	Val	Arg	Lys	Pro	Met	Arg	Asp	Cys
		355					360					365			
Ile	Arg	Cys	Ala	Lys	Cys	Val	Gly	Val	Cys	Pro	Met	Gly	Leu	Asn	Pro
	370					375					380				
Ala	Phe	Leu	Met	Arg	Asp	Thr	Leu	Tyr	Lys	Ser	Trp	Glu	Thr	Ala	Glu
	385				390					395					400
Lys	Gly	Asn	Val	Val	Asp	Cys	Ile	Glu	Cys	Gly	Ser	Cys	Ser	Phe	Thr
			405						410					415	
Cys	Pro	Ala	Asn	Arg	Pro	Leu	Leu	Asp	Tyr	Ile	Arg	Gln	Ala	Lys	Lys
			420					425					430		
Thr	Val	Met	Gly	Ile	Gln	Arg	Ala	Arg	Lys	Gln					
	435						440								

(2) INFORMATION FOR SEQ ID NO:415

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

Met	Lys	Arg	Ile	Gln	Leu	Thr	Leu	Ile	Ala	Leu	Phe	Ala	Ala	Val	Ala
1			5						10					15	
Gly	Leu	Val	Ala	Gln	Asn	Ala	Tyr	Glu	Gly	Val	Ile	Ser	Tyr	Lys	Ile
		20					25					30			
Ser	Leu	Asp	Lys	Thr	Gly	Asn	Lys	Val	Val	Leu	Asn	Gly	Ala	Ala	Asp
		35					40					45			
Met	Ser	Asn	Leu	Lys	Leu	Lys	Ser	Thr	Gln	Met	Ile	Ile	Val	Thr	Pro
	50					55					60				
Ile	Leu	Arg	Ser	Glu	Asp	Gly	Thr	Ser	Arg	Val	Glu	Phe	Pro	Ser	Val
	65				70				75				80		
Val	Ile	Thr	Gly	Arg	Asn	Arg	Thr	Lys	Ala	Leu	Lys	Arg	Glu	Ile	Ala
			85					90					95		
Phe	Ser	Ser	Ala	Leu	Pro	Gln	Ala	Lys	His	Ala	Ala	Gln	Tyr	Ile	Arg

100	105	110
Arg His Asn Gly Lys Ser Glu Gln Phe Ala Phe Thr Gly Glu His Ala		
115	120	125
Tyr Ala Ser Trp Met Met Asp Ala Lys Phe Val Val Arg Glu Glu Val		
130	135	140
Arg Gly Cys Ala Lys Cys Pro Val Gly Leu Ser Ser Asn Ile Val Pro		
145	150	155
Phe Asp Pro Leu Phe Asn Pro Ala Glu Ala Pro Tyr Leu Leu Ala His		
165	170	175
Ile Thr Pro Ala Glu Glu Val Glu Lys Gln Arg Glu Ser Ser Phe Asp		
180	185	190
Ala Tyr Ile Asn Phe Lys Val Asn Lys Ala Asp Val Leu Pro Glu Tyr		
195	200	205
Arg Asn Asn Lys Ala Glu Leu Glu Lys Ile Lys Glu Phe Val Ser Thr		
210	215	220
Val Lys Ala Asn Pro Asn Tyr Ser Val Asn Lys Met Ile Ile Glu Gly		
225	230	235
Phe Ala Ser Pro Glu Ala Ser Ile Ala His Asn Lys Ala Leu Ser Glu		
245	250	255
Arg Arg Ala Lys Arg Leu Ala Glu Glu Leu Val Arg Lys Tyr Gly Lys		
260	265	270
Thr Leu Pro Asn Ile Thr Thr Glu Phe Gly Gly Glu Asp Trp Lys Gly		
275	280	285
Leu Lys Leu Ala Ile Glu Lys Ser Asp Ile Ala Asp Arg Asp Arg Val		
290	295	300
Leu Glu Ile Ile Asn Ser Asp Lys Tyr Ala Asp Asp Ala Arg Glu		
305	310	315
Gln Ala Leu Lys Gln Leu Ser Ser Tyr Arg Tyr Ile Leu Asp Gln Ile		
325	330	335
Tyr Pro Asn Leu Arg Arg Asn Thr Ile Thr Met Gly Tyr Ile Val Arg		
340	345	350
Asp Tyr Thr Leu Glu Glu Ala Arg Glu Ile Ile Lys Thr Ala Pro Lys		
355	360	365
Glu Leu Ser Glu Ala Glu Met Tyr Arg Val Ala Met Ser Tyr Pro Glu		
370	375	380
Gly His Gln Glu Arg Leu Phe Ala Leu Asn Thr Thr Leu Lys Tyr Phe		
385	390	395
Pro Glu Ser Val Thr Gly Arg Ile Asn Leu Ala Val Ala Ala Phe Asn		
405	410	415
Gly Gly Asp Val Gln Gln Ala Ile Ala Leu Leu Ser Pro Ile Gln Thr		
420	425	430
Glu Lys Gly Val Ser Asn Ile Leu Gly Ala Ala Tyr Ala Arg Thr Gly		
435	440	445
Asp Phe Ala Arg Ala Glu Thr Phe Phe Arg Lys Ala Val Ala Glu Gly		
450	455	460
Asp Ala Asn Ala Gln Arg Asn Leu Asp Met Leu Leu Gly Lys Lys		
465	470	475

(2) INFORMATION FOR SEQ ID NO:416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

Met Ala Glu Lys Arg Asp Tyr Tyr Glu Val Leu Gly Val Ser Lys Asn	
1	5
Ala Thr Asp Asp Glu Leu Lys Lys Ala Tyr Arg Lys Lys Ala Ile Gln	10
20	25
Tyr His Pro Asp Lys Asn Pro Gly Asp Lys Glu Ala Glu Glu His Phe	30
35	40
Lys Glu Val Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Gln Lys Arg	45
50	55
Ser Gln Tyr Asp Gln Phe Gly His Ala Gly Leu Gly Gly Ala Ala Gly	60

65		70		75		80									
Gly	Gly	Phe	Ser	Gly	Gly	Met	Ser	Met	Glu	Asp	Ile	Phe	Ser	Arg	
			85					90					95		
Phe	Gly	Asp	Leu	Phe	Gly	Gly	Phe	Gly	Phe	Gly	Gly	Phe	Ser	Asp	
			100				105					110			
Met	Gly	Gly	Gly	Ser	Arg	Arg	Arg	Val	Arg	Arg	Gly	Ser	Asp	Leu	Arg
			115				120					125			
Val	Arg	Val	Lys	Leu	Ser	Leu	Ala	Asp	Ile	Ser	Lys	Gly	Val	Glu	Lys
			130				135					140			
Lys	Val	Lys	Val	Lys	Lys	Gln	Val	Val	Cys	Ser	Lys	Cys	Arg	Gly	Asp
			145			150				155					160
Gly	Thr	Glu	Glu	Ala	Asn	Gly	Lys	Thr	Thr	Cys	Gln	Thr	Cys	His	Gly
				165					170					175	
Thr	Gly	Val	Val	Thr	Arg	Val	Ser	Asn	Thr	Phe	Leu	Gly	Ala	Met	Gln
			180					185						190	
Thr	Gln	Ser	Thr	Cys	Pro	Thr	Cys	His	Gly	Glu	Gly	Glu	Ile	Ile	Thr
			195				200					205			
Lys	Pro	Cys	Ser	Lys	Cys	Lys	Gly	Glu	Gly	Val	Glu	Ile	Gly	Glu	Glu
			210			215					220				
Val	Ile	Ser	Phe	His	Ile	Pro	Ala	Gly	Val	Ala	Glu	Gly	Met	Gln	Met
					230					235					240
Ser	Val	Asn	Gly	Lys	Gly	Asn	Ala	Ala	Pro	Arg	Gly	Gly	Val	Asn	Gly
				245					250					255	
Asp	Leu	Ile	Val	Val	Ile	Ala	Glu	Glu	Pro	Asp	Pro	Asn	Leu	Ile	Arg
			260					265					270		
Asn	Gly	Asn	Asp	Leu	Ile	Tyr	Asn	Leu	Leu	Ile	Ser	Val	Pro	Leu	Ala
			275				280					285			
Ile	Lys	Gly	Gly	Ser	Val	Glu	Val	Pro	Thr	Ile	Asp	Gly	Arg	Ala	Lys
			290			295					300				
Ile	Arg	Ile	Glu	Ala	Gly	Thr	Gln	Pro	Gly	Lys	Met	Leu	Arg	Leu	Arg
					310					315					320
Asn	Lys	Gly	Leu	Pro	Ser	Val	Asn	Gly	Tyr	Gly	Met	Gly	Asp	Gln	Leu
				325					330					335	
Val	Asn	Val	Asn	Val	Tyr	Ile	Pro	Glu	Ser	Ile	Asp	Ala	Lys	Asp	Glu
			340					345					350		
Gln	Ala	Ile	Ala	Ala	Met	Glu	Asn	Ser	Asp	Ser	Phe	Lys	Pro	Thr	Asp
			355			360					365				
Ala	Ala	Arg	Lys	Asp	Ile	Asp	Lys	Lys	Tyr	Arg	Glu	Met	Leu	Asp	
			370			375					380				

(2) INFORMATION FOR SEQ ID NO:417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

Met	Lys	Lys	Leu	Ile	Leu	Ala	Thr	Leu	Gly	Leu	Met	Ala	Ile	Ala	Met
1			5						10				15		
Leu	Ser	Cys	Ser	Ser	Asn	Asn	Lys	Asp	Leu	Glu	Asn	Lys	Gly	Glu	Ala
			20					25				30			
Thr	Leu	Leu	Val	Thr	Phe	Gly	Ser	Ser	Tyr	Lys	Ala	Pro	Arg	Glu	Thr
			35				40					45			
Tyr	Ala	Lys	Ile	Glu	Lys	Thr	Phe	Ala	Ala	Ala	Tyr	Pro	Asp	Gln	Arg
			50			55			60						
Ile	Ser	Trp	Thr	Tyr	Thr	Ser	Ser	Ile	Ile	Arg	Lys	Lys	Leu	Ala	Gln
			65			70			75				80		
Gln	Gly	Ile	Tyr	Ile	Asp	Ala	Pro	Asp	Glu	Ala	Leu	Glu	Lys	Leu	Ala
			85					90				95			
Arg	Leu	Gly	Tyr	Lys	Lys	Ile	Asn	Val	Gln	Ser	Leu	His	Val	Ile	Pro
			100				105					110			
Gly	Arg	Glu	Tyr	Asp	Glu	Met	Ile	Asp	Phe	Val	Asn	Lys	Phe	Lys	Ala
			115				120					125			
Ala	His	Ser	Asp	Ile	Thr	Val	Lys	Val	Gly	Ala	Pro	Leu	Phe	Asp	Thr

130		135		140	
Asp Glu Asp Met Arg Glu Val Ala Glu Ile Leu His Lys Arg Phe Gln					
145	150	155	160		
Gln Thr Ile Glu Lys Gly Glu Ala Ile Val Phe Met Gly His Gly Thr					
	165	170	175		
Glu His Ala Ala Asn Asp Arg Tyr Ala Arg Ile Asn Lys Ile Met Lys					
	180	185	190		
Asn Tyr Ser Lys Phe Met Ile Val Gly Thr Val Glu Ser Asp Pro Ser					
	195	200	205		
Ile Asn Asp Val Ile Ala Glu Leu Lys Glu Thr Gly Ala Thr Ala Val					
	210	215	220		
Thr Met Met Pro Leu Met Ser Val Ala Gly Asp His Ala Thr Asn Asp					
225	230	235	240		
Met Ala Gly Asp Glu Asp Asp Ser Trp Lys Thr Leu Leu Thr Asn Ala					
	245	250	255		
Gly Tyr Thr Val Ser Ile Asp Lys Leu Asp Asn Gly Asn Phe Ser Ala					
	260	265	270		
Leu Gly Asp Ile Glu Glu Ile Arg Asn Ile Trp Leu Lys His Met Lys					
	275	280	285		
Ala Thr Ser Ala Arg					
290					

(2) INFORMATION FOR SEQ ID NO:418

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

Met Thr Ser Val Ser His Leu Arg Thr Ile Ser Val Ala Gly Ile Leu					
1	5	10	15		
Ala Ala Leu Gly Gly Ala Val Leu Ile Leu Phe Gly Val Asn Leu Phe					
	20	25	30		
Leu Gly Ser Val Ala Ile Pro Met Ser Glu Ile Phe Arg His Leu Phe					
	35	40	45		
Ser Asp Arg Pro Glu Gly Gly Glu Ala Leu Val His Tyr Asn Ile Leu					
	50	55	60		
Trp Lys Ser Arg Leu Pro Glu Ala Leu Thr Ala Ala Phe Ala Gly Ala					
65	70	75	80		
Gly Leu Ser Val Ser Gly Leu Gln Met Gln Thr Val Phe Arg Asn Pro					
	85	90	95		
Leu Ala Gly Pro Ser Val Leu Gly Ile Ser Ser Gly Ala Ser Leu Gly					
	100	105	110		
Val Ala Leu Val Val Leu Leu Ser Gly Ser Leu Gly Gly Val Ala Leu					
	115	120	125		
Ser Ser Leu Gly Tyr Met Gly Glu Val Ala Met Asn Ile Ala Ala Ala					
	130	135	140		
Val Gly Ser Leu Ala Val Met Gly Leu Ile Val Phe Val Ser Thr Lys					
145	150	155	160		
Val Arg Ser His Val Thr Leu Leu Ile Ile Gly Val Met Ile Gly Tyr					
	165	170	175		
Val Ala Thr Ala Val Ile Gly Val Phe Lys Phe Phe Ser Ile Glu Glu					
	180	185	190		
Asp Ile Arg Ala Tyr Val Ile Trp Gly Leu Gly Ser Phe Ser Arg Ala					
	195	200	205		
Thr Asp Ser Gln Leu Ser Phe Phe Ala Ile Leu Met Leu Ile Phe Ile					
	210	215	220		
Pro Ala Gly Met Leu Leu Val Lys Gln Leu Asn Leu Leu Leu Gly					
225	230	235	240		
Glu Ser Tyr Ala Arg Asn Leu Gly Leu Asn Thr Arg Arg Ala Arg Leu					
	245	250	255		
Leu Val Ile Ser Ser Ala Gly Leu Leu Ile Ala Thr Val Thr Ala Tyr					
	260	265	270		
Cys Gly Pro Ile Gly Phe Leu Gly Met Ala Val Pro His Leu Ala Arg					

275	280	285
Val Ile Phe His Thr Ser Asp His Arg Ile Leu Met Pro Ala Thr Cys		
290	295	300
Leu Ile Gly Ser Ala Leu Ala Leu Phe Cys Asn Ile Ile Ala Arg Met		
305	310	315
Pro Gly Phe Glu Gly Ala Leu Pro Val Asn Ser Val Thr Ala Leu Val		
	325	330
Gly Ala Pro Ile Ile Val Thr Val Leu Phe Arg Arg Arg Arg Phe Lys		
	340	345
Glu Glu Thr Asp		350
355		

(2) INFORMATION FOR SEQ ID NO:419

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

Met	Arg	Thr	Lys	Thr	Ile	Phe	Phe	Ala	Ile	Ile	Ser	Phe	Ile	Ala	Leu
1				5					10					15	
Leu	Ser	Ser	Ser	Leu	Ser	Ala	Gln	Ser	Lys	Ala	Val	Leu	Thr	Gly	Ser
			20				25						30		
Val	Ser	Asp	Ala	Glu	Thr	Gly	Glu	Pro	Leu	Ala	Gly	Ala	Arg	Ile	Glu
		35				40						45			
Val	Lys	His	Thr	Asn	Ile	Val	Ala	Gly	Ala	Asp	Ala	Gly	Gly	His	Phe
	50				55				60						
Glu	Ile	Lys	Asn	Leu	Pro	Ala	Gly	Gln	His	Thr	Ile	Ile	Cys	Ser	Leu
65				70					75					80	
Gly	Gly	Tyr	Gly	Gln	Lys	Glu	Glu	Val	Val	Ala	Ile	Glu	Ala	Gly	Gln
			85					90						95	
Thr	Lys	Thr	Ile	Ser	Phe	Ala	Leu	Arg	Leu	Arg	Thr	Asn	Asn	Leu	Glu
		100					105					110			
Glu	Val	Val	Val	Thr	Gly	Thr	Gly	Thr	Arg	Tyr	Arg	Leu	Val	Asp	Ala
	115				120							125			
Pro	Val	Ala	Thr	Glu	Val	Leu	Thr	Ala	Lys	Asp	Ile	Ala	Ser	Phe	Ser
	130				135					140					
Ala	Pro	Thr	Ser	Glu	Ala	Leu	Leu	Gln	Gly	Leu	Ser	Pro	Ser	Phe	Asp
145			150					155						160	
Phe	Gly	Pro	Asn	Leu	Met	Gly	Ser	Phe	Met	Gln	Leu	Asn	Gly	Leu	Ser
		165					170						175		
Ser	Lys	Tyr	Ile	Leu	Ile	Leu	Ile	Asp	Gly	Lys	Arg	Val	Tyr	Gly	Asp
	180				185							190			
Val	Gly	Gly	Gln	Ala	Asp	Leu	Ser	Arg	Ile	Ser	Pro	Asp	Gln	Ile	Glu
	195				200						205				
Arg	Ile	Glu	Leu	Val	Lys	Gly	Ala	Ser	Ser	Ser	Leu	Tyr	Gly	Ser	Asp
	210				215						220				
Ala	Ile	Ala	Gly	Val	Ile	Asn	Val	Ile	Thr	Lys	Lys	Asn	Thr	Asn	Arg
225			230					235						240	
Leu	Ser	Ala	Tyr	Thr	Ser	His	Arg	Ile	Ser	Lys	Tyr	Asn	Asp	Arg	Gln
		245						250					255		
Thr	Asn	Thr	Ser	Leu	Asp	Ile	Asn	Ile	Gly	Lys	Phe	Ser	Ser	Asn	Thr
	260				265							270			
Asn	Tyr	Phe	Phe	Tyr	His	Thr	Asp	Gly	Trp	Gln	Asn	Ser	Pro	Phe	Glu
	275				280							285			
Ile	Lys	Lys	Lys	Lys	Gly	Ser	Gly	Glu	Pro	Val	Leu	Glu	Glu	Thr	Tyr
	290				295						300				
Lys	Lys	Thr	Phe	Arg	Ala	Gln	Glu	Asn	Gln	Gly	Val	Ser	Gln	Ser	Leu
305			310					315						320	
Ser	Tyr	Tyr	Ala	Thr	Asn	Asn	Leu	Ser	Phe	Ser	Gly	Asn	Val	Gln	Tyr
		325						330					335		
Asn	Lys	Arg	Gln	Ile	Phe	Thr	Pro	Thr	Phe	Ser	Glu	Lys	Lys	Ala	Tyr
	340				345							350			
Asp	Met	Asp	Tyr	Arg	Ala	Leu	Thr	Ala	Ser	Leu	Gly	Thr	Asn	Tyr	Leu


```

      35      40      45
Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser
50      55      60
Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala
65      70      75      80
Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala
      85      90      95
Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln
100      105      110
Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala
115      120      125
Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly
130      135      140
Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala
145      150      155      160
Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met Ala Arg
165      170      175
Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu Val Asp
180      185      190
Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn Glu Thr
195      200      205
Tyr Leu Ile Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe Pro Lys
210      215      220
Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile Ala Glu
225      230      235      240
Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe Leu Ser
245      250      255
Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala Leu Asn
260      265      270
Glu Glu Lys Val Arg Phe Lys Ile Thr Phe Ile Lys Asn Met Gly Thr
275      280      285
Tyr Ala Ala Trp Lys Ala Thr Lys Thr Thr Gly Gln Tyr Asp Leu Lys
290      295      300
Thr Phe Glu Val Lys Ala Thr Leu Ala Asp Lys Asp Lys Ala Gln Lys
305      310      315      320
Leu Arg Pro Gly Met Ser Val Ile Ile Arg Lys
325      330

```

(2) INFORMATION FOR SEQ ID NO:421

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

```

Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser Phe Ser Val Leu Leu
1      5      10      15
Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val Val Tyr Leu Gln Asp
20      25      30
Ile Gln Thr Phe Asn Arg Glu Ile Ala Lys Pro Tyr Asp Val Lys
35      40      45
Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val Ser Ser Arg Asp Pro
50      55      60
Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr Thr Arg Ala Leu Ala
65      70      75      80
Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly Phe Leu Val Asp Ser
85      90      95
Lys Gly Tyr Ile Asn Tyr Pro Ile Leu Gly Gln Ile Tyr Val Glu Gly
100      105      110
Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln Lys Arg Ile Ile Ser
115      120      125
Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val Gln Leu Gln Asn Phe
130      135      140
Lys Val Ser Val Leu Gly Glu Val Asn His Pro Gly Ser Met Ser Val

```



```

145          150          155          160
Lys Gly Glu Arg Ile Thr Leu Leu Glu Ala Ile Gly Met Ala Gly Asp
          165          170          175
Leu Thr Ile Tyr Gly Arg Arg Asp Arg Val Phe Val Ile Arg Glu Thr
          180          185          190
Asp Gly His Arg Glu Val Phe Gln Thr Asp Leu Arg Lys Ala Asp Leu
          195          200          205
Leu Ala Ser Pro Val Tyr Tyr Leu His Gln Asn Asp Val Ile Tyr Val
          210          215          220
Glu Pro Asn Asp Lys Lys Thr Gln Met Ser Glu Ile Asn Gln Asn Asn
225          230          235          240
Asn Val Asn Val Trp Leu Ser Val Thr Ser Thr Leu Val Ser Ile Ser
          245          250          255
Thr Leu Thr Ile Thr Ile Ile Asp Lys Thr Lys
          260          265

```

(2) INFORMATION FOR SEQ ID NO:422

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

```

Met Lys Lys Thr Asn Leu Phe Leu Ser Leu Leu Val Ile Phe Ile Thr
1          5          10          15
Gly Ser Phe Met Thr Ala Cys Ala Gln Lys Ser Lys Thr Asn Lys Leu
          20          25          30
Thr Glu Glu Asp Arg Ser Arg Asn Glu Tyr Val Gln Ser Met Asp Val
          35          40          45
Leu Ser Asn Ile Ile Gly Asn Val Arg Leu Tyr Phe Val Asp Thr Ile
          50          55          60
Ser Ile Lys His Met Thr Arg Arg Gly Ile Asp Ala Met Leu Gly Gly
65          70          75          80
Leu Asp Pro Tyr Thr Glu Tyr Ile Pro Tyr Glu Glu Met Asp Glu Leu
          85          90          95
Lys Leu Met Thr Thr Gly Glu Tyr Ala Gly Val Gly Ala Ile Ile Ser
          100          105          110
Gln Arg Pro Asp Ser Ala Val Ile Ile Gln Arg Pro Met Glu Gly Met
          115          120          125
Pro Ala Asp Glu Ala Gly Leu Ile Ala Gly Asp Arg Ile Leu Thr Ile
          130          135          140
Asp Gly Lys Asp Phe Arg Lys Ser Thr Thr Pro Lys Val Ser Gln Ala
145          150          155          160
Leu Lys Gly Ile Ala Gly Thr Val Ala Lys Val Thr Val Met Arg Tyr
          165          170          175
Gly Glu Thr Lys Pro Arg Thr Phe Ser Val Lys Arg Gln Lys Val Ile
          180          185          190
Met Asn Ser Val Thr Tyr Ser Gly Met Leu Asp Gly Ser Ile Gly Tyr
          195          200          205
Ile Arg Leu Asn Asn Phe Thr Asp Lys Ser Ala Glu Glu Val Arg Thr
          210          215          220
Ala Leu Leu Asp Leu Arg Asp Lys Gln Gly Ala Lys Gly Leu Ile Leu
225          230          235          240
Asp Leu Arg Gly Asn Gly Gly Gly Leu Met Gln Ala Ala Ile Glu Ile
          245          250          255
Val Asn Leu Phe Val Pro Lys Gly Lys Glu Val Val Thr Thr Lys Gly
          260          265          270
Arg Ile Ala Glu Ser Ala Ser Val Phe Arg Thr Leu Thr Glu Pro Ile
          275          280          285
Asp Thr Lys Leu Pro Ile Val Val Leu Ile Asp Gly Gln Ser Ala Ser
          290          295          300
Ser Ser Glu Ile Val Ala Gly Ala Leu Gln Asp Met Asp Arg Ala Val
305          310          315          320
Leu Met Gly Gln Lys Ser Tyr Gly Lys Gly Leu Val Gln Thr Thr Arg

```


195					200					205					
Asp	Pro	Glu	Arg	Val	Arg	Thr	Leu	Leu	Gln	Arg	Ser	Ala	Asn	Leu	Gln
210						215					220				
Phe	Trp	Arg	Thr	Tyr	Lys	Phe	Glu	Glu	Val	Ser	Gly	Asp	Leu	Ile	Ala
225					230					235					240
Ala	Asn	Asp	Arg	Leu	Ser	Glu	Leu	Ala	Met	Asn	Asn	Thr	Asp	Ala	Thr
				245					250					255	
Pro	Glu	Thr	Glu	Pro	Ala	Thr	Thr	Asp	Ser	Val	Ala	Ala	Thr	Ala	Asp
				260				265					270		
Ser	Ala	Ala	Val	Gln	Ala	Val	Ala	Asp	Ser	Ala	Thr	Val	Ala	Gln	Lys
				275				280					285		
Glu	Ala	Lys	Asp	Ala	Thr	Arg	Lys	Asp	Ala	Leu	Phe	Ser	Leu	Leu	Thr
290					295						300				
Pro	Val	Asn	Arg	Gly	Gly	Ala	Val	Val	Gly	Val	Ala	Arg	Arg	Ala	Asn
305				310						315					320
Met	Ala	Gln	Ile	Ser	Glu	Met	Leu	Gln	Gln	Ala	His	Asp	Leu	Lys	Val
				325					330					335	
Thr	Arg	Glu	Asp	Val	Leu	Phe	Leu	Trp	Gly	Ala	Lys	Ala	Ile	Glu	Asp
				340				345					350		
Pro	Glu	Thr	Lys	Lys	Glu	Thr	Asp	Leu	Tyr	Glu	Leu	Tyr	Ala	Ile	Arg
				355			360					365			
Thr	Asn	Arg	Thr	Gly	Asp	Pro	Asp	Leu	Gly	Gly	Asp	Val	Val	Thr	Ser
370					375						380				
Ala	Lys	Ser	Asp	Ile	Gln	Asn	Asp	Phe	Gly	Arg	Ser	Glu	Pro	Ile	Val
385					390					395					400
Ser	Met	Thr	Met	Asn	Glu	Glu	Gly	Ala	Arg	Lys	Trp	Ala	Arg	Ile	Thr
				405					410					415	
Lys	Asp	Asn	Val	Gly	Arg	Ala	Ile	Ala	Ile	Val	Leu	Asp	Gly	Val	Val
				420				425					430		
Tyr	Ser	Ala	Pro	Asn	Val	Asn	Asp	Glu	Ile	Thr	Gly	Gly	Arg	Ser	Gln
				435			440					445			
Ile	Ser	Gly	His	Phe	Thr	Val	Glu	Glu	Ala	Gly	Asp	Leu	Ala	Asn	Val
				450			455				460				
Leu	Asn	Ser	Gly	Lys	Met	Asp	Ala	Thr	Val	Ser	Ile	Glu	Gln	Glu	Asn
465					470					475				480	
Val	Ile	Gly	Pro	Thr	Leu	Gly	Ala	Glu	Ser	Ile	Lys	Ala	Gly	Phe	Leu
				485					490					495	
Ser	Phe	Leu	Leu	Ala	Leu	Val	Ile	Leu	Met	Cys	Tyr	Met	Cys	Leu	Ala
				500				505					510		
Tyr	Gly	Phe	Leu	Pro	Gly	Leu	Ile	Ala	Asn	Gly	Ala	Leu	Ile	Val	Asn
				515			520					525			
Ser	Phe	Phe	Thr	Leu	Gly	Val	Leu	Ala	Ser	Phe	His	Ala	Val	Leu	Thr
				530			535				540				
Leu	Ser	Gly	Ile	Ala	Gly	Leu	Val	Leu	Thr	Leu	Gly	Met	Ala	Val	Asp
545					550					555				560	
Ala	Asn	Val	Leu	Ile	Phe	Glu	Arg	Ile	Lys	Glu	Glu	Leu	Arg	Ala	Gly
				565					570					575	
Lys	Thr	Pro	Ile	Arg	Ala	Val	Thr	Asp	Gly	Tyr	Gly	Asn	Ala	Phe	Ser
				580				585					590		
Ala	Ile	Phe	Asp	Ser	Asn	Val	Thr	Thr	Ile	Ile	Thr	Gly	Ile	Ile	Leu
				595			600					605			
Phe	Leu	Tyr	Gly	Thr	Gly	Pro	Ile	Arg	Gly	Phe	Ala	Thr	Thr	Leu	Ile
				610			615				620				
Ile	Gly	Leu	Ile	Ala	Ser	Phe	Ile	Thr	Ala	Val	Phe	Leu	Thr	Arg	Ile
625					630					635				640	
Val	Phe	Glu	Lys	Leu	Ala	Lys	Lys	Gly	Arg	Leu	Asp	Lys	Ile	Thr	Phe
				645					650					655	
Thr	Thr	Ser	Ile	Thr	Arg	Asn	Leu	Leu	Val	Asn	Pro	Ser	Tyr	Asn	Ile
				660				665					670		
Leu	Gly	Lys	Arg	Lys	Thr	Gly	Phe	Ile	Ile	Pro	Val	Ile	Ile	Ile	Val
				675			680					685			
Leu	Gly	Leu	Ile	Ala	Ser	Phe	Thr	Ile	Gly	Leu	Asn	Arg	Gly	Ile	Glu
				690			695				700				
Phe	Ser	Gly	Gly	Arg	Asn	Tyr	Val	Val	Lys	Phe	Asp	Gln	Pro	Val	Ser
705					710					715				720	
Ser	Glu	Ala	Val	Arg	Ser	Ala	Leu	Ser	Ser	Pro	Leu	Gln	Glu	Lys	Val
				725					730					735	
Leu	Val	Thr	Ser	Ile	Gly	Thr	Glu	Gly	Thr	Glu	Val	Arg	Ile	Ser	Thr
				740				745					750		
Asn	Tyr	Lys	Ile	Gln	Glu	Glu	Ser	Glu	Glu	Thr	Glu	Ala	Glu	Ile	Thr
				755				760					765		
Asp	Lys	Leu	Tyr	Gln	Ser	Leu	Lys	Gly	Phe	Tyr	Thr	Gln	Gln	Pro	Thr
				770			775				780				
Ala	Asp	Gln	Phe	Leu	Asp	Asn	Ile	Ile	Ser	Ser	Gln	Lys	Val	Ser	Pro
785					790					795				800	
Ser	Met	Ser	Ser	Asp	Ile	Thr	Arg	Gly	Ala	Ile	Trp	Ala	Val	Leu	Leu
				805					810					815	

```

Ser Met Ile Phe Met Ala Ile Tyr Ile Leu Ile Arg Phe Arg Asp Ile
      820      825      830
Ser Phe Ser Ala Gly Val Phe Val Ser Val Ala Ala Thr Thr Phe Cys
      835      840      845
Ile Ile Ala Leu Tyr Ala Leu Leu Trp Lys Ile Leu Pro Phe Thr Met
      850      855      860
Glu Ile Asp Gln Asn Phe Ile Ala Ala Ile Leu Ala Ile Ile Gly Tyr
      865      870      875      880
Ser Leu Asn Asp Thr Val Val Val Phe Asp Arg Ile Arg Glu Thr Met
      885      890      895
Lys Leu Tyr Pro Asn Arg Asp Arg Tyr Gln Val Ile Asn Asp Ala Leu
      900      905      910
Asn Ser Thr Leu Gly Arg Thr Leu Asn Thr Ser Leu Thr Thr Phe Ile
      915      920      925
Val Met Leu Val Ile Phe Ile Phe Gly Gly Ala Thr Met Arg Ser Phe
      930      935      940
Thr Phe Ser Ile Leu Leu Gly Ile Val Ile Gly Thr Tyr Ser Thr Leu
      945      950      955      960
Phe Val Ala Thr Pro Leu Ala Tyr Glu Ile Gln Lys Arg Lys Leu Asn
      965      970      975
Lys Ala Ala Lys Lys
      980

```

(2) INFORMATION FOR SEQ ID NO:424

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

```

Met Lys Arg Met Thr Leu Phe Phe Leu Cys Leu Leu Thr Ser Ile Gly
1      5      10      15
Trp Ala Met Ala Gln Asn Arg Thr Val Lys Gly Thr Val Ile Ser Ser
      20      25      30
Glu Asp Asn Glu Pro Leu Ile Gly Ala Asn Val Val Val Val Gly Asn
      35      40      45
Thr Thr Ile Gly Ala Ala Thr Asp Leu Asp Gly Asn Phe Thr Leu Ser
      50      55      60
Val Pro Ala Asn Ala Lys Met Leu Arg Val Ser Tyr Ser Gly Met Thr
65      70      75      80
Thr Lys Glu Val Ala Ile Ala Asn Val Met Lys Ile Val Leu Asp Pro
      85      90      95
Asp Ser Lys Val Leu Glu Gln Val Val Val Leu Gly Tyr Gly Thr Gly
      100      105      110
Gln Lys Leu Ser Thr Val Ser Gly Ser Val Ala Lys Val Ser Ser Glu
      115      120      125
Lys Leu Ala Glu Lys Pro Val Ala Asn Ile Met Asp Ala Leu Gln Gly
      130      135      140
Gln Val Ala Gly Met Gln Val Met Thr Thr Ser Gly Asp Pro Thr Ala
145      150      155      160
Val Ala Ser Val Glu Ile His Gly Thr Gly Ser Leu Gly Ala Ser Ser
      165      170      175
Ala Pro Leu Tyr Ile Val Asp Gly Met Gln Thr Ser Leu Asp Val Val
      180      185      190
Ala Thr Met Asn Pro Asn Asp Phe Glu Ser Met Ser Val Leu Lys Asp
      195      200      205
Ala Ser Ala Thr Ser Ile Tyr Gly Ala Arg Ala Ala Asn Gly Val Val
      210      215      220
Phe Ile Gln Thr Lys Lys Gly Lys Met Ser Glu Arg Gly Arg Ile Thr
225      230      235      240
Phe Asn Ala Ser Tyr Gly Ile Ser Gln Ile Leu Asn Thr Lys Pro Leu
      245      250      255
Asp Asn Met Met Thr Gly Asp Glu Leu Leu Asp Phe Gln Val Lys Ala
      260      265      270

```

Gly Phe Trp Gly Asn Asn Gln Thr Val Gln Lys Val Lys Asp Met Ile
 275 280 285
 Leu Ala Gly Ala Glu Asp Leu Tyr Gly Asn Tyr Asp Ser Leu Lys Asp
 290 295 300
 Glu Tyr Gly Lys Thr Leu Phe Pro Val Asp Phe Asn His Asp Ala Asp
 305 310 315 320
 Trp Leu Lys Ala Leu Phe Lys Thr Ala Pro Thr Ser Gln Gly Asp Ile
 325 330 335
 Ser Phe Ser Gly Gly Ser Gln Gly Thr Ser Tyr Tyr Ala Ser Ile Gly
 340 345 350
 Tyr Phe Asp Gln Glu Gly Met Ala Arg Glu Pro Ala Asn Phe Lys Arg
 355 360 365
 Tyr Ser Gly Arg Leu Asn Phe Glu Ser Arg Ile Asn Glu Trp Leu Lys
 370 375 380
 Val Gly Ala Asn Leu Ser Gly Ala Ile Ala Asn Arg Arg Ser Ala Asp
 385 390 395 400
 Tyr Phe Gly Lys Tyr Tyr Met Gly Ser Gly Thr Phe Gly Val Leu Thr
 405 410 415
 Met Pro Arg Tyr Tyr Asn Pro Phe Asp Val Asn Gly Asp Leu Ala Asp
 420 425 430
 Val Tyr Tyr Met Tyr Gly Ala Thr Arg Pro Ser Met Thr Glu Pro Tyr
 435 440 445
 Phe Ala Lys Met Arg Pro Phe Ser Ser Glu Ser His Gln Ala Asn Val
 450 455 460
 Asn Gly Phe Ala Gln Ile Thr Pro Ile Lys Gly Leu Thr Leu Lys Ala
 465 470 475 480
 Gln Ala Gly Val Asp Ile Thr Asn Thr Arg Thr Ser Ser Lys Arg Met
 485 490 495
 Pro Asn Asn Pro Tyr Asp Ser Thr Pro Leu Gly Glu Arg Arg Glu Arg
 500 505 510
 Ala Tyr Arg Asp Val Ser Lys Ser Phe Thr Asn Thr Ala Glu Tyr Lys
 515 520 525
 Phe Ser Ile Asp Glu Lys His Asp Leu Thr Ala Leu Met Gly His Glu
 530 535 540
 Tyr Ile Glu Tyr Glu Gly Asp Val Ile Gly Ala Ser Ser Lys Gly Phe
 545 550 555 560
 Glu Ser Asp Lys Leu Met Leu Leu Ser Gln Gly Lys Thr Gly Asn Ser
 565 570 575
 Leu Ser Leu Pro Glu His Arg Val Ala Glu Tyr Ala Tyr Leu Ser Phe
 580 585 590
 Phe Ser Arg Phe Asn Tyr Gly Phe Asp Lys Trp Met Tyr Ile Asp Phe
 595 600 605
 Ser Val Arg Asn Asp Gln Ser Ser Arg Phe Gly Ser Asn Asn Arg Ser
 610 615 620
 Ala Trp Phe Tyr Ser Val Gly Gly Met Phe Asp Ile Tyr Asn Lys Phe
 625 630 635 640
 Ile Gln Glu Ser Asn Trp Leu Ser Asp Leu Arg Leu Lys Met Ser Tyr
 645 650 655
 Gly Thr Thr Gly Asn Ser Glu Ile Gly Asn Tyr Asn His Gln Ala Leu
 660 665 670
 Val Thr Val Asn Asn Tyr Thr Glu Asp Ala Met Gly Leu Ser Ile Ser
 675 680 685
 Thr Ala Gly Asn Pro Asp Leu Ser Trp Glu Lys Gln Ser Gln Phe Asn
 690 695 700
 Phe Gly Leu Ala Ala Gly Ala Phe Asn Asn Arg Leu Ser Ala Glu Val
 705 710 715 720
 Asp Phe Tyr Val Arg Thr Thr Asn Asp Met Leu Ile Asp Val Pro Met
 725 730 735
 Pro Tyr Ile Ser Gly Phe Phe Ser Gln Tyr Gln Asn Val Gly Ser Met
 740 745 750
 Lys Asn Thr Gly Val Asp Leu Ser Leu Lys Gly Thr Ile Tyr Gln Asn
 755 760 765
 Lys Asp Trp Asn Val Tyr Ala Ser Ala Asn Phe Asn Tyr Asn Arg Gln
 770 775 780
 Glu Ile Thr Lys Leu Phe Phe Gly Leu Asn Lys Tyr Met Leu Pro Asn
 785 790 795 800
 Thr Gly Thr Ile Trp Glu Ile Gly Tyr Pro Asn Ser Phe Tyr Met Ala
 805 810 815
 Glu Tyr Ala Gly Ile Asp Lys Lys Thr Gly Lys Gln Leu Trp Tyr Val
 820 825 830
 Pro Gly Gln Val Asp Ala Asp Gly Asn Lys Val Thr Thr Ser Gln Tyr
 835 840 845
 Ser Ala Asp Leu Glu Thr Arg Ile Asp Lys Ser Val Thr Pro Pro Ile
 850 855 860
 Thr Gly Gly Phe Ser Leu Gly Ala Ser Trp Lys Gly Leu Ser Leu Asp
 865 870 875 880
 Ala Asp Phe Ala Tyr Ile Val Gly Lys Trp Met Ile Asn Asn Asp Arg

305					310					315				320	
Ala	Leu	Phe	Lys	Thr	Ala	Pro	Thr	Ser	Gln	Gly	Asp	Ile	Ser	Phe	Ser
				325					330					335	
Gly	Gly	Ser	Gln	Gly	Thr	Ser	Tyr	Tyr	Ala	Ser	Ile	Gly	Tyr	Phe	Asp
			340					345					350		
Gln	Glu	Gly	Met	Ala	Arg	Glu	Pro	Ala	Asn	Phe	Lys	Arg	Tyr	Ser	Gly
		355					360					365			
Arg	Leu	Asn	Phe	Glu	Ser	Arg	Ile	Asn	Glu	Trp	Leu	Lys	Val	Gly	Ala
	370					375					380				
Asn	Leu	Ser	Gly	Ala	Ile	Ala	Asn	Arg	Arg	Ser	Ala	Asp	Tyr	Phe	Gly
	385					390				395					400
Lys	Tyr	Tyr	Met	Gly	Ser	Gly	Thr	Phe	Gly	Val	Leu	Thr	Met	Pro	Arg
			405						410					415	
Tyr	Tyr	Asn	Pro	Phe	Asp	Val	Asn	Gly	Asp	Leu	Ala	Asp	Val	Tyr	Tyr
		420						425					430		
Met	Tyr	Gly	Ala	Thr	Arg	Pro	Ser	Met	Thr	Glu	Pro	Tyr	Phe	Ala	Lys
		435					440					445			
Met	Arg	Pro	Phe	Ser	Ser	Glu	Ser	His	Gln	Ala	Asn	Val	Asn	Gly	Phe
	450					455					460				
Ala	Gln	Ile	Thr	Pro	Ile	Lys	Gly	Leu	Thr	Leu	Lys	Ala	Gln	Ala	Gly
	465					470				475					480
Val	Asp	Ile	Thr	Asn	Thr	Arg	Thr	Ser	Ser	Lys	Arg	Met	Pro	Asn	Asn
				485					490					495	
Pro	Tyr	Asp	Ser	Thr	Pro	Leu	Gly	Glu	Arg	Arg	Glu	Arg	Ala	Tyr	Arg
		500						505					510		
Asp	Val	Ser	Lys	Ser	Phe	Thr	Asn	Thr	Ala	Glu	Tyr	Lys	Phe	Ser	Ile
	515						520					525			
Asp	Glu	Lys	His	Asp	Leu	Thr	Ala	Leu	Met	Gly	His	Glu	Tyr	Ile	Glu
	530					535					540				
Tyr	Glu	Gly	Asp	Val	Ile	Gly	Ala	Ser	Ser	Lys	Gly	Phe	Glu	Ser	Asp
	545					550				555					560
Lys	Leu	Met	Leu	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Asn	Ser	Leu	Ser	Leu
			565						570					575	
Pro	Glu	His	Arg	Val	Ala	Glu	Tyr	Ala	Tyr	Leu	Ser	Phe	Phe	Ser	Arg
		580						585					590		
Phe	Asn	Tyr	Gly	Phe	Asp	Lys	Trp	Met	Tyr	Ile	Asp	Phe	Ser	Val	Arg
	595					600						605			
Asn	Asp	Gln	Ser	Ser	Arg	Phe	Gly	Ser	Asn	Asn	Arg	Ser	Ala	Trp	Phe
	610					615					620				
Tyr	Ser	Val	Gly	Gly	Met	Phe	Asp	Ile	Tyr	Asn	Lys	Phe	Ile	Gln	Glu
	625					630				635					640
Ser	Asn	Trp	Leu	Ser	Asp	Leu	Arg	Leu	Lys	Met	Ser	Tyr	Gly	Thr	Thr
			645						650					655	
Gly	Asn	Ser	Glu	Ile	Gly	Asn	Tyr	Asn	His	Gln	Ala	Leu	Val	Thr	Val
		660						665					670		
Asn	Asn	Tyr	Thr	Glu	Asp	Ala	Met	Gly	Leu	Ser	Ile	Ser	Thr	Ala	Gly
	675						680					685			
Asn	Pro	Asp	Leu	Ser	Trp	Glu	Lys	Gln	Ser	Gln	Phe	Asn	Phe	Gly	Leu
	690					695					700				
Ala	Ala	Gly	Ala	Phe	Asn	Asn	Arg	Leu	Ser	Ala	Glu	Val	Asp	Phe	Tyr
	705					710				715					720
Val	Arg	Thr	Thr	Asn	Asp	Met	Leu	Ile	Asp	Val	Pro	Met	Pro	Tyr	Ile
			725						730					735	
Ser	Gly	Phe	Phe	Ser	Gln	Tyr	Gln	Asn	Val	Gly	Ser	Met	Lys	Asn	Thr
		740						745					750		
Gly	Val	Asp	Leu	Ser	Leu	Lys	Gly	Thr	Ile	Tyr	Gln	Asn	Lys	Asp	Trp
		755					760					765			
Asn	Val	Tyr	Ala	Ser	Ala	Asn	Phe	Asn	Tyr	Asn	Arg	Gln	Glu	Ile	Thr
	770					775					780				
Lys	Leu	Phe	Phe	Gly	Leu	Asn	Lys	Tyr	Met	Leu	Pro	Asn	Thr	Gly	Thr
	785					790				795					800
Ile	Trp	Glu	Ile	Gly	Tyr	Pro	Asn	Ser	Phe	Tyr	Met	Ala	Glu	Tyr	Ala
			805						810					815	
Gly	Ile	Asp	Lys	Lys	Thr	Gly	Lys	Gln	Leu	Trp	Tyr	Val	Pro	Gly	Gln
		820						825					830		
Val	Asp	Ala	Asp	Gly	Asn	Lys	Val	Thr	Thr	Ser	Gln	Tyr	Ser	Ala	Asp
		835					840				845				
Leu	Glu	Thr	Arg	Ile	Asp	Lys	Ser	Val	Thr	Pro	Pro	Ile	Thr	Gly	Gly
	850					855					860				
Phe	Ser	Leu	Gly	Ala	Ser	Trp	Lys	Gly	Leu	Ser	Leu	Asp	Ala	Asp	Phe
	865					870				875					880
Ala	Tyr	Ile	Val	Gly	Lys	Trp	Met	Ile	Asn	Asn	Asp	Arg	Tyr	Phe	Thr
			885					890						895	
Glu	Asn	Ala	Gly	Gly	Leu	Met	Gln	Leu	Asn	Lys	Asp	Lys	Met	Leu	Leu
		900						905					910		
Asn	Ala	Trp	Thr	Glu	Asp	Asn	Lys	Glu	Thr	Asp	Val	Pro	Lys	Leu	Gly
		915					920					925			

Gln Ser Pro Gln Phe Asp Thr His Leu Leu Glu Asn Ala Ser Phe Leu
 930 935 940
 Arg Leu Lys Asn Leu Lys Leu Thr Tyr Val Leu Pro Asn Ser Leu Phe
 945 950 955 960
 Ala Gly Gln Asn Val Ile Gly Gly Ala Arg Val Tyr Leu Met Ala Arg
 965 970 975
 Asn Leu Leu Thr Val Thr Lys Tyr Lys Gly Phe Asp Pro Glu Ala Gly
 980 985 990
 Gly Asn Val Gly Lys Asn Gln Tyr Pro Asn Ser Lys Gln Tyr Val Ala
 995 1000 1005
 Gly Ile Gln Leu Ser Phe
 1010

(2) INFORMATION FOR SEQ ID NO:426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

Met Lys Lys Lys Asn Phe Leu Leu Leu Gly Ile Phe Val Ala Leu Leu
 1 5 10 15
 Thr Phe Ile Gly Ser Met Gln Ala Gln Gln Ala Lys Asp Tyr Phe Asn
 20 25 30
 Phe Asp Glu Arg Gly Glu Ala Tyr Phe Ser Phe Lys Val Pro Asp Arg
 35 40 45
 Ala Val Leu Gln Glu Leu Ala Leu Ile Met Ser Ile Asp Glu Phe Asp
 50 55 60
 Pro Val Thr Asn Glu Ala Ile Ala Tyr Ala Ser Glu Glu Glu Phe Glu
 65 70 75 80
 Ala Phe Leu Arg Tyr Gly Leu Lys Pro Thr Phe Leu Thr Pro Pro Ser
 85 90 95
 Met Gln Arg Ala Val Glu Met Phe Asp Tyr Arg Ser Gly Glu Lys Tyr
 100 105 110
 Glu Trp Asn Ala Tyr Pro Thr Tyr Glu Ala Tyr Ile Ser Met Met Glu
 115 120 125
 Glu Phe Gln Thr Lys Tyr Pro Ser Leu Cys Thr Thr Ser Val Ile Gly
 130 135 140
 Lys Ser Val Lys Asp Arg Lys Leu Met Ile Cys Lys Leu Thr Ser Ser
 145 150 155 160
 Ala Asn Thr Gly Lys Lys Pro Arg Val Leu Tyr Thr Ser Thr Met His
 165 170 175
 Gly Asp Glu Thr Thr Gly Tyr Val Val Leu Leu Arg Leu Ile Asp His
 180 185 190
 Leu Leu Ser Asn Tyr Glu Ser Asp Pro Arg Ile Lys Asn Ile Leu Asp
 195 200 205
 Lys Thr Glu Val Trp Ile Cys Pro Leu Thr Asn Pro Asp Gly Ala Tyr
 210 215 220
 Arg Ala Gly Asn His Thr Val Gln Gly Ala Thr Arg Tyr Asn Ala Asn
 225 230 235 240
 Asn Val Asp Leu Asn Arg Asn Phe Lys Asp Asp Val Ala Gly Asp His
 245 250 255
 Pro Asp Gly Lys Pro Trp Gln Pro Glu Ala Thr Ala Phe Met Asp Leu
 260 265 270
 Glu Gly Asn Thr Ser Phe Val Leu Gly Ala Asn Ile His Gly Gly Thr
 275 280 285
 Glu Val Val Asn Tyr Pro Trp Asp Asn Lys Lys Glu Arg His Ala Asp
 290 295 300
 Asp Glu Trp Tyr Lys Leu Ile Ser Arg Asn Tyr Ala Ala Ala Cys Gln
 305 310 315 320
 Ser Ile Ser Ala Ser Tyr Met Thr Ser Glu Thr Asn Ser Gly Ile Ile
 325 330 335
 Asn Gly Ser Asp Trp Tyr Val Ile Arg Gly Ser Arg Gln Asp Asn Ala
 340 345 350

Asn Tyr Phe His Arg Leu Arg Glu Ile Thr Leu Glu Ile Ser Asn Thr
 355 360 365
 Lys Leu Val Pro Ala Ser Gln Leu Pro Lys Tyr Trp Asn Leu Asn Lys
 370 375 380
 Glu Ser Leu Leu Ala Leu Ile Glu Glu Ser Leu Tyr Gly Ile His Gly
 385 390 395 400
 Thr Val Thr Ser Ala Ala Asn Gly Gln Pro Leu Lys Cys Gln Ile Leu
 405 410 415
 Ile Glu Asn His Asp Lys Arg Asn Ser Asp Val Tyr Ser Asp Ala Thr
 420 425 430
 Thr Gly Tyr Tyr Val Arg Pro Ile Lys Ala Gly Thr Tyr Thr Val Lys
 435 440 445
 Tyr Lys Ala Glu Gly Tyr Pro Glu Ala Thr Arg Thr Ile Thr Ile Lys
 450 455 460
 Asp Lys Glu Thr Val Ile Met Asp Ile Ala Leu Gly Asn Ser Val Pro
 465 470 475 480
 Leu Pro Val Pro Asp Phe Thr Ala Ser Pro Met Thr Ile Ser Val Gly
 485 490 495
 Glu Ser Val Gln Phe Gln Asp Gln Thr Thr Asn Asn Pro Thr Asn Trp
 500 505 510
 Glu Trp Thr Phe Glu Gly Gly Gln Pro Ala Met Ser Thr Glu Gln Asn
 515 520 525
 Pro Leu Val Ser Tyr Ser His Pro Gly Gln Tyr Asp Val Thr Leu Lys
 530 535 540
 Val Trp Asn Ala Ser Gly Ser Asn Thr Ile Thr Lys Glu Lys Phe Ile
 545 550 555 560
 Thr Val Asn Ala Val Met Pro Val Ala Glu Phe Val Gly Thr Pro Thr
 565 570 575
 Glu Ile Glu Glu Gly Gln Thr Val Ser Phe Gln Asn Gln Ser Thr Asn
 580 585 590
 Ala Thr Asn Tyr Val Trp Ile Phe Asp Gly Gly Thr Pro Ala Thr Ser
 595 600 605
 Glu Asp Glu Asn Pro Thr Val Leu Tyr Ser Lys Ala Gly Gln Tyr Asp
 610 615 620
 Val Thr Leu Lys Ala Ile Ser Ala Ser Gly Glu Thr Val Lys Thr Lys
 625 630 635 640
 Glu Lys Tyr Ile Thr Val Lys Lys Ala Pro Val Pro Ala Pro Val Ala
 645 650 655
 Asp Phe Glu Gly Thr Pro Arg Lys Val Lys Lys Gly Glu Thr Val Thr
 660 665 670
 Phe Lys Asp Leu Ser Thr Asn Asn Pro Thr Ser Trp Leu Trp Val Phe
 675 680 685
 Glu Gly Gly Ser Pro Ala Thr Ser Thr Glu Gln Asn Pro Val Val Thr
 690 695 700
 Tyr Asn Glu Thr Gly Lys Tyr Asp Val Gln Leu Thr Ala Thr Asn Glu
 705 710 715 720
 Gly Gly Ser Asn Val Lys Lys Ala Glu Asp Tyr Ile Glu Val Ile Leu
 725 730 735
 Asp Asp Ser Val Glu Asp Ile Val Ala Gln Thr Gly Ile Val Ile Arg
 740 745 750
 Pro Gln Asn Gly Thr Lys Gln Ile Leu Ile Glu Ala Asn Ala Ala Ile
 755 760 765
 Lys Ala Ile Val Leu Tyr Asp Ile Asn Gly Arg Val Val Leu Lys Thr
 770 775 780
 Thr Pro Asn Gln Leu Arg Ser Thr Val Asp Leu Ser Ile Leu Pro Glu
 785 790 795 800
 Gly Ile Tyr Thr Ile Asn Ile Lys Thr Glu Lys Ser Ala Arg Thr Glu
 805 810 815
 Lys Ile His Ile Gly
 820

(2) INFORMATION FOR SEQ ID NO:427

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

```
Met Arg Leu Ile Lys Ala Phe Leu Val Gln Leu Leu Leu Leu Pro Ile
1      5      10      15
Phe Phe Tyr Lys Arg Phe Ile Ser Pro Leu Thr Pro Pro Ser Cys Arg
20      25      30
Phe Thr Pro Ser Cys Ser Ser Tyr Ala Ile Glu Ala Leu Arg Lys Tyr
35      40      45
Gly Pro Gly Lys Gly Leu Leu Ser Ile Lys Arg Ile Leu Arg Cys
50      55      60
His Pro Trp Gly Gly Ser Gly Tyr Asp Pro Val Pro
65      70      75
```

(2) INFORMATION FOR SEQ ID NO:428

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 859 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

```
Met Ala Tyr Asp Phe Thr Gln Thr Phe Arg Asn Ser Leu Glu Tyr Ser
1      5      10      15
Tyr Gln Glu Ala Thr Arg Leu Gly Val Val Ala Val Thr Gln Asp Met
20      25      30
Leu Val Leu Gly Ile Ile Arg Asp Gly Asp Asn Gly Ala Ile Asp Ile
35      40      45
Met Arg His Tyr Gly Ile Asn Leu Tyr Glu Leu Lys Arg Leu Ile Glu
50      55      60
Leu Glu Ala Ile Ala Glu Ser Leu Pro Ala Ser Pro Glu Gly Ser Pro
65      70      75      80
Ile Phe Thr Pro Ser Ala Arg Glu Ala Ile Asp Asp Ala Thr Asp Ile
85      90      95
Cys Ala Asp Met Glu Asp Glu Ala Val Ser Pro Val His Leu Leu Leu
100      105      110
Ser Ile Leu Asn Ser Thr Gln Glu Ser Leu Val Gln Lys Ile Phe Met
115      120      125
Lys Gln Gly Ile Lys Tyr Asp Thr Ile Leu Ser Asp Tyr Phe Gly Gln
130      135      140
Arg Asn Pro Ser Glu Gly Lys Ser Pro Ser Glu Met Glu Ile Leu Asp
145      150      155      160
Gly Tyr Gln Asp Asn Asp Phe Asp Asp Glu Glu Asp Glu Ser Ser Pro
165      170      175
Pro Ser Gly Asn Ser Gly Thr Gly Gly Gly Ser Gly Asp Ala Pro Glu
180      185      190
Gln Asn Thr Gly Gly Asp Thr Thr Thr Thr Arg Ser Gly Gly
195      200      205
Asp Thr Pro Ala Leu Asp Thr Phe Gly Thr Asp Ile Thr Ala Met Ala
210      215      220
Ala Ala Gly Lys Leu Asp Pro Val Val Gly Arg Glu Gln Glu Ile Glu
225      230      235      240
Arg Val Ile Gln Ile Leu Ser Arg Arg Lys Lys Asn Asn Pro Val Leu
245      250      255
Ile Gly Glu Pro Gly Val Gly Lys Ser Ala Ile Val Glu Gly Leu Ala
260      265      270
Glu Arg Ile Val Asn Arg Lys Val Ser Arg Ile Leu Phe Asp Lys Arg
275      280      285
Ile Ile Ser Leu Asp Leu Ala Gln Met Val Ala Gly Thr Lys Tyr Arg
290      295      300
Gly Gln Phe Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Leu Lys Lys
305      310      315      320
Asn Pro Gln Ile Ile Leu Phe Ile Asp Glu Ile His Thr Ile Val Gly
325      330      335
```

Ala Gly Ser Ala Ala Gly Ser Met Asp Thr Ala Asn Met Leu Lys Pro
 340 345 350
 Ala Leu Ala Arg Gly Gln Val Gln Cys Ile Gly Ala Thr Thr Leu Asp
 355 360 365
 Glu Tyr Arg Lys Asn Ile Glu Lys Asp Gly Ala Leu Glu Arg Arg Phe
 370 375 380
 Gln Lys Val Pro Ile Ala Pro Ser Thr Ala Glu Glu Thr Leu Thr Ile
 385 390 395 400
 Leu Gln Asn Ile Lys Glu Lys Tyr Glu Asp Tyr His Gly Val Arg Tyr
 405 410 415
 Thr Asp Glu Ala Ile Lys Ala Ala Val Glu Leu Thr Asp Arg Tyr Val
 420 425 430
 Ser Asp Arg Phe Phe Pro Asp Lys Ala Ile Asp Ala Met Asp Glu Ala
 435 440 445
 Gly Ala Ser Val His Ile Thr Asn Val Val Ala Pro Lys Glu Ile Glu
 450 455 460
 Ile Leu Glu Ala Glu Leu Ala Ser Val Arg Glu Asn Lys Leu Ser Ala
 465 470 475 480
 Val Lys Ala Gln Asn Tyr Glu Leu Ala Ala Ser Phe Arg Asp Gln Glu
 485 490 495
 Arg Arg Thr Gln Gln Gln Ile Ala Glu Glu Lys Lys Lys Trp Glu Glu
 500 505 510
 Gln Met Ser Lys His Arg Glu Thr Val Asp Glu Asn Val Val Ala His
 515 520 525
 Val Val Ala Leu Met Thr Gly Val Pro Ala Glu Arg Leu Ser Thr Gly
 530 535 540
 Glu Gly Glu Arg Leu Arg Thr Met Ala Asp Asp Leu Lys Thr Lys Val
 545 550 555 560
 Val Gly Gln Asp Thr Ala Ile Glu Lys Met Val His Ala Ile Gln Arg
 565 570 575
 Asn Arg Leu Gly Leu Arg Asn Glu Lys Lys Pro Ile Gly Ser Phe Leu
 580 585 590
 Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Tyr Leu Ala Lys Lys Leu
 595 600 605
 Ala Glu Tyr Leu Phe Glu Asp Glu Asn Ala Met Ile Arg Val Asp Met
 610 615 620
 Ser Glu Tyr Met Glu Lys Phe Ser Val Ser Arg Leu Val Gly Ala Pro
 625 630 635 640
 Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu Arg Val
 645 650 655
 Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu Ile Glu Lys Ala
 660 665 670
 His Ala Asp Val Phe Asn Leu Leu Gln Val Met Asp Glu Gly Gln
 675 680 685
 Leu Thr Asp Ser Leu Gly Arg Arg Val Asn Phe Lys Asn Thr Val Ile
 690 695 700
 Ile Ile Thr Ser Asn Val Gly Thr Arg Gln Leu Lys Asp Phe Gly Gln
 705 710 715 720
 Gly Ile Gly Phe Arg Ser Glu Lys Asp Glu Glu Ala Asn Lys Glu His
 725 730 735
 Ser Arg Ser Val Ile Gln Lys Ala Leu Asn Lys Thr Phe Ser Pro Glu
 740 745 750
 Phe Leu Asn Arg Leu Asp Asp Ile Ile Leu Phe Asp Gln Leu Gly Lys
 755 760 765
 Thr Glu Ile Arg Arg Met Val Asp Ile Glu Leu Lys Ala Val Leu Ala
 770 775 780
 Arg Ile His Arg Ala Gly Tyr Asp Leu Val Leu Thr Asp Glu Ala Lys
 785 790 795 800
 Asp Val Ile Ala Thr Lys Gly Tyr Asp Leu Gln Tyr Gly Ala Arg Pro
 805 810 815
 Leu Lys Arg Thr Leu Gln Asn Glu Val Glu Asp Arg Leu Thr Asp Leu
 820 825 830
 Ile Leu Ser Gly Gln Ile Glu Lys Gly Gln Thr Leu Thr Leu Ser Ala
 835 840 845
 Arg Asp Gly Glu Ile Ile Val Gln Glu Gln Ala
 850 855

(2) INFORMATION FOR SEQ ID NO:429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

```
Met Asn Tyr Leu Tyr Ile Leu Ile Thr Leu Leu Leu Ser Gly Phe Phe
1      5      10      15
Ser Gly Ala Glu Ile Ala Phe Leu Ser Ser Asp Lys Leu Arg Leu Glu
      20      25      30
Leu Asp Arg Asn Arg Gly Asp Leu Thr Gly Arg Ala Leu Asn Leu Leu
      35      40      45
Tyr Arg His Pro Asp Gln Leu Val Thr Thr Leu Leu Val Gly Asn Asn
      50      55      60
Ile Val Leu Val Val Tyr Gly Leu Leu Met Ala Gly Leu Leu Ala Ala
      65      70      75      80
Pro Leu Ala Gln Trp Ile Asp Asn Asp Ala Met Ile Val Val Leu Gln
      85      90      95
Ser Val Leu Ser Thr Ile Ile Ile Leu Phe Thr Gly Glu Phe Leu Pro
      100      105      110
Lys Ala Ile Phe Lys Thr Asn Ala Asn Met Met Met Arg Val Phe Ala
      115      120      125
Leu Pro Ile Val Ala Ile Tyr Tyr Leu Leu Tyr Pro Leu Ser Lys Leu
      130      135      140
Phe Thr Gly Leu Ser Arg Ser Phe Ile Arg Leu Val Asp Lys Asn Tyr
      145      150      155      160
Val Pro Thr Thr Val Gly Leu Gly Arg Val Asp Leu Asp His Tyr Leu
      165      170      175
Ala Glu Asn Met Ser Gly Glu Asn Glu Gln Asn Asp Leu Thr Thr Glu
      180      185      190
Val Lys Ile Ile Gln Asn Ala Leu Asp Phe Ser Gly Ile Gln Val Arg
      195      200      205
Asp Cys Met Ile Pro Arg Asn Glu Met Ile Ala Cys Glu Leu Gln Thr
      210      215      220
Asp Ile Glu Val Leu Lys Thr Thr Phe Ile Asp Thr Gly Leu Ser Lys
      225      230      235      240
Ile Ile Ile Tyr Arg Gln Asn Ile Asp Asp Val Val Gly Tyr Ile His
      245      250      255
Ser Ser Glu Met Phe Arg Gly Gln Asp Trp Gln Lys Arg Ile Asn Thr
      260      265      270
Thr Val Phe Val Pro Glu Ser Met Tyr Ala Asn Lys Leu Met Arg Leu
      275      280      285
Leu Met Gln Arg Lys Lys Ser Ile Ala Ile Val Ile Asp Glu Leu Gly
      290      295      300
Gly Thr Ala Gly Met Val Thr Leu Glu Asp Leu Val Glu Glu Ile Phe
      305      310      315      320
Gly Asp Ile Glu Asp Glu His Asp Thr Arg Lys Ile Ile Ala Lys Gln
      325      330      335
Leu Gly Pro His Thr Tyr Leu Val Ser Gly Arg Met Glu Ile Asp Asp
      340      345      350
Val Asn Glu Arg Phe Gly Leu Ser Leu Pro Glu Ser Asp Asp Tyr Leu
      355      360      365
Thr Val Ala Gly Phe Ile Leu Asn Ser His Gln Asn Ile Pro Gln Ala
      370      375      380
Asn Glu Val Val Glu Ile Ala Pro Tyr Thr Phe Thr Ile Leu Arg Ser
      385      390      395      400
Ser Ser Thr Lys Ile Glu Leu Val Lys Met Ser Ile Asp Asp Gln Ser
      405      410      415
Asn
```

(2) INFORMATION FOR SEQ ID NO:430

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

```
Met Lys Gln Asn Tyr Phe Lys Arg Val Cys Ser Leu Leu Trp Leu Val
1      5      10      15
Leu Pro Met Leu Ile Met Pro Leu Glu Val Ala Ala Gln Glu Ile Ile
      20      25      30
Pro Asn Glu Glu Val Leu Glu Ser Leu Thr Phe Val Ala Pro Val Glu
      35      40      45
Glu Thr Asp Ala Ile Glu Ala Glu Val Glu Ala Leu Gln Glu Ile Val
      50      55      60
Ala Thr Glu Glu Ile Ala Glu Gln Ala Val Arg Ser Tyr Thr Tyr Thr
      65      70      75      80
Val Tyr Arg Asp Gly Val Lys Ile Ala Ser Gly Leu Thr Glu Pro Thr
      85      90      95
Phe Leu Asp Glu Asp Val Pro Ala Gly Glu His Thr Tyr Cys Val Glu
      100     105     110
Val Gln Tyr Gln Gly Gly Val Ser Asp Lys Val Cys Val Asp Val Glu
      115     120     125
Val Lys Asp Phe Lys Pro Val Thr Asn Leu Thr Gly Thr Ala Ser Asn
      130     135     140
Asp Glu Val Ser Leu Asp Trp Asp Gly Val Glu Glu Lys Ala Glu Glu
      145     150     155     160
Pro Ala Ser Asp Lys Ala Val Ser Tyr Asn Val Tyr Lys Asn Gly Thr
      165     170     175
Leu Ile Gly Asn Thr Ala Glu Thr His Tyr Val Glu Thr Gly Val Ala
      180     185     190
Asn Gly Thr Tyr Ile Tyr Glu Val Glu Val Lys Tyr Pro Asp Gly Val
      195     200     205
Ser Pro Lys Val Ala Val Thr Val Thr Val Thr Asn Ser Ser Leu Ser
      210     215     220
Asn Val Asp Gly Gln Ala Pro Tyr Thr Leu Arg Val Glu Gly Lys Lys
      225     230     235     240
Ile Ile Ala Glu Ala His Gly Met Ile Thr Leu Tyr Asp Ile Asn Gly
      245     250     255
Arg Thr Val Ala Val Ala Pro Asn Arg Leu Glu Tyr Met Ala Gln Thr
      260     265     270
Gly Phe Tyr Ala Val Arg Phe Asp Val Gly Asn Lys His His Val Ser
      275     280     285
Lys Ile Gln Val Arg
290
```

(2) INFORMATION FOR SEQ ID NO:431

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```
Met Ile Pro Leu Ser Glu Ser Phe Glu Ser Gly Ile Pro Ala Ile Trp
1      5      10      15
Lys Thr Ile Asp Ala Asp Gly Asp Gly Tyr Asn Trp Met His Leu Thr
      20      25      30
Asn Phe Thr Gly Gln Ser Gly Leu Cys Val Ser Ser Ala Ser Tyr Ile
      35      40      45
Gly Gly Val Gly Ala Leu Thr Pro Asp Asn Tyr Leu Ile Thr Pro Glu
      50      55      60
Leu Lys Leu Pro Thr Asp Ala Leu Val Glu Ile Ile Tyr Trp Val Cys
      65      70      75      80
```

```

Thr Gln Asp Leu Thr Ala Pro Ser Glu His Tyr Ala Val Tyr Ser Ser
      85          90          95
Ser Thr Gly Asn Asn Ala Ala Asp Phe Val Asn Leu Leu Tyr Glu Glu
      100        105        110
Thr Leu Thr Ala Lys Arg Ile Gln Ser Pro Glu Leu Ile Arg Gly Asn
      115        120        125
Arg Thr Gln Gly Val Trp Tyr Gln Arg Lys Val Val Leu Pro Asn Asp
      130        135        140
Thr Lys Tyr Val Ala Phe Arg His Phe Asn Ser Thr Asp Asn Phe Trp
      145        150        155        160
Leu Asn Leu Asp Glu Val Ser Ile Leu Tyr Thr Pro Leu Pro Arg Arg
      165        170        175
Ala Pro Cys Pro His Pro Gly Gly Tyr Thr Tyr Ser Val Phe Arg Asp
      180        185        190
Gly Gln Lys Ile Ala Ser Gly Leu Ser Ala Leu Ala Tyr Ile Asp Thr
      195        200        205
Asp Val Pro Tyr Gly Thr Gln Asp Tyr Cys Val Gln Val Asn Tyr Leu
      210        215        220
Gln Gly Asp Ser Tyr Lys Val Cys Lys Asn Ile Val Val Ala Asn Ser
      225        230        235        240
Ala Asn Ile Tyr Gly Ala Asp Lys Pro Phe Ala Leu Thr Val Val Gly
      245        250        255
Lys Thr Ile Val Ala Ser Ala Phe Lys Gly Glu Ile Thr Leu Tyr Asp
      260        265        270
Ile Arg Gly Arg Leu Ile Ala Ser Gly Cys Asp Thr Leu Arg Tyr Lys
      275        280        285
Ala Glu Asn Gly Phe Tyr Leu Ile Lys Ile Gln Val Asn Gly Thr Val
      290        295        300
Tyr Thr Glu Lys Ile Gln Ile Gln
305          310

```

(2) INFORMATION FOR SEQ ID NO:432

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala
1      5      10      15
Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
      20      25      30
Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
      35      40      45
Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
      50      55      60
Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
65      70      75      80
Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
      85      90      95
Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
      100     105     110
Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp
      115     120     125
Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu
      130     135     140
Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp
      145     150     155     160
Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro
      165     170     175
Trp Asn Asn Lys Glu Pro Leu Leu Pro Asn Gly Asn His Ala Tyr Thr
      180     185     190
Gly Cys Val Ala Thr Ala Ala Ala Gln Ile Met Arg Tyr His Ser Trp
      195     200     205

```

Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val
 210 215 220
 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met
 225 230 235 240
 Pro Gly Asn Pro Asp Leu Asp Asn Leu Thr Gln Ser Gln Val Asp Ala
 245 250 255
 Tyr Ala Thr Leu Met Arg Asp Val Ser Ala Ser Val Ser Met Ser Phe
 260 265 270
 Tyr Glu Asn Gly Ser Gly Thr Tyr Ser Val Tyr Val Val Gly Ala Leu
 275 280 285
 Arg Asn Asn Phe Arg Tyr Lys Arg Ser Leu Gln Leu His Val Arg Ala
 290 295 300
 Leu Tyr Thr Ser Gln Glu Trp His Asp Met Ile Arg Gly Glu Leu Ala
 305 310 315 320
 Ser Gly Arg Pro Val Tyr Tyr Ala Gly Asn Asn Gln Ser Ile Gly His
 325 330 335
 Ala Phe Val Cys Asp Gly Tyr Ala Ser Asp Gly Thr Phe His Phe Asn
 340 345 350
 Trp Gly Trp Gly Gly Val Ser Asn Gly Phe Tyr Lys Leu Thr Leu Leu
 355 360 365
 Ser Pro Thr Ser Leu Gly Ile Gly Gly Glu Gly Ile Gly Phe Thr Ile
 370 375 380
 Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu
 385 390 395 400
 Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala
 405 410 415
 Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn
 420 425 430
 Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys
 435 440 445
 Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser
 450 455 460
 Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn
 465 470 475 480
 Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr
 485 490 495
 Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val
 500 505 510
 Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Thr
 515 520 525
 Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val
 530 535 540
 Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn
 545 550 555 560
 Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser
 565 570 575
 Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala
 580 585 590
 Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp
 595 600 605
 Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser
 610 615 620
 Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val
 625 630 635 640
 Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
 645 650 655
 Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
 660 665 670
 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val
 675 680 685
 Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
 690 695 700
 Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
 705 710 715 720
 Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
 725 730 735
 Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
 740 745 750
 Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
 755 760 765
 Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
 770 775 780
 Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
 785 790 795 800
 Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
 805 810 815
 Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val

820 825 830
 Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
 835 840

(2) INFORMATION FOR SEQ ID NO:433

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...290
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

```

Met Lys Lys Leu Phe Leu Ser Leu Thr Ser Leu Val Met Val Phe Ala
 1                    5                10                15
Val Ala Ser Cys Asp Ile Ile Asp Lys Asp Gln Thr Leu Leu Pro Ala
    20                25                30
Pro Thr Asn Val Thr Pro Asp Asn Pro Asp Asp Asn Pro Ser Glu Ile
    35                40                45
Asp Ile Thr Gln Thr His Thr Glu Lys Tyr Val Leu Ala Glu Glu Phe
    50                55                60
Thr Gly Gln Lys Cys Leu Asn Cys Pro Lys Gly His Arg Lys Leu Ala
    65                70                75                80
Ala Leu Lys Glu Gln Tyr Gly Lys Arg Leu Thr Val Val Gly Ile His
    85                90                95
Ala Gly Pro Gly Ser Leu Val Pro Pro Leu Phe Arg Thr Glu Ala Gly
    100               105               110
Asp Ala Tyr Tyr Ser Lys Phe Ala Asn Asn Thr Pro Leu Pro Ala Leu
    115               120               125
Met Val Ser Arg Lys Lys Phe Gly Ser Ser Tyr Val Tyr Asp Lys Ser
    130               135               140
Tyr Lys Thr Trp Asp Val Pro Ile Ala Glu Gln Met Glu Gln Lys Ala
    145               150               155               160
Lys Ile Asn Ile Phe Ala Val Ala Glu Tyr Thr Asp Thr Gln Lys Ile
    165               170               175
Lys Val Thr Val Lys Gly Lys Ile Leu Glu Gly Asn Thr Leu Pro Lys
    180               185               190
Ser Met Val Gln Val Tyr Leu Leu Glu Asp Lys Leu Ile Ala Pro Gln
    195               200               205
Val Asp Gly Asn Thr Thr Val Glu Asn Tyr Glu His Asn His Val Leu
    210               215               220
Arg Gly Ala Val Asn Gly Ile Trp Gly Glu Glu Phe Val Asn Leu Lys
    225               230               235               240
Asp Tyr Leu Tyr Thr Tyr Ala Val Glu Pro Leu Ser Gly Met Ser Phe
    245               250               255
Val Ala Glu Asn Tyr Ser Ile Val Ala Phe Val Tyr Asp Val Gln Thr
    260               265               270
Phe Glu Val Tyr Asp Val Val His Val Lys Ile Asn Pro Gln Ser Asp
    275               280               285
Gly Lys
    290
  
```

(2) INFORMATION FOR SEQ ID NO:434

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

```

Met Lys Lys Ser Ser Val Val Ala Ser Val Leu Ala Val Ala Leu Val
1      5      10      15
Phe Ala Gly Cys Gly Leu Asn Asn Met Ala Lys Gly Gly Leu Ile Gly
20      25      30
Ala Gly Val Gly Gly Ala Ile Gly Ala Gly Val Gly Asn Val Ala Gly
35      40      45
Asn Thr Ala Val Gly Ala Ile Val Gly Thr Ala Val Gly Gly Ala Ala
50      55      60
Gly Ala Leu Ile Gly Lys Lys Met Asp Lys Gln Lys Lys Glu Leu Glu
65      70      75      80
Ala Ala Val Pro Asp Ala Thr Ile Gln Thr Val Asn Asp Gly Glu Ala
85      90      95
Ile Leu Val Thr Phe Asp Ser Gly Ile Leu Phe Ala Thr Asn Ser Ser
100     105     110
Thr Leu Ser Pro Asn Ser Arg Thr Ala Leu Thr Lys Phe Ala Ala Asn
115     120     125
Met Asn Lys Asn Pro Asp Thr Asp Ile Arg Ile Val Gly His Thr Asp
130     135     140
Asn Thr Gly Ser Asp Lys Ile Asn Asp Pro Leu Ser Glu Arg Arg Ala
145     150     155     160
Ala Ser Val Tyr Ser Phe Leu Asn Ser Gln Gly Val Ser Met Ser Arg
165     170     175
Met Ala Ala Glu Gly Arg Gly Ser His Glu Pro Val Ala Asp Asn Ser
180     185     190
Thr Val Ala Gly Arg Ser Ala Asn Arg Arg Val Glu Val Tyr Ile Leu
195     200     205
Pro Asn Ala Lys Met Ile Glu Gln Ala Gln Gln Gly Thr Leu Lys
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:435

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```

Met Ser Lys Lys Ser Ile Leu Leu Leu Cys Cys Ser Leu Cys Phe Ile
1      5      10      15
Ser Ala Thr Lys Ala Val Thr Pro Val Arg Asn Val Arg Asn Ser Gln
20      25      30
Val Asn Ser Lys Ala Lys Thr Glu Arg Thr Lys Pro Ser Asp Ser Val
35      40      45
Arg Tyr Ile Ser Asn Met Ile Ala Asp Arg Leu Glu Phe Arg Asn Lys
50      55      60
Ile Ser Ser Glu Lys Glu Val Arg Lys Ala Glu Tyr Glu Asn Arg Leu
65      70      75      80
Ala Met Glu Ala Leu Asn Tyr Pro Ala Ile Asp Leu Tyr Gly Glu Asp
85      90      95
Ser Trp Ser Glu Tyr Val Asn Pro Phe Val Gly Ala Gly Thr Asp Val
100     105     110
Glu Ile Pro Asn Ser Tyr Asp Ile Asp Cys Ser Ser Phe Val Met Pro
115     120     125
Val Glu Asp Lys Gln Val Thr Ser Gln Phe Gly Tyr Arg Arg Arg Phe
130     135     140
Gly Arg Met His Tyr Gly Ile Asp Leu Ser Val Asn Arg Gly Asp Thr
145     150     155     160
Ile Arg Ala Ala Phe Asp Gly Lys Val Arg Val Arg Ser Tyr Glu Ala
165     170     175

```

Arg Gly Tyr Gly Tyr Tyr Ile Val Leu Arg His Pro Asn Gly Leu Glu
 180 185 190
 Thr Val Tyr Gly His Met Ser Arg Gln Leu Val Asp Glu Asn Gln Ile
 195 200 205
 Val Arg Ala Gly Gln Pro Ile Gly Leu Gly Gly Ser Thr Gly Arg Ser
 210 215 220
 Thr Gly Pro His Leu His Phe Glu Thr Arg Phe Met Gly Ile Pro Ile
 225 230 235 240
 Asn Pro Ser Thr Ile Ile Asp Phe Asp Asn Gly Val Pro Leu Arg Asp
 245 250 255
 Ile Tyr Thr Phe Lys Arg Gly Ser Asn Ser Arg Tyr Ala Lys Ala Ser
 260 265 270
 Lys Thr Ser Ser Arg Tyr Ala Lys Lys Gly Lys Lys Gly Arg Gln Ala
 275 280 285
 Ser Ser Pro Met Thr Tyr Arg Ile Lys Lys Gly Asp Thr Leu Glu Thr
 290 295 300
 Ile Ala Lys Arg His Gly Thr Ser Val Gln Lys Leu Cys Ala Thr Asn
 305 310 315 320
 Gly Ile Gly Lys Ser Lys Ile Leu Thr Pro Gly Lys Ala Leu Arg Ile
 325 330 335
 Lys

(2) INFORMATION FOR SEQ ID NO:436

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

Met Ala Lys Ile Asn Phe Tyr Ala Glu Gly Val Ser Leu Pro Arg Ile
 1 5 10 15
 Arg Arg Arg Ile Val Gly Lys Trp Ile Ala Glu Val Cys Ser Arg Tyr
 20 25 30
 Gly Lys Ala Val Gly Glu Ile Ser Tyr Leu Phe Cys Asp Asp Glu Tyr
 35 40 45
 Ile Leu Lys Ala Asn Gln Glu Phe Leu Asp His Asp Tyr Tyr Thr Asp
 50 55 60
 Ile Ile Thr Phe Asp Ser Cys Glu Ala Asp Thr Val Asn Gly Asp Leu
 65 70 75 80
 Leu Ile Ser Leu Asp Thr Val Arg Ser Asn Ala Arg Ala Leu Asp Leu
 85 90 95
 Arg Tyr Glu Asp Glu Leu His Arg Val Ile Ile His Gly Ile Leu His
 100 105 110
 Leu Cys Gly Leu Lys Asp Lys Ser Lys Lys Asp Glu Ala Gln Met Arg
 115 120 125
 Ala Ala Glu Glu Lys Ala Leu Val Met Leu Arg Glu Thr Ile Gly Ser
 130 135 140
 Glu Leu Ser Leu Leu His Thr
 145 150

(2) INFORMATION FOR SEQ ID NO:437

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

```

Met Lys Val Lys Tyr Leu Met Leu Thr Leu Val Gly Ala Ile Ala Leu
1      5      10      15
Asn Ala Ser Ala Gln Glu Asn Thr Val Pro Ala Thr Gly Gln Leu Pro
20      25      30
Ala Lys Asn Val Ala Phe Ala Arg Asn Lys Ala Gly Ser Asn Trp Phe
35      40      45
Val Thr Leu Gln Gly Gly Val Ala Ala Gln Phe Leu Asn Asp Asn Asn
50      55      60
Asn Lys Asp Leu Met Asp Arg Leu Gly Ala Ile Gly Ser Leu Ser Val
65      70      75      80
Gly Lys Tyr His Ser Pro Phe Phe Ala Thr Arg Leu Gln Ile Asn Gly
85      90      95
Gly Gln Ala His Thr Phe Leu Gly Lys Asn Gly Glu Gln Glu Ile Asn
100     105     110
Thr Asn Phe Gly Ala Ala His Phe Asp Phe Met Phe Asp Val Val Asn
115     120     125
Tyr Phe Ala Pro Tyr Arg Glu Asn Arg Phe Phe His Leu Ile Pro Trp
130     135     140
Val Gly Val Gly Tyr Gln His Lys Phe Ile Gly Ser Glu Trp Ser Lys
145     150     155     160
Asp Asn Val Glu Ser Leu Thr Ala Asn Val Gly Val Met Met Ala Phe
165     170     175
Arg Leu Gly Lys Arg Val Asp Phe Val Ile Glu Ala Gln Ala Ala His
180     185     190
Ser Asn Leu Asn Leu Ser Arg Ala Tyr Asn Ala Lys Lys Thr Pro Val
195     200     205
Phe Glu Asp Pro Ala Gly Arg Tyr Tyr Asn Gly Phe Gln Gly Met Ala
210     215     220
Thr Ala Gly Leu Asn Phe Arg Leu Gly Ala Val Gly Phe Asn Ala Ile
225     230     235     240
Unk Pro Met Asp Tyr Ala Leu Ile Asn Asp Leu Asn Gly Gln Ile Asn
245     250     255
Arg Leu Arg Ser Glu Val Glu Glu Leu Ser Lys Arg Pro Val Ser Cys
260     265     270
Pro Glu Cys Pro Glu Val Thr Pro Val Thr Lys Thr Glu Asn Ile Leu
275     280     285
Thr Glu Lys Ala Val Leu Phe Arg Phe Asp Ser His Val Val Asp Lys
290     295     300
Asp Gln Leu Ile Asn Leu Tyr Asp Val Ala Gln Phe Val Lys Glu Thr
305     310     315     320
Asn Glu Pro Ile Thr Val Val Gly Tyr Ala Asp Pro Thr Gly Asn Thr
325     330     335
Gln Tyr Asn Glu Lys Leu Ser Glu Arg Arg Ala Lys Ala Val Val Asp
340     345     350
Val Leu Thr Gly Lys Tyr Gly Val Pro Ser Glu Leu Ile Ser Val Glu
355     360     365
Trp Lys Gly Asp Ser Thr Gln Pro Phe Ser Lys Lys Ala Trp Asn Arg
370     375     380
Val Val Ile Val Arg Ser Lys
385     390

```

(2) INFORMATION FOR SEQ ID NO:438

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

Met Thr Tyr Arg Ile Met Lys Ala Lys Ser Leu Leu Leu Ala Leu Ala
 1 5 10 15
 Gly Leu Ala Cys Thr Phe Ser Ala Thr Ala Gln Glu Ala Thr Thr Gln
 20 25 30
 Asn Lys Ala Gly Met His Thr Ala Phe Gln Arg Asp Lys Ala Ser Asp
 35 40 45
 His Trp Phe Ile Asp Ile Ala Gly Gly Ala Gly Met Ala Leu Ser Gly
 50 55 60
 Trp Asn Asn Asp Val Asp Phe Val Asp Arg Leu Ser Ile Val Pro Thr
 65 70 75 80
 Phe Gly Ile Gly Lys Trp His Glu Pro Tyr Phe Gly Thr Arg Leu Gln
 85 90 95
 Phe Thr Gly Phe Asp Ile Tyr Gly Phe Pro Gln Gly Ser Lys Glu Arg
 100 105 110
 Asn His Asn Tyr Phe Gly Asn Ala His Leu Asp Phe Met Phe Asp Leu
 115 120 125
 Thr Asn Tyr Phe Gly Val Tyr Arg Pro Asn Arg Val Phe His Ile Ile
 130 135 140
 Pro Trp Ala Gly Ile Gly Phe Gly Tyr Lys Phe His Ser Glu Asn Ala
 145 150 155 160
 Asn Gly Glu Lys Val Gly Ser Lys Asp Asp Met Thr Gly Thr Val Asn
 165 170 175
 Val Gly Leu Met Leu Lys Phe Arg Leu Ser Arg Val Val Asp Phe Asn
 180 185 190
 Ile Glu Gly Gln Ala Phe Ala Gly Lys Met Asn Phe Ile Gly Thr Lys
 195 200 205
 Arg Gly Lys Ala Asp Phe Pro Val Met Ala Thr Ala Gly Leu Thr Phe
 210 215 220
 Asn Leu Gly Lys Thr Glu Trp Thr Glu Ile Val Pro Met Asp Tyr Ala
 225 230 235 240
 Leu Val Asn Asp Leu Asn Asn Gln Ile Asn Ser Leu Arg Gly Gln Val
 245 250 255
 Glu Glu Leu Ser Arg Arg Pro Val Ser Cys Pro Glu Cys Pro Glu Pro
 260 265 270
 Thr Gln Pro Thr Val Thr Arg Val Val Val Asp Asn Val Val Tyr Phe
 275 280 285
 Arg Ile Asn Ser Ala Lys Ile Asp Arg Asn Gln Glu Ile Asn Val Tyr
 290 295 300
 Asn Thr Ala Glu Tyr Ala Lys Thr Asn Asn Ala Pro Ile Lys Val Val
 305 310 315 320
 Gly Tyr Ala Asp Glu Lys Thr Gly Thr Ala Ala Tyr Asn Met Lys Leu
 325 330 335
 Ser Glu Arg Arg Ala Lys Ala Val Ala Lys Met Leu Glu Lys Tyr Gly
 340 345 350
 Val Ser Ala Asp Arg Ile Thr Ile Glu Trp Lys Gly Ser Ser Glu Gln
 355 360 365
 Ile Tyr Glu Glu Asn Ala Trp Asn Arg Ile Val Val Met Thr Ala Ala
 370 375 380
 Glu
 385

(2) INFORMATION FOR SEQ ID NO:439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

Met Glu Phe Phe Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val
 1 5 10 15
 Val Leu Ser Gln Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys
 20 25 30
 Lys Val Asp Thr Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu

35	40	45
Ala Leu Ala Thr Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp		
50	55	60
Arg Phe Gly Leu Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile		
65	70	75
Ala Ala Leu Val Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro		80
	85	90
Pro Leu Tyr Gln Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn		95
	100	105
Cys Cys Val Leu Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr		110
	115	120
Leu Leu Gln Ser Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr		125
	130	135
Leu Ala Met Val Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr		140
145	150	155
Asn Leu Pro Lys Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala		160
	165	170
Gly Ile Leu Ala Met Ala Phe Met Gly Phe Ser Gly Ile Ala		175
	180	185
		190

(2) INFORMATION FOR SEQ ID NO:440

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

Met Leu Phe Ile Ala Ala Val Phe Val Asn Asn Val Val Leu Ser Gln	
1	5
Phe Leu Gly Ile Cys Pro Phe Leu Gly Val Ser Lys Lys Val Asp Thr	
	20
Ser Ile Gly Met Gly Ala Ala Val Thr Phe Val Leu Ala Leu Ala Thr	
	35
Leu Val Thr Phe Leu Ile Gln Lys Phe Val Leu Asp Arg Phe Gly Leu	
50	55
Gly Phe Met Gln Thr Ile Ala Phe Ile Leu Val Ile Ala Ala Leu Val	
65	70
Gln Met Val Glu Ile Ile Leu Lys Lys Val Ser Pro Pro Leu Tyr Gln	
	85
Ala Leu Gly Val Phe Leu Pro Leu Ile Thr Thr Asn Cys Cys Val Leu	
	100
Gly Val Ala Ile Leu Val Ile Gln Lys Asp Tyr Thr Leu Leu Gln Ser	
	115
Phe Val Tyr Ala Ile Ser Thr Ala Ile Gly Phe Thr Leu Ala Met Val	
	130
Thr Phe Ala Gly Ile Arg Glu Gln Leu Asp Met Thr Asn Leu Pro Lys	
145	150
Ala Met Lys Gly Ile Pro Ser Ala Leu Leu Ala Ala Gly Ile Leu Ala	
	165
Met Ala Phe Met Gly Phe Ser Gly Ile Ala	
	180
	185

(2) INFORMATION FOR SEQ ID NO:441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```
Met Lys Gln Leu Asn Ile Ile Ser Phe Ile Ile Ala Phe Leu Phe Leu
1      5      10      15
Gly Thr Ser Ala Ser Ala Gln Gln Ser Gly Gly Ser Val Thr Gly Thr
20      25      30
Val Val Asp Lys Ser Ser Lys Glu Pro Ile Ala Tyr Val Gln Val Phe
35      40      45
Val Lys Gly Thr Thr Leu Gly Thr Ser Thr Asp Ala Asn Gly Asn Tyr
50      55      60
Ser Ile Lys Gly Ile Pro Ser Gly Asn Gln Thr Ile Val Ala Arg Leu
65      70      75      80
Met Gly Tyr Ser Thr Cys Glu Glu Lys Val His Ile Glu Lys Gly Gly
85      90      95
Ser Arg His Val Asp Leu Tyr Leu Thr Glu Glu Ile Leu Ser Leu Asp
100     105     110
Gly Val Val Val Ser Ala Asn Arg Asn Glu Thr Phe Arg Arg Gln Ala
115     120     125
Pro Ser Leu Val Thr Val Leu Ser Pro Glu Leu Phe Leu Lys Thr Asn
130     135     140
Ser Thr Asn Leu Ser Gln Gly Leu Lys Phe Gln Pro Gly Leu Arg Val
145     150     155     160
Glu Asp Asn Cys Gln Asn Cys Gly Phe Asn Gln Val Arg Ile Asn Gly
165     170     175
Leu Glu Gly Ala Tyr Ser Gln Ile Leu Ile Asp Ser His Pro Ile Phe
180     185     190
Ser Ser Leu Ala Gly Val Tyr Gly Leu Glu Gln Met Pro Ala Asn Met
195     200     205
Ile Glu Arg Val Glu Val Ile Arg Gly Gly Gly Ser Ala Leu Phe Gly
210     215     220
Ser Asn Ala Val Gly Gly Val Ile Asn Val Ile Thr Lys Glu Pro Leu
225     230     235     240
Arg Asn Ser Ala Glu Ile Ser His Ser Thr Met Thr Phe Asp His Ala
245     250     255
Lys Gly Trp Gly Ser Phe Gln Asn Thr Thr Gln Phe Asn Gly Ser Met
260     265     270
Leu Thr Glu Asp Arg Lys Ala Gly Val Met Val Phe Gly Gln His Asn
275     280     285
Tyr Arg Pro Gly Gln Asp Ile Asp Gly Asp Asn Phe Thr Glu Leu Pro
290     295     300
Asn Leu Arg Asn Arg Ser Leu Gly Phe Arg Ser Tyr Tyr Lys Thr Gly
305     310     315     320
Leu Tyr Ser Lys Ala Thr Leu Glu Tyr His Ser Met Gln Glu Tyr Arg
325     330     335
Arg Gly Gly Asp Arg Leu Asp Asn Pro Pro Phe Glu Ala Gln Ile Ala
340     345     350
Glu Tyr Leu Gln His Tyr Ile Asn Gly Gly Ser Phe Lys Phe Asp Gln
355     360     365
Gly Phe Ser Gly Gly Lys Asp Phe Phe Ser Leu Tyr Ala Ser Ala Gln
370     375     380
Asp Val Gln Arg Arg Ser Tyr Tyr Gly Gly Gly Asp Tyr Thr Glu Asn
385     390     395     400
Leu Leu Asn Gly Ala Val Gln Ser Gly Ser Thr Glu Ser Asp Glu Tyr
405     410     415
Asn Asp Ala Phe Thr Ala Leu Thr Ser Tyr Gly Thr Thr Lys Gly Phe
420     425     430
Asp Leu Gln Gly Gly Gly Met Tyr Arg His Thr Phe Gly Glu Asn Trp
435     440     445
Asp Phe Thr Gly Gly Leu Glu Tyr Ile Tyr Gly Gln Leu Asp Asp Arg
450     455     460
Ser Gly Tyr Arg Pro Ser Lys Ile Asp Gln Asn Thr Ser Thr Phe Ser
465     470     475     480
Gln Tyr Asp Gln Leu Glu Tyr Lys Thr Glu Lys Leu Ser Ala Leu Ile
485     490     495
Gly Ala Arg Ile Asp Tyr Val Leu Leu Asn Gln Asp Gly Lys Arg Tyr
500     505     510
Ile Asp Pro Leu Phe Ile Phe Ser Pro Arg Ala Asn Val Arg Tyr Asn
515     520     525
Pro Asn Lys Asn Leu Ser Phe Arg Leu Ser Tyr Ser Glu Gly Phe Arg
530     535     540
Ala Pro Gln Tyr Phe Asp Glu Asp Leu His Val Glu Leu Ala Gly Gly
```


145					150					155				160
Ile	Val	Gln	Lys	Tyr	Phe	Ser	Glu	Lys	Gly	Tyr	Arg	Asp	Ala	Ser
				165					170					175
Arg	Ile	Thr	Gln	Glu	Pro	Asp	Leu	Ser	Lys	Asp	Gly	Phe	Val	Asn
			180					185					190	
Leu	Ile	Ser	Ile	Glu	Lys	Lys	Ser	Lys	Thr	Lys	Val	Asn	Glu	Ile
		195					200					205		
Phe	Ser	Gly	Asn	Lys	Ala	Leu	Ser	Asn	His	Lys	Leu	Arg	Met	Ala
	210					215				220				
Lys	Asn	Thr	Asn	Ala	Lys	Phe	Ser	Leu	Arg	Lys	His	Ile	Arg	Ser
	225				230					235				240
Phe	Leu	Lys	Leu	Phe	Ser	Thr	His	Lys	Phe	Val	Glu	Glu	Ser	Tyr
			245						250				255	
Glu	Asp	Leu	Val	Arg	Leu	Ile	Glu	Lys	Tyr	Gln	Glu	Tyr	Gly	Tyr
		260						265					270	
Asp	Ala	Glu	Ile	Leu	Thr	Asp	Ser	Val	Val	Lys	Ala	Pro	Asp	Gly
	275					280					285			
Arg	Val	Asp	Ile	Tyr	Leu	Asn	Ile	Glu	Glu	Gly	Gln	Lys	Tyr	Tyr
	290					295					300			
Lys	Asp	Val	Asn	Phe	Val	Gly	Asn	Ser	Gln	Tyr	Pro	Ser	Glu	Tyr
	305				310					315				320
Glu	Arg	Val	Leu	Gly	Ile	Lys	Ser	Gly	Asp	Val	Tyr	Asn	Gln	Arg
			325						330				335	
Leu	Ala	Lys	Arg	Leu	Asn	Glu	Asp	Glu	Asp	Ala	Val	Gly	Asn	Leu
		340					345						350	
Tyr	Asn	Asn	Gly	Tyr	Ile	Phe	Ala	Trp	Val	Asp	Pro	Val	Glu	Thr
	355					360					365			
Val	Val	Gly	Asp	Ser	Val	Ser	Leu	Asp	Ile	Arg	Ile	Ala	Glu	Gly
	370				375					380				
Gln	Ala	Asn	Ile	Asn	Lys	Val	Ile	Ile	Lys	Gly	Asn	Thr	Val	Val
	385				390					395				400
Glu	Asp	Val	Val	Arg	Glu	Leu	Tyr	Thr	Lys	Pro	Gly	Gln	Leu	Phe
			405					410					415	
Ser	Arg	Glu	Asp	Ile	Ile	Asn	Ser	Ile	Arg	Leu	Ile	Asn	Gln	Leu
	420						425						430	
His	Phe	Asp	Ala	Glu	Lys	Ser	Ile	Pro	Arg	Pro	Ile	Pro	Asn	Pro
	435					440				445				
Thr	Gly	Thr	Val	Asp	Ile	Glu	Tyr	Asp	Leu	Val	Pro	Arg	Ser	Ser
	450				455					460				
Gln	Leu	Glu	Leu	Ser	Val	Gly	Trp	Ser	Gln	Ser	Gly	Leu	Leu	Phe
	465				470					475				480
Gly	Ala	Ile	Lys	Phe	Thr	Asn	Phe	Ser	Val	Gly	Asn	Leu	Leu	His
			485						490				495	
Ser	Met	Tyr	Lys	Lys	Gly	Ile	Ile	Pro	Gln	Gly	Asp	Gly	Gln	Thr
		500					505						510	
Ser	Leu	Ser	Ala	Gln	Thr	Asn	Gly	Lys	Tyr	Tyr	Gln	Gln	Tyr	Ser
	515					520					525			
Thr	Phe	Met	Asp	Pro	Trp	Phe	Gly	Gly	Lys	Arg	Pro	Asp	Met	Phe
	530					535					540			
Phe	Ser	Ala	Phe	Tyr	Ser	Lys	Thr	Thr	Ala	Ile	Asp	Ser	Lys	Phe
	545				550					555				560
Asn	Ser	Asn	Ala	Gly	Asn	Tyr	Tyr	Asn	Ala	Tyr	Tyr	Asn	Ser	Tyr
			565						570				575	
Asn	Asn	Tyr	Asn	Ser	Tyr	Tyr	Asn	Gly	Met	Ser	Asn	Tyr	Thr	Gly
		580						585					590	
Leu	Tyr	Thr	Gln	Ala	Ser	Asp	Pro	Asp	Arg	Ser	Leu	Gln	Met	Leu
		595					600					605		
Thr	Ser	Ile	Gly	Tyr	Gly	Lys	Arg	Leu	Thr	Trp	Pro	Asp	Asn	Trp
	610					615					620			
Gln	Ile	Tyr	Thr	Ser	Leu	Asn	Tyr	Thr	Tyr	Tyr	Arg	Leu	Arg	Asn
	625				630						635			640
Ser	Tyr	Asn	Thr	Phe	Gln	Asn	Phe	His	His	Gly	Ser	Ala	Asn	Asp
			645					650					655	
Asn	Leu	Glu	Leu	Arg	Leu	Ser	Arg	Thr	Ser	Ile	Asp	Asn	Pro	Ile
		660						665				670		
Thr	Arg	Ser	Gly	Ser	Asp	Phe	Met	Val	Ser	Val	Ala	Ala	Thr	Leu
	675						680				685			
Tyr	Ser	Leu	Trp	Asp	Asn	His	Asp	Tyr	Ala	Ser	Gln	Asn	Leu	Ser
	690				695						700			
Ser	Asp	Arg	Tyr	Arg	Phe	Ile	Glu	Tyr	His	Lys	Trp	Lys	Phe	Arg
	705				710					715				720
Arg	Val	Phe	Thr	Pro	Leu	Leu	Asn	Pro	Ala	Thr	His	Lys	Tyr	Thr
			725						730				735	
Val	Leu	Met	Ser	Arg	Val	Glu	Gly	Ala	Val	Leu	Gly	Ser	Tyr	Asn
		740						745				750		
Asn	Lys	Lys	Ser	Pro	Phe	Gly	Thr	Phe	Tyr	Met	Gly	Gly	Asp	Gly
	755					760					765			


```

Ser Ser Tyr Tyr Gly Gly Tyr Met Asn Glu Thr Ile Gly Leu Arg Gly
770      775      780
Tyr Lys Asn Gly Ser Ile Ala Gly Asn Asn Tyr Asp Tyr Ala Tyr Ala
785      790      795      800
Tyr Met Arg Leu Thr Met Glu Leu Arg Phe Pro Ile Leu Phe Glu Asn
      805      810      815
Ser Phe Asn Ala Trp Leu Leu Ala Phe Ala Glu Ala Gly Asn Ala Trp
      820      825      830
Arg Ser Ile Asp Asn Tyr Asn Pro Phe Asn Leu Lys Arg Ser Ala Gly
      835      840      845
Val Gly Leu Arg Val Thr Leu Pro Met Val Gly Met Leu Gly Ile Asp
      850      855      860
Trp Gly Tyr Gly Phe Asp Arg Pro Asp Asn Ser Leu Gln Arg Gly Gly
865      870      875      880
Ser Asn Val His Phe Val Leu Gly Gln Glu Phe
      885      890

```

(2) INFORMATION FOR SEQ ID NO:443

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...174
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

```

Met Asn Gly Asp Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu
1      5      10      15
Ala Val Ala Phe Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met
      20      25      30
Glu Tyr Ile Leu Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln
      35      40      45
Leu Glu Gln Val Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu
      50      55      60
Asn Glu Ala Gln Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe
65      70      75      80
Leu Ser Ala Ala Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys
      85      90      95
Glu Gln Gln Ala Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly
      100      105      110
Glu Leu Tyr Lys Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu
      115      120      125
Ile Trp Asn Ala Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met
      130      135      140
Val Leu Asp Arg Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile
145      150      155      160
Asp Ile Ser Asp Leu Val Leu Ser Lys Met Gly Phe Ser Lys
      165      170

```

(2) INFORMATION FOR SEQ ID NO:444

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

```
Met Lys Arg Phe Leu Ile Leu Ile Gly Phe Ala Leu Ala Val Ala Phe
1      5      10      15
Ser Gly Phe Ser Gln Lys Phe Ala Leu Val Asp Met Glu Tyr Ile Leu
      20      25      30
Arg Asn Ile Pro Asp Tyr Glu Met Met Asn Glu Gln Leu Glu Gln Val
      35      40      45
Ser Lys Lys Trp Gln Asn Glu Ile Glu Ala Leu Glu Asn Glu Ala Gln
      50      55      60
Ser Met Tyr Lys Lys Tyr Gln Ser Asp Leu Val Phe Leu Ser Ala Ala
      65      70      75      80
Gln Lys Lys Thr Gln Glu Glu Ala Ile Val Lys Lys Glu Gln Gln Ala
      85      90      95
Ser Glu Leu Lys Arg Lys Tyr Phe Gly Pro Glu Gly Glu Leu Tyr Lys
      100      105      110
Lys Arg Ser Asp Leu Met Lys Pro Ile Gln Asp Glu Ile Trp Asn Ala
      115      120      125
Ile Lys Glu Ile Ala Lys Arg Asn Asn Tyr Gln Met Val Leu Asp Arg
      130      135      140
Gly Thr Ser Gly Ile Ile Phe Ala Ser Pro Ser Ile Asp Ile Ser Asp
      145      150      155      160
Leu Val Leu Ser Lys Met Gly Phe Ser Lys
      165      170
```

(2) INFORMATION FOR SEQ ID NO:445

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```
Met Lys Lys Phe Phe Leu Met Leu Leu Met Ala Leu Pro Leu Ser Leu
1      5      10      15
Leu Ala Gln Lys Val Ala Val Val Asn Thr Glu Glu Ile Ile Ser Lys
      20      25      30
Met Pro Glu Gln Val Ala Ala Thr Lys Gln Leu Asn Glu Leu Ala Glu
      35      40      45
Lys Tyr Arg Leu Asp Leu Lys Ser Met Asp Asp Glu Phe Ala Lys Lys
      50      55      60
Thr Glu Glu Phe Val Lys Glu Lys Asp Ser Leu Glu Asn Ile Arg
      65      70      75      80
Asn Arg Arg Gln Gln Glu Leu Gln Asp Ile Gln Thr Arg Tyr Gln Gln
      85      90      95
Ser Tyr Gln Thr Met Gln Glu Asp Leu Gln Lys Arg Gln Gln Leu
      100      105      110
Phe Ala Pro Ile Gln Gln Lys Val Ala Asp Ala Ile Lys Lys Val Gly
      115      120      125
Asp Glu Glu Asn Cys Ala Tyr Ile Met Glu Ala Gly Met Met Leu Tyr
      130      135      140
Thr Gly Ala Thr Ala Ile Asp Leu Thr Ala Lys Val Lys Ala Lys Leu
      145      150      155      160
Gly Ile Lys
```

(2) INFORMATION FOR SEQ ID NO:446

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```
Met Lys Glu Ala Ile Pro Arg Lys Asn Lys Tyr Ile Lys Leu Asn Gly
1      5      10      15
Ile Tyr Arg Leu Ser Phe Ile Leu Leu Cys Cys Leu Leu Cys Ser Gln
20      25      30
Ala Ala Met Ala Gln Gly Val Arg Val Ser Gly Tyr Val Leu Asp Arg
35      40      45
Gly Glu Lys Pro Ile Pro Phe Ala Gly Val Lys Val Arg Gly Thr Gly
50      55      60
Thr Gly Ala Thr Thr Asn Leu Lys Gly Tyr Tyr Glu Phe Arg Met Lys
65      70      75      80
Ala Thr Thr Asp Ser Ile Thr Ile Glu Phe Ser Ser Met Gly Tyr Gln
85      90      95
Gly Val Ser Arg Ser Phe Pro Ser Leu Thr Lys Asp Thr Arg Leu Asn
100     105     110
Val Arg Leu Ala Glu Ala Glu Met Glu Leu Ser Ser Val Thr Val Gln
115     120     125
Ala Thr Lys Arg Arg Leu Asn Thr Met Glu Arg Val Asn Thr Arg Asp
130     135     140
Leu Arg Val Asn Ala Gly Pro Thr Gly Gly Val Glu Ser Leu Ile Ser
145     150     155     160
Thr Tyr Ala Gly Val Thr Gln Asn Asn Glu Leu Ser Ser Gln Tyr Ser
165     170     175
Val Arg Gly Gly Ser Tyr Asp Glu Asn Met Val Tyr Val Asn Gly Val
180     185     190
Glu Val Tyr Arg Pro Leu Leu Val Arg Ser Ala Gln Gln Glu Gly Leu
195     200     205
Ser Phe Val Asn Pro Asp Leu Thr Gln Ser Val Gln Phe Ser Ala Gly
210     215     220
Gly Phe Thr Ala Asp Tyr Gly Asp Lys Met Ser Ser Val Leu Asp Ile
225     230     235     240
Arg Tyr Lys Gln Pro Gln Glu Lys Glu Gly Ala Val Leu Leu Gly Met
245     250     255
Leu Gln Ser Ser Ala Tyr Tyr Gly Ser Ser Ala Gly Ala Phe Ser Gln
260     265     270
Ile Thr Gly Val Arg Tyr Lys Ser Ala Lys Ser Leu Leu Gly Thr Thr
275     280     285
Asp Thr Lys Ala Glu Tyr Asp Pro Ile Tyr Ala Asp Gly Gln Thr Phe
290     295     300
Met Thr Tyr Arg Phe Ser Pro Lys Leu Ser Val Ser Phe Leu Gly Asn
305     310     315     320
Ile Ser Gln Thr Arg Tyr Lys Phe Val Pro Gln Thr Arg Glu Thr Ser
325     330     335
Phe Gly Thr Leu Ser Asp Ala Lys Lys Leu Lys Ile Phe Phe Asp Gly
340     345     350
Gln Glu Gln Asp Arg Phe Leu Thr Tyr Phe Gly Ala Phe Ser Met Asn
355     360     365
Phe Val Pro Asp Asp Lys Gln Arg His Thr Val Thr Leu Ser Ala Phe
370     375     380
Asn Ser Asn Glu Arg Glu Thr Tyr Asp Ile Gln Gly Glu Tyr Phe Leu
385     390     395     400
Asn Asp Val Gln Leu Gly Ala Asp Gly Thr Ala Ser Met Ala Ser Gly
405     410     415
Ser Glu Asn Ser Asn Gly Leu Gly Ile Gly Arg Asn His Glu His Ala
420     425     430
Arg Asn Arg Leu Ser Tyr Arg Val Leu Asn Met Gly Tyr Arg Gly Glu
435     440     445
Met Lys Leu Asn Glu Lys His Arg Leu Gln Ala Gly Val Ser Ala Gln
450     455     460
Met Glu Lys Ile Ala Asp His Ile Ser Glu Trp Glu Arg Arg Asp Ser
465     470     475     480
Val Gly Tyr Asn Leu Pro His Ser Glu Thr Val Leu Leu Met Tyr Asn
485     490     495
Asn Leu Tyr Ala Asp Thr Gln Met Arg Gly Thr Arg Leu Ser Ala Phe
500     505     510
Val Gln Asp Arg Phe Asn Phe Ser Met Gly Gly Gly Thr Phe Ser Leu
```

```

      515              520              525
Ile Pro Gly Ile Arg Ala Ser Trp Trp Ser Phe Asn Lys Glu Leu Leu
530              535              540
Val Ser Pro Arg Ile Ser Val Gly Tyr Ser Pro Glu Ser Asn Pro Ala
545              550              555              560
Leu Val Leu Arg Ala Ala Ala Gly Leu Tyr Tyr Gln Ala Pro Phe Tyr
      565              570              575
Lys Glu Leu Arg Gln Thr His Lys Asp Ala Glu Gly Asn Asn Val Val
      580              585              590
Val Leu Asn Glu Lys Ile Arg Ser Ser Gln Gly Ala Phe His Ile Leu Ala
      595              600              605
Gly Ala Asp Tyr Thr Phe Glu Met Gly Gly Arg Lys Tyr Lys Phe Thr
      610              615              620
Ala Glu Ala Tyr Tyr Lys Ser Leu Phe Asn Ile Asn Pro Tyr Ile Ile
625              630              635              640
Glu Asn Val Lys Ile Arg Tyr Leu Gly Glu Asn Ile Gly Ser Gly Tyr
      645              650              655
Ala Ala Gly Ile Asp Leu Lys Leu Phe Gly Glu Leu Val Pro Gly Val
      660              665              670
Asp Ser Trp Leu Thr Ala Ser Ile Ile Lys Ala Arg Gln Lys Leu Asp
      675              680              685
Gly Tyr Gly Ser Leu Pro Leu Met Asn Ala Pro Thr Tyr Asn Phe Ser
      690              695              700
Phe Phe Leu Gln Glu Tyr Val Pro Gly Asn Lys Arg Ile Thr Ala Thr
705              710              715              720
Leu Arg Ala Ala Leu Ser Gly Gly Leu Pro Gln Leu Asn Pro Ser Lys
      725              730              735
Gly Leu Ser Ser Pro Ala Phe Thr Ala Pro Ala Tyr Lys Arg Val Asp
      740              745              750
Leu Gly Val Met Tyr Lys Trp Leu Asp Pro Asp Asp Ser Phe Ala Gly
      755              760              765
Arg Ser Lys Trp Leu Met Gly Val Lys Gly Ala Tyr Ile Gly Ala Asp
      770              775              780
Leu Phe Asn Leu Phe Asp Met Thr Asn Val Asn Ser Tyr Tyr Trp Val
785              790              795              800
Ser Asp Ala Tyr Gln Gln Gln Tyr Ala Val Pro Asn Tyr Leu Thr Arg
      805              810              815
Arg Gln Phe Asn Leu Arg Leu Leu Val Glu Phe
      820              825

```

(2) INFORMATION FOR SEQ ID NO:447

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

```

Met Tyr Ser Gly His His Lys Ile His Tyr Pro Phe Leu Ile Leu Leu
1              5              10              15
Val Cys Leu Ala Phe Ala Ala Cys Lys Ser Val Lys Leu Lys Asp Ala
      20              25              30
Glu Lys Ala His Asp Arg Gln Glu Tyr Thr Lys Ala Ala Asp Met Tyr
      35              40              45
Asn Thr Leu Tyr Arg Arg Thr Arg Arg Lys Gln Val Glu Met Lys Ala
      50              55              60
Tyr Thr Ala Phe Arg Ser Gly Glu Asn Tyr Arg Ala Ala Gly Arg Gln
65              70              75              80
Ala Lys Ala Leu Arg Gly Tyr Leu Asn Ala Arg Arg Tyr Gly Tyr Pro
      85              90              95
Asp Ser Val Val Leu Leu Arg Leu Ala Gln Thr Tyr Gln Gln Gly Gly
      100              105              110
Asn Tyr Lys Glu Ala Glu Val Leu Phe Arg Gly Tyr Leu Glu Ala Tyr
      115              120              125
Pro Lys Ser Tyr Phe Ala Ala Ile Gly Leu Glu Gly Cys Leu Phe Ala

```

130	135	140
Arg Gln Gln Lys Glu Tyr Pro Thr Arg Tyr Arg Ile Arg Arg Ala Ala		
145	150	155
Glu Trp Asn Ser Ala Arg Gly Asp Phe Gly Pro Ala Tyr Ala Pro Asp		160
	165	170
Ala Ser Ala Leu Tyr Phe Thr Ser Ser Arg Ser Lys Asp Asp Gly Leu		175
	180	185
Asp Asn Ser Ser Ile Thr Gly Leu Lys Pro Asn Asp Ile Tyr Ile Ile		190
	195	200
Lys Arg Asp Ala Gln Gly Arg Trp Gly Arg Pro Asp Ser Val Ser Gly		205
	210	215
Gly Ile Asn Thr Pro Trp Asp Glu Gly Val Pro Thr Ile Thr Pro Asp		220
225	230	235
Gly Ser Thr Ile Tyr Thr Leu Ala Gln Gln Gly Ala Asp Tyr Asp		240
	245	250
Arg Thr Val Gln Ile Tyr Ser Ala Ala Arg Ser Gly Glu Gly Gly Trp		255
	260	265
Ser Asn Gly Ser Leu Val Asp Ile Met Arg Asp Ser Leu Arg Met Ala		270
	275	280
Ala His Pro Ser Met Ser Ala Ser Gly Asp Tyr Leu Tyr Phe Val Ser		285
	290	295
Asn Ile Gly Gly Ser Tyr Gly Gly Lys Asp Ile Tyr Arg Val Lys Val		300
305	310	315
Ser Asp Arg Ser Tyr Gly Ser Pro Glu Asn Leu Gly Pro Asp Ile Asn		320
	325	330
Thr Pro Gly Asp Glu Met Phe Pro Phe Ile Asp Gly Asp Ser Thr Leu		335
	340	345
Phe Phe Ala Ser Asp Gly His Ala Gly Leu Gly Gly Leu Asp Ile Phe		350
	355	360
Lys Ala Thr Leu Asp Ser Thr Gly Gln Trp His Val Val Asn Met Gly		365
	370	375
Gln Pro Val Asn Ser Ser Ala Asp Asp Phe Gly Leu Ala Val Glu Pro		380
385	390	395
Lys Gly Lys Asn Lys Glu Glu Ala Leu Pro Asp Asn Gly Val Lys Gly		400
	405	410
Val Phe Cys Ser Asn Arg Gly Asp Ala Arg Gly Trp Pro His Leu Phe		415
	420	425
His Phe Glu Leu Pro Ala Ile Tyr Thr Glu Ile Gln Gly Tyr Val Met		430
	435	440
Asp Arg Glu Glu Asn Pro Ile Ala Gly Ala Thr Val Arg Ile Val Gly		445
	450	455
Glu Arg Gly Pro Val Gly Gln Gly Phe Val Thr Thr Arg Asp Asp Gly		460
465	470	475
Ser Tyr Lys Met Ser Val Gln Gly Asp Thr Arg Tyr Val Met Leu Ala		480
	485	490
Gly Ala Ser Gly Tyr Leu Asn Gln Tyr Val Glu Leu Lys Thr Asp Thr		495
	500	505
Ala Lys Gln Ser Glu Thr Tyr Tyr Val Asp Phe Phe Leu Ala Ser Arg		510
	515	520
Glu Lys Ala Glu Gly Leu Gln Asn Ile Phe Tyr Asp Phe Asp Lys Ala		525
	530	535
Thr Leu Arg Pro Glu Ser Met Lys Ser Leu Asp Glu Leu Ile Arg Ile		540
545	550	555
Leu Thr Asp Asn Pro Asp Ile Arg Ile Glu Leu Gly Ser His Ala Asp		560
	565	570
Arg Lys Gly Pro Asp Ala Tyr Asn Leu Gly Leu Ser Asp Arg Arg Ala		575
	580	585
Lys Ser Val Val Asp Tyr Leu Thr Ser Arg Gly Ile Ala Ala Asp Arg		590
	595	600
Leu Thr Trp Lys Gly Tyr Gly Lys Ser Val Pro Lys Thr Val Thr Ala		605
	610	615
Lys Ile Ala Glu Arg His Asp Phe Leu Lys Glu Gly Asp Val Leu Thr		620
625	630	635
Glu Glu Phe Val Ala Pro Leu Thr Glu Glu Gln Ser Val Cys Asp		640
	645	650
Gln Leu Asn Arg Arg Thr Glu Phe Arg Val Ile Glu Glu Glu Leu Arg		655
	660	665
		670

(2) INFORMATION FOR SEQ ID NO:448

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

```
Met Lys Lys Phe Phe Phe Ala Leu Leu Ser Ile Gly Ile Ser Ala Gln
1      5      10      15
Ala Phe Ala Lys Thr Asp Asn Val Pro Thr Asp Ser Leu Arg Val His
20      25      30
Asn Leu Gln Thr Val Thr Val Tyr Ser Thr Arg Thr Ala Val Pro Leu
35      40      45
Lys Lys Ile Pro Ala Lys Met Glu Leu Ile Ser Ser Arg Asn Ile Lys
50      55      60
Gln Ser Gly Phe Asn Asn Met Thr Asp Ile Leu Lys Thr Gln Ser Ser
65      70      75      80
Leu Asp Val Ile Gln Tyr Pro Gly Phe Ser Ser Asn Ile Gly Ile Arg
85      90      95
Gly Phe Lys Pro Ser Gly Lys Tyr Val Thr Val Leu Val Asn Gly Ile
100     105     110
Pro Ala Gly Thr Asp Asn Ile Ser Thr Leu Asn Thr Ser Asn Ile Glu
115     120     125
Gln Ile Glu Ile Leu Lys Gly Pro Phe Ser Ser Ile Tyr Gly Thr Asn
130     135     140
Ala Met Gly Gly Val Val Asn Ile Ile Thr His Lys Ser Lys Asp Lys
145     150     155     160
Ile His Gly Asn Val Ser Leu Phe Gly Gly Ser Tyr Gln Thr Met Ala
165     170     175
Gly Ser Phe Asn Leu Gly Gly Arg Phe Glu Asp Ile Phe Ser Phe Asp
180     185     190
Leu Ser Leu Gly Leu Asp Lys Gln Asn Lys Asp Tyr Lys Thr Gly Ser
195     200     205
Asn Asn Phe Leu Ser Leu Ser Lys Leu Glu Glu Ala Ile Val Asp Val
210     215     220
Asn Ala Thr Lys Asn Lys Lys Met Lys Gly Ser Asp Tyr Thr Val Ala
225     230     235     240
Thr Gly Arg Leu Arg Phe Gly Ile Asp Phe Thr Pro Glu Trp Ser Leu
245     250     255
Asn Leu Tyr Gln Asn Val Phe Leu Gly Asp Ala Ile Pro Val Gly Gly
260     265     270
Ser Ile Trp Gly Val Tyr Gly Glu Ser Lys Lys Asn Leu Asn Arg Ser
275     280     285
Ser Thr Ser Phe Glu Leu Leu Gly Lys His Gly Cys His Thr Leu Gln
290     295     300
Phe Ser Pro Tyr Phe Asn Ile Glu Lys Ser Glu Asn Tyr Asn Asn Ala
305     310     315     320
Asp Pro Thr Gly Phe Ile Asn Tyr Lys Ser Asp Tyr Tyr Thr Tyr Gly
325     330     335
Ala Leu Leu Gln Asp Lys Ile Ser Phe Gly Gly Gln Asn Ile Val Leu
340     345     350
Gly Val Asp Ser Arg Asn Met Thr Met Glu Ser Glu Arg Phe Glu Gln
355     360     365
Ala Gly Val Asn Thr Lys Pro Tyr Asn Pro Gly Tyr Ala Thr Asn Asn
370     375     380
Ile Gly Leu Phe Gly Gln Ala Asn Phe Tyr Leu Leu Asn Asp Ala Leu
385     390     395     400
Ser Ile Ser Ala Gly Ala Arg Ala Asp Phe Met Phe Phe Asp Leu Lys
405     410     415
Ala Asn Glu Tyr Leu Asn Asn Glu Ala Lys Gln Glu Thr His Asn Val
420     425     430
Ile Asn Pro Asn Val Gly Ile Lys Tyr Glu Phe Val Lys Gly Leu Thr
435     440     445
Ala His Gly Thr Phe Gly Ser Ala Phe Ser Ala Pro Asp Ala Phe Gln
450     455     460
Lys Ala Gly Gln Tyr Val Gly Pro Phe Gly Thr Thr Ile Gly Asn Pro
465     470     475     480
Asp Leu Lys Pro Glu Lys Ser Met Thr Trp Asp Phe Gly Ile Gly Tyr
485     490     495
Ser Asn Ala Arg Cys Gly Ile Gln Ala Asp Val Thr Leu Thr Tyr Phe
500     505     510
His Thr Asp His Lys Asp Leu Ile Leu Ser Ser Pro Asp Tyr Ala Asn
515     520     525
```

```

Asn Ile Thr Thr Tyr Ile Asn Ala Asp Lys Ala Arg Met Ser Gly Ile
530          535          540
Glu Ala Leu Leu Ser Tyr Asp Phe Gly Ser Leu Phe Ala Asn Lys Phe
545          550          555          560
Ser Leu Arg Ala Phe Ala Asn Ala Thr Ile Met Leu Asn Ser Glu Met
565          570          575
Lys Lys Ser Gln Thr Asp Ala Pro Trp Ser Glu Met Tyr Tyr Val Arg
580          585          590
Lys Gln Asn Ile Thr Phe Gly Ile Glu Tyr Arg Gly Lys Glu Gly Leu
595          600          605
Glu Val Met Leu Asn Gly Arg Phe Met Gly Arg Arg Ile Glu Gln Asn
610          615          620
Trp Tyr Ala Tyr Tyr Pro Glu Val Arg Pro Glu Leu Gln Gln Leu Leu
625          630          635          640
Ala Ala Glu Glu Pro Glu Leu Ala Ala Gln Gly Leu Leu Arg His Pro
645          650          655
Gln Ala Met Val Phe Asn Ala Ser Ala Tyr Tyr His Met Asn Lys Tyr
660          665          670
Leu Thr Phe Gly Val Asn Leu Asn Ile Leu Asp Glu Leu Tyr Thr
675          680          685
Glu Lys Asp Gly Tyr His Met Pro Gly Arg Asn Ile Met Gly Lys Val
690          695          700
Met Val Asn Phe
705

```

(2) INFORMATION FOR SEQ ID NO:449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

```

Met Asn Arg Phe Ser Asn His Trp Pro Cys Ile Leu Val Gly Phe Val
1          5          10          15
Leu Trp Phe Val Ser Ala Ser Arg Thr Val Ala Gln Asn Ala Ser Glu
20          25          30
Thr Thr Val Ser Tyr Asp Thr Asp Thr Ala Val Leu Ser Glu Ala Asp
35          40          45
Val Leu Arg Ile Ala Leu Ser Glu Asn Ala Thr Val Lys Val Ala Asp
50          55          60
Met Asp Val Arg Lys Gln Glu Tyr Ala Arg Arg Ala Ala Arg Ala Asp
65          70          75          80
Leu Phe Pro Lys Val Asp Leu Asn Gly Val Tyr Ser His Thr Leu Lys
85          90          95
Lys Gln Val Leu Tyr Ile Asp Met Pro Gly Phe Ser Ser Ser Glu Gly
100          105          110
Ile Glu Met Gly Arg Thr His Asn Thr Gln Gly Gly Val Asn Val Ser
115          120          125
Met Pro Leu Val Ser Ala Gln Leu Trp Lys Ser Ile Ala Met Thr Gly
130          135          140
Glu Gln Leu Asp Leu Ala Leu Glu Lys Ala Arg Ser Ser Arg Ile Asp
145          150          155          160
Leu Val Ala Glu Val Lys Lys Ala Tyr Leu Ser Val Leu Leu Ala Glu
165          170          175
Asp Ser Tyr Gly Val Phe Lys Arg Ser Tyr Asp Asn Ala Leu Ala Asn
180          185          190
Tyr Lys Asn Ile Ser Asp Lys Phe Asp Arg Gly Leu Val Ala Glu Tyr
195          200          205
Asp Lys Ile Arg Ala Asn Val Gln Val Arg Asn Ile Glu Pro Asn Leu
210          215          220
Leu Gln Ala Gln Asn Ser Val Ala Leu Ala Leu Trp Gln Leu Lys Val
225          230          235          240
Leu Met Ser Met Glu Val Glu Thr Pro Ile Arg Leu Ser Gly Ser Leu
245          250          255

```

```

Ser Asp Tyr Lys Glu Gln Val Tyr Thr Gly Tyr Phe Ala Ala Asp Thr
      260      265      270
Leu Ile Ser Asn Asn Ser Ser Leu Arg Gln Leu Asp Ile Gln Arg Arg
      275      280      285
Leu Ala Val Ser Ala Asp Lys Leu Asn Lys Tyr Ser Phe Leu Pro Thr
      290      295      300
Leu Asn Leu Gly Gly Gln Tyr Thr Tyr Ser Leu Asn Ser Asn Asp Ile
      305      310      315      320
Lys Phe Trp Gly Glu Gly Gln Arg Trp Thr Pro Phe Ser Thr Ile Ser
      325      330      335
Leu Ser Leu Tyr Ile Pro Ile Phe Asn Gly Gly Lys Arg Leu Tyr Asn
      340      345      350
Val Lys Gln Ser Ala Leu Ser Ile Arg Gln Ile Asp Leu Gln Arg Arg
      355      360      365
His Ile Glu Gln Ser Ile Arg Met Gly Ile Lys Asn Gln Asn Asp Arg
      370      375      380
Leu Arg Thr Cys Met Gln Arg Phe Val Ala Ser Glu Glu Ala Val Arg
      385      390      395      400
Ser Ala Glu Lys Gly Tyr Gln Ile Ala Glu Lys Arg Tyr Gln Thr Gly
      405      410      415
Glu Gly Thr Leu Val Glu Leu Asn Asp Ala Asp Val Ala Leu Leu Gln
      420      425      430
Ala Arg Leu Asn Tyr Asn Gln Ala Ile Phe Asp Phe Met Thr Ala Lys
      435      440      445
Ala Glu Leu Asp Lys Met Asn Gly Met Gly Ile Pro Glu Gln
      450      455      460

```

(2) INFORMATION FOR SEQ ID NO:450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

```

Met Trp Gly Asp Ser His Gly Val Ala Pro Asn Gln Val Arg Arg Thr
1      5      10      15
Leu Val Lys Val Ala Leu Ser Glu Ser Leu Pro Pro Gly Ala Lys Gln
      20      25      30
Ile Arg Ile Gly Phe Ser Leu Pro Lys Glu Thr Glu Glu Lys Val Thr
      35      40      45
Ala Leu Tyr Leu Leu Val Ser Asp Ser Leu Ala Val Arg Asp Leu Pro
      50      55      60
Asp Tyr Lys Gly Arg Val Ser Tyr Asp Ser Phe Pro Ile Ser Lys Glu
      65      70      75      80
Asp Arg Thr Thr Ala Leu Ser Ala Asp Ser Val Ala Gly Arg Arg Phe
      85      90      95
Phe Tyr Leu Ala Ala Asp Ile Gly Pro Val Ala Ser Phe Ser Arg Ser
      100      105      110
Asp Thr Leu Thr Ala Arg Val Glu Glu Val Ala Val Asp Gly Arg Pro
      115      120      125
Leu Pro Leu Lys Glu Leu Ser Pro Ala Ser Arg Arg Leu Tyr Arg Gly
      130      135      140
Tyr Glu Ala Leu Phe Val Pro Gly Asp Gly Gly Ser Arg Asn Tyr Arg
      145      150      155      160
Ile Pro Ala Ile Leu Lys Thr Ala Asn Gly Thr Leu Ile Ala Met Ala
      165      170      175
Asp Arg Arg Lys Tyr Asn Gln Thr Asp Leu Pro Glu Asp Ile Asp Ile
      180      185      190
Val Met Arg Arg Ser Thr Asp Gly Gly Lys Ser Trp Ser Asp Pro Arg
      195      200      205
Ile Ile Val Gln Gly Glu Gly Arg Asn His Gly Phe Gly Asp Val Ala
      210      215      220
Leu Val Gln Thr Gln Ala Gly Lys Leu Leu Met Ile Phe Val Gly Gly
      225      230      235      240

```


Val Gly Leu Trp Gln Ser Thr Pro Asp Arg Pro Gln Arg Thr Tyr Ile
 245 250 255
 Ser Glu Ser Arg Asp Glu Gly Leu Thr Trp Ser Pro Pro Arg Asp Ile
 260 265 270
 Thr His Phe Ile Phe Gly Lys Asp Cys Ala Asp Pro Gly Arg Ser Arg
 275 280 285
 Trp Leu Ala Ser Phe Cys Ala Ser Gly Gln Gly Leu Val Leu Pro Ser
 290 295 300
 Gly Arg Ile Thr Phe Val Ala Ala Ile Arg Glu Ser Gly Gln Glu Tyr
 305 310 315 320
 Val Leu Asn Asn Tyr Val Leu Tyr Ser Asp Asp Glu Gly Asp Thr Trp
 325 330 335
 Gln Leu Ser Asp Cys Ala Tyr Arg Arg Gly Asp Glu Ala Lys Leu Ser
 340 345 350
 Leu Met Pro Asp Gly Arg Val Leu Met Ser Ile Arg Asn Gln Gly Arg
 355 360 365
 Gln Glu Ser Arg Gln Arg Phe Phe Ala Leu Ser Ser Asp Asp Gly Leu
 370 375 380
 Thr Trp Glu Arg Ala Lys Gln Phe Glu Gly Ile His Asp Pro Gly Cys
 385 390 395 400
 Asn Gly Ala Met Leu Gln Val Lys Arg Asn Gly Arg Asp Gln Val Leu
 405 410 415
 His Ser Leu Pro Leu Gly Pro Asp Gly Arg Arg Asp Gly Ala Val Tyr
 420 425 430
 Leu Phe Asp His Val Ser Gly Arg Trp Ser Ala Pro Val Val Val Asn
 435 440 445
 Ser Gly Ser Ser Ala Tyr Ser Asp Met Thr Leu Leu Ala Asp Gly Thr
 450 455 460
 Ile Gly Tyr Phe Val Glu Glu Gly Asp Glu Ile Ser Leu Val Phe Ile
 465 470 475 480
 Arg Phe Val Leu Asp Asp Leu Phe Asp Val Arg Gln
 485 490

(2) INFORMATION FOR SEQ ID NO:451

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Met Lys Lys Glu Lys Leu Trp Ile Ala Ile Val Ala Gly Leu Ala Phe
 1 5 10 15
 Val Leu Gly Leu Tyr Ala Leu Gly Arg Ser Val Ala Gln Leu Arg Arg
 20 25 30
 Ser Gln Pro Ser Val Thr Val Thr Gly Met Ala Glu Arg Asn Phe Lys
 35 40 45
 Ser Asp Leu Ile Val Trp Thr Ala Ser Tyr Gln Leu Gln Met Met Asp
 50 55 60
 Leu Glu Ser Ala Tyr Lys Ala Leu Lys Glu Lys Gln Ile Leu Val Ala
 65 70 75 80
 Asp Tyr Leu Lys Asn Lys Gln Leu Pro Asp Ser Ser Tyr Ile Phe Ser
 85 90 95
 Ser Val Ala Ile Ser Lys Glu Tyr Asn Tyr Tyr Tyr Asp Pro Arg Gln
 100 105 110
 Glu Gln Asn Val Arg Thr Phe Ala Gly Tyr Leu Leu Ser Gln Thr Val
 115 120 125
 Thr Val Thr Ser Gln Asp Ile Glu His Val Glu Lys Ile Ser Arg Asp
 130 135 140
 Ile Thr Glu Leu Ile Asn Gln Gly Val Glu Ile Thr Ser Asp Arg Pro
 145 150 155 160
 Ala Tyr Tyr Tyr Thr Lys Leu Asn Asp Leu Lys Val Glu Met Leu Arg
 165 170 175
 Asn Ala Ser Glu Asp Ala Phe Asn Arg Ala Ser Val Ile Ala Glu Gly
 180 185 190

Ser Gly Ser Ser Val Gly Lys Met Leu Ser Ser Ser Met Gly Val Phe
 195 200 205
 Gln Ile Val Gly Leu Asn Ser Asn Glu Asp Tyr Ser Trp Gly Gly Ser
 210 215 220
 Phe Asn Thr Ser Ser Lys Met Lys Thr Ala Ser Ile Thr Val Lys Ala
 225 230 235 240
 Ser Phe Ala Leu Lys
 245

(2) INFORMATION FOR SEQ ID NO:452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

Met Lys Lys Thr Ile Ala Ile Ile Ala Ser Ala Leu Leu Ala Leu Gly
 1 5 10 15
 Ala Val Gly Cys Lys Lys Asn Ala Asp Thr Thr Ala Val Ser Glu Lys
 20 25 30
 Asp Ser Ile Ala Leu Ser Met Gly Ile Leu Tyr Gly Gln Asp Phe Ala
 35 40 45
 Asn Gln Phe Glu Met Ser Arg Leu Gln Gly Gln Pro Ile Asp Ser Val
 50 55 60
 Ala Phe Leu Asp Gly Phe Lys Tyr Gly Ile Asp Thr Thr Arg Phe Ser
 65 70 75 80
 Tyr Asn Leu Gly Ala Ile Tyr Ala Ser Asn Ile Ala Arg Gln Leu Ala
 85 90 95
 His Asp Ser Ile Asp Ile Asp Lys Phe Tyr Ala Ala Met Arg Ala Ala
 100 105 110
 Leu Leu Lys Asp Thr Val Ser Ile Ala Met Lys Pro Ala Asp Ala Gln
 115 120 125
 Ala Phe Met Gln Arg Ile Gln Ala Lys Lys Gln Arg Glu Asn Asn Met
 130 135 140
 Lys Gln Phe Gly Gln Asn Ile Glu Lys Gly Asn Glu Tyr Ile Asp Thr
 145 150 155 160
 Phe Lys Lys Glu Asp Gly Val Thr Val Thr Thr Gly Leu Ala Tyr
 165 170 175
 Lys Thr Leu Gln Glu Gly Thr Gly Ala Thr Pro Ser Leu Ala Asp Thr
 180 185 190
 Val Arg Val Lys Tyr Val Gly Thr Leu Val Asp Gly Lys Glu Phe Asp
 195 200 205
 Lys Asn Glu Glu Gly Ile Glu Phe Ala Val Thr Gly Val Ile Lys Gly
 210 215 220
 Trp Thr Glu Met Leu Gln Leu Met Lys Val Gly Gln Lys Val Arg Val
 225 230 235 240
 Val Ile Pro Gln Glu Leu Ala Tyr Gly Glu Thr Gly Asn Tyr Thr Ile
 245 250 255
 Glu Pro Phe Ser Thr Leu Thr Phe Glu Met Glu Leu Ile Gly Ile Lys
 260 265 270
 Pro Gly Lys Lys
 275

(2) INFORMATION FOR SEQ ID NO:453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

```
Met Lys Val Leu Arg Gln Val Phe Leu Pro Ile Leu Phe Val Leu Leu
1          5          10          15
Thr Gly Ala Cys Ser Thr Thr Lys Asn Leu Pro Glu Gly Glu Gln Leu
20          25          30
Tyr Ile Gly Met Gly Lys Thr Gln Ile Leu Arg Gln Asp Lys Ser His
35          40          45
Ala Gly Gln Gln Ala Leu Thr Glu Val Glu Ser Thr Leu Lys Val Thr
50          55          60
Pro Asn Gly Ala Ile Phe Gly Ser Ala Ser Ala Ser Leu Pro Lys Ile
65          70          75          80
Pro Phe Gly Leu Trp Leu Tyr Asn Ser Phe Val Gly Asp Ser Thr Val
85          90          95
Ile Ser Lys Trp Ile Phe Asp Lys Phe Ala Ala Lys Pro Val Phe Ile
100         105         110
Ser Gln Val Lys Ser Asp Ser Arg Ala Lys Val Ala Thr Asn Ile Leu
115         120         125
Arg Glu His Gly Tyr Phe Asp Ala Lys Val Lys Ser Ser Val Thr Thr
130         135         140
Leu Lys Lys Asp Ser Leu Lys Ala Lys Ile Ser Tyr Thr Val Asp Met
145         150         155         160
Ala Ser Pro Tyr His Tyr Asp Ser Ile Ile Pro Leu Pro Ile Ser Thr
165         170         175
Phe Pro Asp Ser Ile Leu Ala Tyr Arg Gln Thr Pro Ser Leu Ile Arg
180         185         190
Lys Gly Asp Gln Phe Asn Leu Ala Lys Leu His Glu Glu Arg Gln Thr
195         200         205
Ile Ser Ala Leu Leu Arg Asp Asn Gly Tyr Tyr Tyr Phe Arg Pro Gln
210         215         220
Asp Ile Ile Tyr Glu Ala Asp Thr Leu Leu Val Arg Gly Ala Val Cys
225         230         235         240
Leu Arg Ala Lys Leu Ser Glu Asp Thr Pro Pro Gln Ala Met Arg Pro
245         250         255
Trp Arg Ile Gly Lys Arg Thr Ala Val Leu Leu Gly Met Asn Gly Glu
260         265         270
Ser Pro Thr Asp Ser Leu Glu Val Glu Asp Met Lys Val Leu Tyr Tyr
275         280         285
Arg Lys Met Pro Val Arg Pro Lys Ile Leu Ala Lys Arg Phe Arg Phe
290         295         300
Phe Ser Gly Asn Leu Tyr Arg Gln Lys Asp Asp Glu Thr Thr Arg Lys
305         310         315         320
Ser Leu Ala Arg Leu Gly Ala Phe Ser Val Ile Asp Leu Asn Phe Leu
325         330         335
Gln Arg Asp Ser Ile Ser Gly Leu Leu Asp Val Arg Leu Leu Thr Thr
340         345         350
Leu Asp Lys Pro Trp Asp Ala Ser Leu Glu Thr Leu Phe Thr Ser Lys
355         360         365
Ser Asn Asp Phe Ile Gly Pro Gly Leu Asn Phe Ala Leu Ala Arg Arg
370         375         380
Asn Val Phe Gly Gly Gly Glu Asn Leu Ser Trp Asn Ile Gly Gly Ser
385         390         395         400
Tyr Glu Trp Glu Thr Gly Asn Arg Pro Glu Asn Ser Ser Asn Arg Leu
405         410         415
Ile Asp Ile Asn Ser Tyr Asn Met Asn Thr Ala Val Asn Leu Ser Phe
420         425         430
Pro Ser Ile Val Phe Pro Gly Leu Leu Asp Lys Tyr Tyr Tyr Tyr Pro
435         440         445
Thr Thr Thr Thr Phe Gln Ala Ser Ala Thr Ala Leu Asn Arg Ala His
450         455         460
Tyr Phe Ser Met Tyr Ser Phe Gly Phe Ser Thr Thr Tyr Glu Phe Gln
465         470         475         480
Pro Ser Lys Glu His Arg His Ala Ile Phe Pro Leu Lys Leu Asn Tyr
485         490         495
Asn Leu Leu Gly His Gln Thr Glu Thr Phe Gln Ala Ile Thr Ala Asn
500         505         510
Asn Pro Pro Leu Leu Leu Ser Leu Gln Ser Gln Phe Leu Ala Gln Met
515         520         525
Gly Tyr Ile Tyr Thr Phe Asn Lys Ser Val Ser Glu Lys Ser Pro His
530         535         540
```

```

His Leu Trp Met Gln Phe Gly Leu Ser Glu Ala Gly Asn Leu Leu Asn
545          550          555          560
Leu Ile Tyr Leu Ala Gly Lys Lys Tyr Ser Asp Thr Lys Asn Phe
          565          570          575
Val Gly Val Pro Phe Ser Gln Phe Ile Lys Ala Thr Gly Glu Leu Arg
          580          585          590
Tyr Ser Tyr Thr Ile Asp Arg Asn Gln Ser Leu Ala Thr Arg Phe Gly
          595          600          605
Thr Gly Val Ile Tyr Ser Tyr Gly Asn Met Arg Val Ala Pro Tyr Ser
610          615          620
Glu Gln Phe Tyr Val Gly Gly Ala Asn Ser Ile Arg Ala Phe Thr Val
625          630          635          640
Arg Ser Ile Gly Pro Gly Arg Phe Asn Pro Asp Ser Asp Asn Gln Tyr
          645          650          655
Ser Tyr Leu Asp Gln Val Gly Glu Phe Lys Leu Glu Ala Asn Val Glu
          660          665          670
Tyr Arg Gly Lys Leu Phe Gly Asp Leu His Ala Ala Val Phe Leu Asp
675          680          685
Ala Gly Asn Val Trp Leu Leu Arg Glu Asp Ser Ser Arg Pro Gly Gly
690          695          700
Ala Leu Ser Glu Val Gly Ser Val Ser Asn Phe Leu Asn Ser Ile Ala
705          710          715          720
Leu Gly Thr Gly Val Gly Leu Arg Tyr Asp Leu Ala Phe Leu Val Val
          725          730          735
Arg Val Asp Val Gly Phe Gly Leu His Leu Pro Tyr Asn Thr Gly Lys
          740          745          750
Lys Gly Tyr Tyr Asn Ile Pro Arg Phe Lys Asp Ala Ile Gly Phe His
          755          760          765
Leu Ala Val Gly Tyr Pro Phe
770          775

```

(2) INFORMATION FOR SEQ ID NO:454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

```

Met Ser Ser His Ser Val Arg Tyr Leu Ile Gly Ile Ala Gly Cys Leu
1          5          10          15
Leu Leu Met Leu Ala Ser Ser Cys Ser Val Thr Arg Tyr Val Pro Asp
          20          25          30
Gly Ser Arg Leu Leu Asp Arg Val Thr Ile Ala Ser Glu Thr Gly Ser
          35          40          45
Ile Ala Leu Pro Glu Asp Ile Arg Asp Tyr Thr Leu Gln Gln Pro Asn
          50          55          60
Tyr Arg Leu Phe Gly Met Thr Arg Trp Leu Leu Arg Val Tyr Ser Ser
65          70          75          80
Ser Asn Pro Asn Ser Asn Ser Trp Trp Asn Arg Ser Leu Arg Lys Met
          85          90          95
Gly Glu Pro Pro Val Leu Ile Asp Ser Val Leu Thr Asp Arg Thr Ala
          100          105          110
Asn Arg Leu Ala Lys Ala Met Ala Gly Asp Gly Phe Leu Asp Ala Thr
          115          120          125
Ala Arg Ala Val Val Asp Thr Gly Leu Tyr Lys Lys Ala Arg Ile Thr
          130          135          140
Tyr Leu Ile Gln Pro Gly Ser Arg Tyr Tyr Ile Arg Asn Met Ala Leu
145          150          155          160
Asp Val Lys Asn Pro Leu Leu Pro Pro Val Ala Leu Gly Asn Ser Leu
          165          170          175
Pro Ser Ala Tyr Lys Val Gly Ile Ser Glu Gly Ser Pro Leu Ser Pro
          180          185          190
Ile Val Leu Asp Glu Glu Arg Lys Ala Ile Ala Arg His Met Arg Asn
          195          200          205

```

Asn Gly Phe Trp Lys Phe Ser Ala Glu Asp Val Tyr Tyr Glu Ala Asp
 210 215 220
 Thr Thr Val Ser Gly Gly Ser Gly Thr Lys Ser Ala Asp Leu Lys Leu
 225 230 235 240
 Val Val Asn Gly Ile Gly Arg Tyr Pro Tyr Arg Ile Gly Arg Val Phe
 245 250 255
 Phe His Ala Asp Tyr Asp Pro Leu Glu Ser Asp Phe Arg Val Gln Glu
 260 265 270
 Leu Pro Arg Ile Asp Ser Ile Ser Arg Gly Asp Tyr Thr Val Tyr Tyr
 275 280 285
 Gly Ser Arg Gly Arg Tyr Ile Arg Ala Ser Ala Leu Thr Arg Ser Val
 290 295 300
 Ser Val Thr Pro Gly Ala Phe Phe Cys Glu Asp Asp Val Glu Arg Ser
 305 310 315 320
 Tyr Ile Lys Leu Asn Ala Leu Pro Ile Val Arg Asn Val Asn Ile Arg
 325 330 335
 Phe Val Glu His Asn Gly Lys Asp Glu Ile Ala Leu Ala Asp Ser Ser
 340 345 350
 Arg Leu Val Asp Cys Tyr Ile Leu Thr Val Pro Ala Lys Ser Lys Ser
 355 360 365
 Phe Glu Ala Glu Val Leu Gly Thr Asn Ser Ala Gly Asp Phe Gly Ala
 370 375 380
 Ala Leu Ser Leu Gly Phe Thr Asp Arg Asn Leu Phe Arg Gly Ala Glu
 385 390 395 400
 Met Phe Asn Ile Lys Leu Lys Gly Ala Tyr Glu Ala Ile Arg Lys Gly
 405 410 415
 Ser His Ser Phe Met Glu Tyr Gly Val Glu Ser Ser Leu Arg Phe Pro
 420 425 430
 Arg Leu Leu Phe Pro Phe Ile Ser Asp Glu Thr Arg Arg Arg Leu Arg
 435 440 445
 Ala Ser Thr Glu Trp Lys Ile Gly Tyr Asn Tyr Gln Thr Arg Pro Glu
 450 455 460
 Phe Asp Arg Val Ile Leu Ser Ala Gln Leu Asn Tyr Ser Trp Gln Thr
 465 470 475 480
 Tyr Leu His Asn Arg Leu Arg His Thr Ile Arg Leu Leu Asp Val Asp
 485 490 495
 Tyr Leu His Leu Pro Tyr Ile Asp Pro Asp Phe Ala Gln Ser Leu Pro
 500 505 510
 Pro Thr Thr Ala Leu Tyr Asn Tyr Thr Glu Gln Phe Ile Leu Gly Ser
 515 520 525
 Ala Tyr Ile Leu Asn Tyr Thr Thr Ala Ser Ser Met Glu Arg Thr Val
 530 535 540
 Ser Asn Pro Phe Thr Ala Arg Phe Ser Ile Gln Thr Ala Gly Asn Leu
 545 550 555 560
 Leu Gln Ala Ile Ser Tyr Leu Thr Asp Ser Pro Lys Asp Glu His Gly
 565 570 575
 Leu Tyr Lys Met Phe Gly Leu His Tyr Ala Gln Phe Val Lys Leu Asp
 580 585 590
 Leu Asp Leu Ala Lys Thr Val Leu Leu Glu Lys Asp Asn Thr Leu Ala
 595 600 605
 Leu His Leu Gly Phe Gly Leu Ala Phe Pro Tyr Gly Asn Ala Arg His
 610 615 620
 Ile Pro Phe Glu Leu Arg Tyr Phe Ala Gly Gly Ser Asn Ser Val Arg
 625 630 635 640
 Gly Trp Ser Val Arg Thr Leu Gly Pro Gly Ser Met Lys Met Thr Pro
 645 650 655
 Asp Lys Thr Phe Phe Asp Gln Met Gly Asp Ile Arg Leu Asp Leu Asn
 660 665 670
 Val Glu Tyr Arg Thr Lys Leu Phe Trp Lys Phe Arg Ala Ala Ala Phe
 675 680 685
 Val Asp Ala Gly Asn Val Trp Thr Ile Lys Glu Tyr Glu Asn Gln Glu
 690 695 700
 Asp Gly Leu Phe Arg Phe Asp Arg Phe Tyr Lys Glu Ile Ala Leu Ala
 705 710 715 720
 Tyr Gly Leu Gly Leu Arg Leu Asp Phe Asp Tyr Phe Leu Val Arg Leu
 725 730 735
 Asp Ala Gly Leu Lys Ala Tyr Asp Pro Gln Gln Thr Gly Arg Tyr Lys
 740 745 750
 Trp Ala Ile Thr Arg Pro Asn Leu Ser Ser Asn Phe Ala Trp His Ile
 755 760 765
 Ala Val Gly Tyr Pro Phe
 770

(2) INFORMATION FOR SEQ ID NO:455

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 867 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

```
Met Arg Lys Arg Ile Leu Gln Leu Phe Leu Thr Ala Leu Leu Leu Ala
1      5      10      15
Leu Gly Ser Ser Leu Ala Ile Ala Gln Thr Val Val Thr Gly Lys Val
20      25      30
Ile Asp Ser Glu Thr Ser Glu Pro Leu Ile Gly Val Ser Val Ser Thr
35      40      45
Gly Gln Gly Ala Ser Leu Arg Gly Val Thr Thr Asp Met Asp Gly Gly
50      55      60
Phe Arg Phe Glu Val Pro Ala Lys Ser Val Leu Thr Phe Arg Cys Val
65      70      75      80
Gly Tyr Ala Thr Val Thr Arg Ser Ile Gly Arg Gly Ser Gln Glu Asp
85      90      95
Leu Gly Thr Ile Leu Leu Asp Pro Gln Ala Ile Gly Leu Asp Glu Ile
100     105     110
Gln Val Ile Ala Ser Val Val Pro Lys Asp Arg Met Thr Pro Val Pro
115     120     125
Val Ser Asn Ile Arg Val Ala Asp Ile Gln Ala Ala Ser Leu Asn Val
130     135     140
Glu Phe Pro Glu Leu Val Lys Ser Thr Pro Ser Thr Tyr Thr Thr Lys
145     150     155     160
Gly Ser Gly Gly Phe Gly Asp Gly Arg Thr Asn Val Arg Gly Phe Asp
165     170     175
Thr Tyr Asn Phe Gly Val Leu Ile Asn Gly Val Pro Val Asn Gly Met
180     185     190
Glu Asp Gly Lys Val Tyr Trp Ser Asn Trp Ser Gly Leu Met Asn Gln
195     200     205
Ala Ser Thr Ile Gln Ile Gln Arg Gly Leu Gly Ala Ser Lys Leu Gly
210     215     220
Ile Ser Ser Val Gly Gly Thr Met Asn Ile Ile Thr Lys Thr Thr Asp
225     230     235     240
Ala Asn Thr Gly Gly Ser Ala Tyr Val Gly Met Gly Asn Asp Gly Leu
245     250     255
His Lys Glu Ser Phe Ser Ile Ser Thr Gly Met Asn Asp Gly Trp Ala
260     265     270
Ile Thr Ile Ala Gly Ser His Met Thr Gly Leu Gly Tyr Val Lys Gly
275     280     285
Leu Lys Gly Arg Ala Phe Ser Tyr Phe Phe Asn Val Ser Lys Lys Phe
290     295     300
Asn Glu Arg His Thr Leu Ser Leu Thr Gly Phe Gly Ala Pro Gln Trp
305     310     315     320
His Asn Gln Arg Ser Ser Lys Tyr Ser Val Ala Asp Tyr Asp Lys Tyr
325     330     335
Gly Ile Arg His Asn Gln Ser Phe Gly Tyr Leu Arg Gly Glu Leu Thr
340     345     350
Pro Thr Ala Tyr Ala Tyr Asn Thr Tyr His Lys Pro Gln Phe Ser Leu
355     360     365
Asn His Phe Trp Lys Met Asp Glu Asn Thr Ser Leu Tyr Thr Ala Unk
370     375     380
Tyr Ala Ser Leu Ala Thr Gly Gly Gly Arg Arg Ala Tyr Gly Lys Asn
385     390     395     400
Ser Lys Trp Val Leu Ile Asn Tyr Asn Thr Gly Gln Pro Tyr Glu Gln
405     410     415
Thr Lys Val Thr Pro Asp Gly Leu Ile Asp Tyr Asp Ala Val Leu Ala
420     425     430
Ala Asn Ala Ala Ala Ser Asn Gly Ser Glu Ala Ile Phe Ala Leu Gly
435     440     445
Ser Asn Ser His Lys Trp Phe Gly Leu Leu Ser Ser Phe Lys Lys Lys
450     455     460
Leu Asn Ser Ser Leu Thr Leu Thr Ala Gly Tyr Asp Gly Arg Tyr Tyr
465     470     475     480
Arg Gly Asp His Tyr Asp Lys Ile Thr Asp Leu Leu Gly Gly Ser Tyr
```

```

      485              490              495
Tyr Ile Glu Asp Pro Lys Thr Lys Leu Ala Tyr His Ala Glu Gly Gln
      500              505              510
Gln Leu Lys Val Gly Asp Ile Val Asn Arg Asp Tyr Thr Gly Glu Ile
      515              520              525
Met Trp His Gly Leu Phe Ala Gln Met Glu His Ser Ser Glu Trp Ile
      530              535              540
Asp Ala Phe Val Ser Gly Ser Ile Asn Tyr Glu Leu Tyr Arg Asn His
      545              550              555              560
Asn Tyr Gly Gly Ser Lys Ser Thr Gly Tyr Leu Pro Gly Val Ser Pro
      565              570              575
Trp Lys Ser Phe Leu Pro Trp Ser Gly Lys Ala Gly Leu Ser Tyr Lys
      580              585              590
Phe Ala Gln Gly His Asn Val Phe Ala Asn Gly Gly Phe Phe Thr Arg
      595              600              605
Ala Pro Leu Phe Gly Asn Ile Tyr Ala Ala Gly Ala Ile Ile Pro Asn
      610              615              620
Asp Lys Ala Asn Met Glu Lys Val Leu Thr Gly Glu Val Gly Tyr Gly
      625              630              635              640
Phe Thr Asn His Lys Asn Phe Glu Phe Asn Ile Asn Gly Tyr Tyr Thr
      645              650              655
Lys Trp Met Asp Arg Val Thr Ser Lys Arg Ile Gly Asn Glu Tyr Val
      660              665              670
Tyr Leu Asn Gly Val Asp Ala Val His Cys Gly Val Glu Ala Glu Val
      675              680              685
Ser Tyr Arg Pro Ile Arg Gln Ile Asp Leu Arg Gly Met Phe Ser Leu
      690              695              700
Gly Asp Trp Thr Trp Gln Asn Asn Val Ser Tyr Thr Ser Tyr Asp Glu
      705              710              715              720
Ala Gly Asn Glu Thr Gly Gln Asp Ile Thr Tyr Ile Lys Gly Leu His
      725              730              735
Val Gly Asp Ala Ala Gln Met Thr Ala Ala Val Ser Ala Asp Ile Glu
      740              745              750
Leu Phe Lys Gly Phe His Val Ile Gly Lys Tyr Asn Phe Leu Gly Lys
      755              760              765
Asn Tyr Ala Gly Phe Asn Pro Ala Thr Arg Asn Ala Gln Gln Tyr Glu
      770              775              780
Ala Asp Gly Lys Glu Ile Val Glu Ser Trp Lys Leu Pro Asp Val Gly
      785              790              795              800
Leu Phe Asp Leu Ser Ala Ser Tyr Asn Phe Lys Leu Gly Ser Leu Ser
      805              810              815
Thr Thr Phe Tyr Phe Asn Met Asp Asn Val Ala Asp Lys Arg Tyr Val
      820              825              830
Ser Asp Ala Asp Asp Asn Ile Ile Gly Lys Lys His Asp Glu Ala Ser
      835              840              845
Ala Leu Val Trp Tyr Gly Phe Gly Arg Thr Trp Ser Thr Gly Ile Arg
      850              855              860
Val Asn Phe
      865

```

(2) INFORMATION FOR SEQ ID NO:456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

```

Met Lys Phe Ser Ile Arg Leu Phe Leu Cys Ile Ile Phe Leu Leu Ser
1          5          10          15
Ala Phe Ile Leu Pro Ala Leu Gly Gln Lys Ser Lys Gln Val Gln Arg
      20          25          30
Leu Glu Lys Gln Arg Lys Glu Ala Leu Lys Ala Ile Glu Lys Thr Asp
      35          40          45
Arg Glu Leu Arg Asn Thr Lys Lys Asp Lys Gln Asp Lys Gln Lys His

```

50	55	60
Leu Asn Leu Leu Asn Lys Lys Gln Val Ala Gln Arg Lys Gln Met Val Gln		
65	70	75
Leu Leu Asp Asn Glu Val Lys Glu Leu Gln Ser Asp Ile Asp Ser Met		80
	85	90
Thr Gly Val Cys His Gln Leu Ser Val Glu Glu Lys Ala Arg Ser Asp		95
	100	105
Glu Tyr Ala Gln Ala Leu Gln Ser Met Gln Lys Arg Lys Arg Ser Leu		110
	115	120
Asp Arg Ile Leu Phe Ile Ser Ser Ala Lys Ser Phe Asp Glu Gly Met		125
	130	135
Arg Arg Met Arg Phe Leu Glu Gln Tyr Ala Ser Ala Tyr Lys Leu Ala		140
	145	150
Ser Val Arg Leu Arg Asp Thr Arg Ser Lys Leu Glu Thr Glu Arg Ala		155
	160	165
Thr Val Glu Asp Ala Lys Lys Glu Lys Gly His Leu Leu Val Ile Arg		170
	175	180
Glu Glu Glu Lys Lys Lys Leu Glu Gly Gln Gln Ala Glu Gln Arg Arg		185
	190	195
Gln Val Gln Ala Leu Gly Ala Lys Gln Lys Asp Leu Glu Ala Gln Leu		200
	205	210
Arg Lys Gln Lys Lys Gln Ala Glu Ala Leu Asn Arg Lys Ile Glu Lys		215
	220	225
Gln Ile Ala Lys Glu Ile Glu Ala Ala Glu Arg Arg Ala Arg Glu Glu		230
	235	240
Arg Glu Arg Leu Ala Arg Glu Ala Lys Ala Lys Gly Lys Pro Val Pro		245
	250	255
Ala Glu Pro Glu Arg Lys Ala Glu Thr Lys Gly Gly Tyr Ala Met Asp		260
	265	270
Ala Ser Glu Arg Ala Leu Ser Gly Ser Phe Ala Gln Asn Lys Gly Arg		275
	280	285
Leu Pro Gly Pro Val Arg Gly Arg Tyr Arg Ile Val Ser Asp Phe Gly		290
	295	300
Val His Gln His Ser Glu Leu Lys Lys Val Gln Val Asn Asn Gly Gly		305
	310	315
Ile Asp Ile Ala Val Ala Thr Gly Ser Asp Ala Thr Ser Val Phe Asp		320
	325	330
Gly Val Val Ser Ser Val Phe Val Ile Pro Gly Tyr Asn Ser Ala Val		335
	340	345
Met Val Arg His Gly Asn Tyr Ile Thr Val Tyr Ala Asn Leu Ser Lys		350
	355	360
Val Tyr Val Asn Ser Gly Thr Arg Val Lys Thr Gly Gln Ala Leu Gly		365
	370	375
Arg Ala Tyr Thr Asp Pro Ser Asn Asn Gln Thr Ile Ile His Phe Glu		380
	385	390
Ile Trp Lys Glu Arg Ser Lys Gln Asn Pro Arg Leu Trp Leu Arg		395
	400	405
	410	415
	420	425
		430

(2) INFORMATION FOR SEQ ID NO:457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

Met Lys Lys Tyr Leu Leu Tyr Ala Ser Leu Leu Thr Ser Val Leu Leu		
1	5	10
Phe Ser Cys Ser Lys Asn Asn Pro Asn Glu Pro Val Glu Asp Arg Ser		15
	20	25
Ile Glu Ile Ser Ile Arg Val Asp Asp Phe Thr Lys Thr Gly Glu Ala		30
	35	40
Val Arg Tyr Glu Arg Asn Gln Gly Ser Ala Ala Glu Arg Leu Ile Thr		45
	50	55
Asn Leu Tyr Leu Leu Leu Phe Asp Gln Ser Gly Ala Asn Pro Ala Lys		60


```

65      70      75      80
Tyr Tyr Ile Thr Gly Asn Thr Phe Thr Gly Gly Thr Trp Leu Pro Asp
      85      90      95
Asp Met Lys Val Lys Leu Asp Met Thr Gln Ser Glu Ala Gly Glu Arg
      100      105      110
Lys Val Tyr Val Val Ala Asn Val Asp Asn Ala Val Lys Thr Ala Leu
      115      120      125
Asp Ala Val Ala Asn Glu Ser Asp Leu Gln Thr Val Lys Arg Thr Thr
      130      135      140
Ala Met Pro Trp Ser Thr Asp Ile Ala Ser Pro Phe Leu Met Ser Gly
      145      150      155
Asn Lys Thr His Asp Phe Leu Ala Asn Arg Leu Leu Asp Asn Val Pro
      165      170      175
Leu Val Arg Ala Ile Ala Lys Val Glu Leu Asn Ile Ser Leu Ser Glu
      180      185      190
Lys Phe Gln Ile Val Pro Ile Ile Val Asn Gly Ser Leu Ser Glu Phe
      195      200      205
Lys Phe Arg Tyr Val Asn Phe Asp Lys Glu Thr Tyr Val Val Lys Pro
      210      215      220
Thr Thr Lys Pro Asp Asn Leu Ile Ser Ser Ala Asn Gly Val Trp Pro
      225      230      235
Gln Ile Thr Asp Trp Thr Val Trp Gly Ala Ser Leu Asn Thr Ser Pro
      245      250      255
Ala Pro Asp Ala Gly Thr Gly Tyr Thr Leu Asp Ala Asn Gly Lys Val
      260      265      270
Thr Ala Leu Arg Ile Val Thr Tyr Leu Asn Glu Arg Asp Ser Lys Gly
      275      280      285
Ala Thr Val Glu Val Ala Leu Pro Arg Val Asp Asp Gly Thr Leu Pro
      290      295      300
Pro Pro Glu Phe Gly Pro Glu Leu Tyr Arg Leu Pro Leu Pro Asp Lys
      305      310      315      320
Ile Leu Arg Asn His Trp Tyr Lys Tyr Glu Val Glu Ile
      325      330

```

(2) INFORMATION FOR SEQ ID NO:458

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

```

Met Ile Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser
1      5      10      15
Arg Gly Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala
      20      25      30
Ala Thr Ala Leu Pro Ala Cys Gly Gly Thr Ala Ser Gly Ser Asp
      35      40      45
Arg Thr Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser
      50      55      60
Ile Ala Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser
65      70      75      80
Asn Pro Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser
      85      90      95
Glu Ala Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg
      100      105      110
Asn Leu Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu
      115      120      125
Met Gly Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser
      130      135      140
Cys Thr Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr
      145      150      155      160
Trp Ser Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp
      165      170      175
Ala Leu Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly

```

```

      180              185              190
His Asp Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp
      195              200              205
Thr Met Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His
      210              215              220
Pro Ser Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val
      225              230              235
Ile Glu Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val
      245              250              255
Ile Asp Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro
      260              265              270
Glu Phe Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala
      275              280              285
Arg Pro Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile
      290              295              300
Leu His Ile Ala Arg Ala Leu Ala His Glu Arg
      305              310              315

```

(2) INFORMATION FOR SEQ ID NO:459

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

```

Met Ile Gly Lys Lys Ile Phe Phe Ile Leu Leu Ala Leu Ile Ala Phe
1           5           10          15
Ser Gly Leu Asn Ala Ala Thr Asp Thr Glu Phe Lys Tyr Pro Thr Asp
      20          25          30
Ala Asn Ile Ile Gly His Val Lys Asp Ser Lys Thr Gly Glu His Leu
      35          40          45
Val Gly Ile Thr Ile Ala Ile Lys Gly Thr Thr Phe Gly Thr Ser Thr
      50          55          60
Asp Ala Thr Gly His Tyr Tyr Leu Arg Asn Leu Arg Pro Gly Glu Ile
      65          70          75          80
Thr Leu Ile Met Arg Gly Met Gly Tyr Lys Ser Gln Glu Arg Val Val
      85          90          95
Arg Val Glu Lys Asp Lys Thr Ile Glu Val Asn Phe Glu Ala Glu Glu
      100         105         110
Asp Ala Ile Asn Leu Asp Glu Val Ile Ser Ala Asn Arg Glu Leu
      115         120         125
Thr Leu Arg Arg Leu Ala Pro Thr Leu Val Asn Val Leu Asn Glu Lys
      130         135         140
Val Phe Ser Gln Val Asn Ala Ser Asn Leu Ala Gln Gly Leu Ser Phe
      145         150         155         160
Gln Pro Gly Val Arg Val Glu Asn Asn Cys Gln Asn Cys Gly Phe Asn
      165         170         175
Gln Val Arg Ile Asn Gly Leu Asp Gly Arg Tyr Ala Gln Ile Leu Ile
      180         185         190
Asp Ser Arg Pro Ile Met Ser Ala Leu Ala Gly Val Tyr Gly Leu Glu
      195         200         205
Gln Ile Pro Ala Asn Met Ile Glu Arg Val Glu Val Arg Gly Gly
      210         215         220
Gly Ser Ala Leu Tyr Gly Ser Ser Ala Ile Ala Gly Val Val Asn Ile
      225         230         235         240
Ile Thr Lys Glu Pro Ser His Asn Ser Phe Thr Phe Asn Glu Ser Leu
      245         250         255
Ser Phe Thr Gly Phe Ser Lys Leu Asp Asn Asn Thr Asn Phe Asn Ala
      260         265         270
Ser Ile Val Ser Asp Asp Asn Arg Ala Gly Ala Met Val Phe Gly Gln
      275         280         285
Ala Arg Tyr Arg Asn His Trp Asp Ala Asn Asn Asp Gly Tyr Ser Glu
      290         295         300
Leu Gly Lys Ile Asp Ala Arg Ser Leu Gly Ala His Ser Tyr Leu Arg

```

305		310		315		320
Leu Ser Asp Tyr Ser Lys Leu Thr Gly Glu Phe His Thr Ile Ser Glu						
	325			330		335
Phe Arg Arg Gly Gly Asp Arg Ile Asp Leu Pro Pro His Val Val Gly						
	340			345		350
Val Ala Glu Gln Thr Asp His Ser Val Phe Ser Gly Asn Leu Lys Tyr						
	355			360		365
Asp Leu Phe Ser Ser Asn Tyr Lys His His Phe Gln Ala Tyr Thr Ser						
	370			375		380
Gly Gln Ile Val Asn Arg Lys Ser Tyr Tyr Gly Gly Ile Gly Glu Ile						
	385			390		395
Asp Val Asn Gly His Pro Gly Gly Thr Glu Gly Tyr Pro Ile Pro Gln						
	405			410		415
Asp Gln Tyr Gly Asp Asn Asn Tyr Gly Val Thr Lys Gly Lys Thr Tyr Met						
	420			425		430
Gly Gly Ile Gln Tyr Ser Tyr Asp Leu Asp Lys Phe Leu Leu Met Pro						
	435			440		445
Ser Gln Leu Leu Phe Gly Ala Glu Tyr Thr Arg Asp Glu Leu Asn Asp						
	450			455		460
Val Met Pro Ile Leu Ser Trp Gln Thr Gly Glu Asp Ala Asn Gly Asn						
	465			470		475
Thr Ile Pro Leu Tyr Pro Glu Leu Asp Gln Asn Ile Asn Asn Tyr Ser						
	485			490		495
Leu Phe Gly Gln Asn Glu Trp Lys Asn Asp Arg Trp Ser Ile Leu Val						
	500			505		510
Gly Ala Arg Leu Asp Lys His Ser Glu Val Lys Asp Met Ile Leu Ser						
	515			520		525
Pro Arg Thr Thr Leu Arg Phe Asn Val Asn Pro Asp Ile Asn Leu Arg						
	530			535		540
Ala Thr Tyr Ala Lys Gly Phe Arg Ala Pro Gln Val Phe Asp Glu Asp						
	545			550		555
Leu His Val Gly Val Val Gly Gly Glu Ala Gln Lys Val Phe Asn Asp						
	565			570		575
Pro Asn Leu Lys Pro Glu Ile Ser His Ala Phe Ser Leu Ser Ala Asp						
	580			585		590
Met Tyr His Arg Phe Gly Asn Val Gln Thr Asn Phe Leu Val Glu Gly						
	595			600		605
Phe Tyr Thr Arg Leu Leu Asp Val Phe Thr Asn Glu Glu Gln Pro Asp						
	610			615		620
Gln His Asp Gly Ile Lys Arg Tyr Thr Arg Ile Asn Gly Ser Gly Ala						
	625			630		635
Lys Val Phe Gly Leu Asn Leu Glu Gly Lys Val Ala Tyr Lys Ser Phe						
	645			650		655
Gln Leu Gln Ala Gly Leu Thr Leu Ala Ser Asn Lys Tyr Asp Glu Ala						
	660			665		670
Gln Glu Trp Gly Leu Asn Thr Val Lys Asp Thr Asn Gly Ala Phe Val						
	675			680		685
Thr Glu Ala Asn Ala Asn Gly Gln Gln Glu Tyr Lys Asn Glu Ser Met						
	690			695		700
Thr Asp Thr Gln Ile Thr Arg Thr Pro Ser Val Tyr Gly Tyr Phe Thr						
	705			710		715
Leu Ala Tyr Asn Pro Ala His Ser Trp Asn Ile Ala Leu Thr Gly Ala						
	725			730		735
Tyr Thr Gly Gln Met Tyr Val Pro His Ala Ile Glu Tyr Gly Val Lys						
	740			745		750
Ser Ala Glu Leu Asp Ile Met Gln Asn Asn Pro Glu Ile Thr Asp Glu						
	755			760		765
Thr Gly Lys Ala Pro Arg Ile Asp Glu Leu Lys Lys Thr Pro Ala Phe						
	770			775		780
Phe Asp Leu Gly Leu Lys Val Gly Tyr Asp Phe His Val Phe Gln Ala						
	785			790		795
Thr Glu Val Gln Leu Tyr Val Gly Met Asn Asn Ile Phe Asn Ser Phe						
	805			810		815
Gln Lys Asp Phe Asp Arg Gly Ala Ala Arg Asp Ser Gly Tyr Ile Tyr						
	820			825		830
Gly Pro Thr Gln Pro Arg Thr Gly Tyr Met Gly Leu Val Val Lys Phe						
	835			840		845

(2) INFORMATION FOR SEQ ID NO:460

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

```
Met Thr Val Lys Arg Ala Val Arg Ile Ala Leu Leu Thr Leu Ile Gly
1          5          10          15
Ile Leu Phe Ser Ser Pro Ser Leu Val Arg Ala Gln Ser Leu Phe Ser
          20          25          30
Thr Glu His Val Leu Gln Leu Tyr Asn Lys Ile Leu Tyr Gly Glu Ser
          35          40          45
Ala Ala Asp Thr Val Ala Glu Lys Thr Ala Gly Glu Ser Ala Phe Pro
          50          55          60
Phe Ile Asp Lys Leu Ile Asn Leu Gly Arg Thr Phe Leu Gly Lys Pro
65          70          75          80
Tyr Arg Tyr Arg Gly Pro Ser Pro Trp Pro Met Asp Cys Ser Gly Tyr
          85          90          95
Val Ser Tyr Leu Tyr Ser Lys Phe Asp Ile Lys Leu Pro Arg Gly Ala
          100         105         110
Ala Ala Gln Ser Gln Tyr Thr Asn Pro Ile Glu Arg Glu Asp Val Arg
          115         120         125
Pro Gly Asp Leu Leu Phe Phe Lys Gly Arg Asn Ala Arg Ser Asn Arg
          130         135         140
Ile Gly His Val Ala Leu Val Val Ser Val Asp Glu Asp Asp Ile Thr
145         150         155         160
Met Met His Ser Arg Asn Ser Arg Gly Ile Val Ile Glu Lys Leu Asn
          165         170         175
Arg Ser Ala Tyr Phe Ser Arg Arg Leu Val Ser Tyr Gly Arg Val Pro
          180         185         190
Gly Ala Lys Arg Val Ile Pro Arg Lys Ser
          195         200
```

(2) INFORMATION FOR SEQ ID NO:461

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```
Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
1          5          10          15
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
          20          25          30
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
          35          40          45
Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
          50          55          60
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
65          70          75          80
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
          85          90          95
Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
          100         105         110
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
          115         120         125
Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
          130         135         140
Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln
```

```

145          150          155          160
Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln
          165          170          175
Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly
          180          185          190
Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu
          195          200          205
Val Gln Tyr Arg Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln
          210          215          220
Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp
225          230          235          240
Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu
          245          250          255
Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser
          260          265          270
Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala
          275          280          285
Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr
          290          295          300
Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser
305          310          315          320
Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn
          325          330          335
Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser
          340          345          350
Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys
          355          360          365
Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala
          370          375          380
Asp Lys Ala Ile Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys
385          390          395          400
Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala
          405          410          415
Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu
          420          425          430
Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp
          435          440          445
Phe Tyr Gln Gly Lys Asp Phe
450          455

```

(2) INFORMATION FOR SEQ ID NO:462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

```

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu
1          5          10          15
Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Cys
          20          25          30
Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala
          35          40          45
Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe
          50          55          60
Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg
65          70          75          80
Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn
          85          90          95
Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln
          100          105          110
Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg
          115          120          125
Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu

```

130	135	140
Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met		
145	150	155
Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Ser Gln Thr Ala Arg Met		160
	165	170
Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser		175
	180	185
Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys		190
	195	200
Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp		205
	210	215
Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp		220
	225	230
Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His		235
	245	250
His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr		255
	260	265
Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val		270
	275	280
Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp		285
	290	295
Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val		300
	305	310
Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser		315
	325	330
His Leu Arg Gln Ala Arg Ala Glu Arg Arg Ala Ala Ile Val Arg Arg		335
	340	345
Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala		350
	355	360
Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr		365
	370	375
Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu		380
	385	390
Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu		395
	405	410
Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys		415
	420	425
Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp		430
	435	440

(2) INFORMATION FOR SEQ ID NO:463

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln Ser Gly Leu Ala Ala Phe	
1	5
Val Ser Met Ala Thr Ala Leu Thr Ala Ser Ala Gln Ile Ser Phe Gly	10
	15
	20
Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser Ala Gly Thr His Ser Phe	25
	30
	35
Asp Asp Ala Met Thr Ile Arg Leu Thr Pro Asp Phe Asn Pro Glu Asp	40
	45
	50
Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln Arg Asp Gly Arg Pro Val	55
	60
	65
Arg Ile Gly Gln Val Ile Pro Val Asp Val Asp Phe Ala Ser Lys Ala	70
	75
	80
	85
Ser His Ile Ser Ser Ile Gly Asp Val Asp Val Tyr Arg Leu Gln Phe	90
	95
	100
Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu Tyr Tyr Asp Ala Phe Asn	105
	110
	115
Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr Thr Pro Asp His Glu Ile	120
	125

130 135 140
 Val Leu Gly Ala Tyr Thr Asn Ala Thr His Arg Arg Asn Gly Ala Phe
 145 150 155 160
 Ala Thr Glu Pro Val Pro Gly Ser Glu Leu Ile Met Asp Tyr Glu Val
 165 170 175
 Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys Ile Ser Gly Ala Gly Tyr
 180 185 190
 Ile Phe Asp Lys Val Gly Gly Arg Pro Val Thr Asp Asn His Tyr Gly
 195 200 205
 Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys Glu Ile Asn Ile Asn Cys
 210 215 220
 Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys Asn Gly Val Val Gln Met
 225 230 235 240
 Ile Met Val Lys Gly Gln Tyr Ile Ser Met Cys Ser Gly Asn Leu Leu
 245 250 255
 Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu Ile Ile Ser Ala Gly His
 260 265 270
 Cys Ala Ser Ile Thr Thr Asn Phe Gly Val Thr Gln Ser Glu Leu Asp
 275 280 285
 Lys Trp Ile Phe Thr Phe His Tyr Glu Lys Arg Gly Cys Ser Asn Gly
 290 295 300
 Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile Ile Gly Ala Ser Met Lys
 305 310 315 320
 Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp Gly Leu Leu Leu Gln Leu
 325 330 335
 Asn Asp Glu Val Pro Leu Arg Tyr Arg Val Tyr Tyr Asn Gly Trp Asp
 340 345 350
 Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala Gly Ile His His Pro Ala
 355 360 365
 Gly Asp Ala Met Lys Ile Ser Ile Leu Lys Lys Thr Pro Ala Leu Asn
 370 375 380
 Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly Thr Asp Asp His Phe Tyr
 385 390 395 400
 Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly Gly Ser Ser Gly Ser Ser
 405 410 415
 Leu Phe Asn Gln Asn Lys His Val Val Gly Thr Leu Thr Gly Gly Ala
 420 425 430
 Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly Arg Leu Asn Ser His Trp
 435 440 445
 Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser Arg Met Asp Ile Tyr Leu
 450 455 460
 Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile Leu Asn Gly Thr Tyr Arg
 465 470 475 480
 Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro Arg Leu Leu Leu Gln Ser
 485 490 495
 Thr Gly Asp Gln Val Glu Leu Asn Trp Thr Ala Val Pro Ala Asp Gln
 500 505 510
 Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His Ile Phe Arg Asn Gly Lys
 515 520 525
 Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr Ser Asp Ala Ile Asp Glu
 530 535 540
 Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr Glu Val Ser Ala Arg Phe
 545 550 555 560
 Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu Ser Tyr Lys Asp Thr Asp
 565 570 575
 Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp Ile Gln Thr Lys Leu Lys
 580 585 590
 Pro Asp Val Thr Pro Leu Pro Gly Gly Gly Val Ser Leu Ser Trp Lys
 595 600 605
 Val Pro Phe Leu Ser Gln Leu Val Ser Arg Phe Gly Glu Ser Pro Asn
 610 615 620
 Pro Val Phe Lys Thr Phe Glu Val Pro Tyr Val Ser Ala Ala Ala Ala
 625 630 635 640
 Gln Thr Pro Asn Pro Pro Val Gly Val Val Ile Ala Asp Lys Phe Met
 645 650 655
 Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile Ala Ala Val Tyr Val Met
 660 665 670
 Pro Ser Ala Pro Asp Ser Thr Phe His Leu Phe Leu Lys Ser Asn Thr
 675 680 685
 Asn Arg Arg Leu Gln Lys Val Thr Thr Pro Ser Asp Trp Gln Ala Gly
 690 695 700
 Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro Phe Pro Val Asn Asn Asp
 705 710 715 720
 His Met Leu Phe Ala Gly Ile Arg Met Pro Asn Lys Tyr Lys Leu Asn
 725 730 735
 Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp Asn Leu Phe Ser Ile Thr
 740 745 750

Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val Ser Phe Glu Gly Tyr Gly
 755 760 765
 Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile Lys Tyr Leu Val Val Asn
 770 775 780
 Thr Asp Ala Pro Lys Ile Asp Met Ser Leu Val Gln Glu Pro Tyr Ala
 785 790 795 800
 Lys Gly Thr Asn Val Ala Pro Phe Pro Glu Leu Val Gly Ile Tyr Val
 805 810 815
 Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln Asp Pro Ser Val Thr Thr
 820 825 830
 Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp Glu Tyr Glu Ile Lys Leu
 835 840 845
 Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly Val Ala Gln Ile Glu Asn
 850 855 860
 Asn Asn Ala Val Val Ala Tyr Pro Ser Val Val Thr Asp Arg Phe Ser
 865 870 875 880
 Ile Lys Asn Ala His Met Val His Ala Ala Ala Leu Tyr Ser Leu Asp
 885 890 895
 Gly Lys Gln Val Arg Ser Trp Asn Asn Leu Arg Asn Gly Val Thr Phe
 900 905 910
 Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr Met Leu Val Met Gln Thr
 915 920 925
 Ala Asn Gly Pro Val Ser Gln Lys Ile Val Lys Gln
 930 935 940

(2) INFORMATION FOR SEQ ID NO:464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

Met Lys Tyr Leu Ile Arg Leu Phe Leu Ser Leu Met Leu Leu Ser Leu
 1 5 10 15
 Trp Thr Gly Cys Thr His Glu Glu Leu Ser Ile Cys Asp Gly Glu Asn
 20 25 30
 Thr Leu Val Leu Arg Val Glu Thr Gly Lys Ala Pro Asn Ala Arg Ala
 35 40 45
 Thr Glu Pro Gly Gln Gly Ile Tyr Asn Glu Asn Lys Val Gly Ser Ile
 50 55 60
 Ser Val Leu Phe Tyr Leu Glu Gly Gln Leu Arg Trp Gln Val Lys Ser
 65 70 75 80
 Thr Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu
 85 90 95
 Gln Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val
 100 105 110
 Val Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser
 115 120 125
 Gln Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro
 130 135 140
 Ala Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala
 145 150 155 160
 Thr Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala
 165 170 175
 Ala Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu
 180 185 190
 Val Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly
 195 200 205
 Phe Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys
 210 215 220
 Thr Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile
 225 230 235 240
 His Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys
 245 250 255


```

Arg Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro
      260      265      270
Asp Asn Thr Ala Lys Pro Tyr Tyr Arg Val Pro Leu Glu Ser Gln
      275      280      285
Asp Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile
      290      295      300
Glu Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly
      305      310      315      320
Thr Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu
      325      330      335
Pro Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn
      340      345      350
Asn Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile
      355      360      365
Ser Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly
      370      375      380
Thr Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr
      385      390      395      400
Ile Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val
      405      410      415
Asn Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala
      420      425      430
Gly Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile
      435      440      445
Val Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu
      450      455      460
Ala Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val
      465      470      475      480
Pro Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr
      485      490      495
Pro Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr
      500      505      510
Pro Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr
      515      520      525
Ser Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala
      530      535      540
Thr Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu
      545      550      555      560
Leu Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn
      565      570      575
Cys Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys
      580      585      590
Phe Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp
      595      600      605
Lys Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly
      610      615      620
Asn Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln
      625      630      635      640
Gly Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val
      645      650      655
Arg Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys
      660      665      670

```

(2) INFORMATION FOR SEQ ID NO:465

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

```

Met Arg Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly
1      5      10      15
Leu Gln Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu
      20      25      30

```

Pro Ser Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu
 35 40 45
 Val Val Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln
 50 55 60
 Val Phe Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu
 65 70 75 80
 Gly Glu Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu
 85 90 95
 Phe Ser Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe
 100 105 110
 Asp Asn Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu
 115 120 125
 Pro Glu Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp
 130 135 140
 Tyr Tyr Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser
 145 150 155 160
 Gln Asp Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr
 165 170 175
 Pro Phe Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys
 180 185 190
 Ile Glu Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys
 195 200 205
 Asn Thr Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr
 210 215 220
 Glu Ala Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg
 225 230 235 240
 Gly Thr Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln
 245 250 255
 Asn Cys Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln
 260 265 270
 Gln Pro His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr
 275 280 285
 Asn Gly Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser
 290 295 300
 Phe Pro Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn
 305 310 315 320
 Phe Ile Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp
 325 330 335
 Gly Lys Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr
 340 345 350
 Leu Ala Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn
 355 360 365
 Val Ser Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser
 370 375 380
 Asp Tyr Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu
 385 390 395 400
 Phe Ile Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu
 405 410 415
 Ile Glu Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His
 420 425 430
 Lys Asn Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu
 435 440 445
 Arg Leu Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile
 450 455 460
 Leu Lys Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu
 465 470 475 480
 Asn Asn Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr
 485 490 495
 Val Trp Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg
 500 505 510
 Leu Asn Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser
 515 520 525
 Ser Ala Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr
 530 535 540
 Thr Tyr Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg
 545 550 555 560
 Ala Thr Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu
 565 570 575
 Phe Tyr Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val
 580 585 590
 Val Gly Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp
 595 600 605
 Thr Tyr Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn
 610 615 620
 Ile Met Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn
 625 630 635 640
 Asn Thr Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu

[illegible]

Val Thr Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg
 1265 1270 1275 1280
 Ile Lys

(2) INFORMATION FOR SEQ ID NO:466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1274 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```

Met Met Cys Ser Leu His Leu Gly Leu Gln Ser Gln Thr Trp His Gly
1      5      10      15
Asp Pro Asp Ser Val Ala Ala Leu Pro Ser Ile Gly Ile Gln Glu Ser
      20      25      30
Ser Cys Thr Arg Ile Thr Phe Glu Val Val Phe Pro Gly Phe Tyr Ser
      35      40      45
Val Glu Lys Arg Glu Gly Asn Gln Val Phe Gln Arg Ile Ser Met Pro
      50      55      60
Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu Ala Glu Leu Pro Val Leu
      65      70      75      80
Lys Lys Met Ile Ala Val Pro Glu Phe Ser Thr Ala Asn Val Ala Val
      85      90      95
Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn Tyr Asn Ile Tyr Pro Asn
      100     105     110
Pro Thr Tyr Val Val Glu Glu Leu Pro Glu Gly Gly Thr Tyr Leu Val
      115     120     125
Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr Ser Gln Asn Val Ser Leu
      130     135     140
Pro Ser Thr His Tyr Val Tyr Ser Gln Asp Gly Tyr Phe Arg Ser Gln
      145     150     155     160
Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe Arg Tyr Asn Pro Val Arg
      165     170     175
Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu Val Thr Ile Thr Phe Asp
      180     185     190
Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr Gly Ile Phe Asn Lys Val
      195     200     205
Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala Asp Gly Lys Ser Ala Ile
      210     215     220
Glu Asn Asp Met Val Phe Ser Arg Gly Thr Thr Tyr Ile Ser Gly
      225     230     235     240
Asn Val Ala Ser Asn Leu Pro Gln Asn Cys Asp Tyr Leu Val Ile Tyr
      245     250     255
Asp Asp Met Phe Asn Val Asn Gln Gln Pro His Asp Glu Ile Lys Arg
      260     265     270
Leu Cys Glu His Arg Ala Phe Tyr Asn Gly Phe Asp Val Ala Ala Val
      275     280     285
Ser Ile Lys Asp Val Leu Asn Ser Phe Pro Ser Asn Ala Thr Ser Tyr
      290     295     300
Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile Arg Ser Val Tyr Asn Gln
      305     310     315     320
Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys Leu Gly Tyr Val Leu Leu
      325     330     335
Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala Asp Thr Asp Asn Thr Lys
      340     345     350
Val Pro Thr Ser Phe Ile His Asn Val Ser Leu Ile Pro Ser His Pro
      355     360     365
Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr Phe Phe Ser Cys Val Ser
      370     375     380
Pro Leu Asp Thr Val Gly Asp Leu Phe Ile Gly Arg Phe Ser Val Thr
      385     390     395     400
Asn Ala His Glu Leu His Asn Leu Ile Glu Lys Thr Ile Asn Lys Glu
      405     410     415

```

Ile Ser Tyr Asn Pro Ile Ala His Lys Asn Ile Leu Tyr Ala Glu Gly
 420 425 430
 Lys Gly Cys Asp Ala Pro Ile Leu Arg Leu Phe Leu Lys Glu Ile Ala
 435 440 445
 Ser Gly Tyr Thr Val Asn Ser Ile Leu Lys Ser Asn Gln Val Ser Ala
 450 455 460
 Ile Asp Ser Ile Phe Asp Cys Leu Asn Asn Gly Ser His His Phe Tyr
 465 470 475 480
 Phe Asn Thr His Gly Met Pro Thr Val Trp Gly Ile Gly Gln Gly Leu
 485 490 495
 Asp Val Asn Thr Leu Thr Ala Arg Leu Asn Asn Thr Ser Ser Gln Gly
 500 505 510
 Leu Cys Thr Ser Leu Ser Cys Ser Ser Ala Val Ala Asp Ser Thr Ile
 515 520 525
 Arg Ser Leu Gly Glu Val Leu Thr Thr Tyr Ala Pro Asn Lys Gly Phe
 530 535 540
 Ser Ala Phe Leu Gly Gly Ser Arg Ala Thr Gln Tyr Ala Val Tyr Leu
 545 550 555 560
 Glu Gly Pro Cys Pro Ser Glu Phe Tyr Glu Tyr Leu Pro Tyr Ser
 565 570 575
 Leu Tyr His Asn Leu Ser Thr Val Val Gly Glu Met Leu Leu Ser Ser
 580 585 590
 Ile Ile Asn Thr Asn Ser Val Asp Thr Tyr Ser Lys Phe Asn Phe Asn
 595 600 605
 Leu Leu Gly Asp Pro Ala Leu Asn Ile Met Ala His Gly Met Glu Val
 610 615 620
 Ser Asn Cys Ile Thr Leu Pro Asn Asn Thr Ile Ile Ser Ser Pro Ile
 625 630 635 640
 Thr Ile Lys Asn Gly Gly Cys Leu Lys Ile Pro Glu Lys Gly Val Leu
 645 650 655
 His Phe Thr Asn Asn Gly Ser Ile Gln Val Met Ser Gly Gly Thr Leu
 660 665 670
 Glu Ile Gly Asn Gln Ala Lys Ile Ser Gly Glu Thr Gly Ala Asn Pro
 675 680 685
 Thr Phe Ile Thr Val Tyr Gly Asp Gly Leu Ala Ile Asn Lys Gln Val
 690 695 700
 Glu Ile Asp Asn Ile Asp Arg Leu Asn Leu Phe Ser Thr His Ser Val
 705 710 715 720
 Met Pro Lys Phe His Phe Asp Ser Val Lys Phe Asn Ser Ala Pro Leu
 725 730 735
 Tyr Thr Thr Asn Cys Ile Val Glu Ile Ser Asn Cys Glu Phe Thr Asn
 740 745 750
 Arg Ser Asp Ile Ile Ser Lys Asn Cys Asp Leu Ser Val Glu Asn Ser
 755 760 765
 Met Phe Ser Ser Ser Gly Ile Thr Val Phe Lys Pro Met Ala Thr Ser
 770 775 780
 Ser Ile Thr Gly Leu Ser Thr Lys Ala Lys Ile Thr Asp Asn Thr Phe
 785 790 795 800
 Phe Ala Thr Gly Asn Phe Ala Tyr His Ile Thr Asn Thr Pro Gly Leu
 805 810 815
 Thr Ala Thr Ser Asn Ala Ala Ile Lys Leu Asp Asn Ile Pro Glu Tyr
 820 825 830
 Tyr Ile Ser Gly Asn Lys Ile Val Asn Cys Asp Glu Ala Leu Val Leu
 835 840 845
 Asn Asn Ser Gly Asn Arg Thr Asn Arg Leu His Asn Ile Thr Arg Asn
 850 855 860
 Val Ile Lys Asn Cys Arg Ile Gly Ser Thr Leu Tyr Asn Ser Tyr Gly
 865 870 875 880
 Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn His Ile Gly Val Arg Leu
 885 890 895
 Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn Ala Pro Val Ile Asn Glu
 900 905 910
 Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg Thr Trp Gln Leu Tyr Ser
 915 920 925
 Ser Asn Gly Thr Phe Pro Leu Asn Phe His Tyr Asn Ser Leu Gln Gly
 930 935 940
 Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp Thr Tyr Thr Asn Arg Tyr
 945 950 955 960
 Ile Asp Val Ser Asn Asn His Trp Gly Asn Asn Asp Leu Phe Asp Pro
 965 970 975
 Asn Gln Val Phe Asn Thr Pro Asp Leu Phe Ile Trp Ile Pro Phe Trp
 980 985 990
 Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn Ser Ser Ala Glu Ala Val
 995 1000 1005
 Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly Asn Ser Asp Tyr Leu Ser
 1010 1015 1020
 Ala Lys Val Ala Leu Lys Met Met Val Glu Thr Tyr Pro Glu Ser Asp

```

1025          1030          1035          1040
Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe Arg Ile Glu Lys Met Ser
          1045          1050          1055
Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr Phe Arg Ser Asn Pro Thr
          1060          1065          1070
Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr Ala Asp Phe Leu Ser Ala
          1075          1080          1085
Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln Ser Ala Ile Asp Trp Tyr
          1090          1095          1100
Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr Gln Asp Ser Val Phe Ala
1105          1110          1115          1120
Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn Met Gln Leu Asp Ser Leu
          1125          1130          1135
Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu Ser Cys Glu Gln Arg Lys
          1140          1145          1150
Ser Leu Glu Ser His Gln Asn Val Lys Asn Tyr Leu Leu Ser Thr Leu
          1155          1160          1165
Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro Leu Glu Cys Asn Lys Ser
          1170          1175          1180
Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile Ser Pro Asn Pro Ala Lys
1185          1190          1195          1200
Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp Asn Pro Ser Cys Ser Val
          1205          1210          1215
Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser Ala Asp Ile Thr Gly Leu
          1220          1225          1230
Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser Ile Gln Phe Asn Thr Ser
          1235          1240          1245
Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr Leu Asn Val Asp Gln Lys
          1250          1255          1260
Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys
1265          1270

```

(2) INFORMATION FOR SEQ ID NO:467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

```

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile
1          5          10          15
Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser
          20          25          30
Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile
          35          40          45
Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu
          50          55          60
Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser
65          70          75          80
Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile
          85          90          95
Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile
          100          105          110
Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr
          115          120          125
Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile
          130          135          140
Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr
145          150          155          160
Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys
          165          170          175
Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe
          180          185          190
Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu

```

		195					200					205				
Pro	Ala	Thr	Asp	Phe	Thr	Val	Ile	Asn	Ile	Gly	Gln	Asn	Val	Gly	Arg	
	210					215					220					
Leu	Thr	Trp	Asn	Tyr	Pro	Glu	Asp	Tyr	Gln	Pro	Glu	Gly	Lys	Gly	Asn	
225					230					235					240	
Glu	Glu	Leu	Gln	Leu	Ser	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Thr	Leu	
				245					250					255		
Leu	Ala	Gln	Ile	Lys	Asp	Val	Ser	Ile	Leu	Glu	Tyr	Val	Asp	Ser	Thr	
			260					265					270			
Tyr	Ser	Leu	Arg	Asp	Asn	Pro	Leu	Gln	Val	Glu	Tyr	Cys	Val	Thr	Ala	
	275					280						285				
Val	Tyr	Asp	Glu	Ser	Ile	Glu	Ser	Ser	Thr	Val	Cys	Gly	Thr	Leu	His	
	290					295					300					
Tyr	Ala	Thr	Asp	Ala	Ile	Leu	Tyr	Glu	Asn	Phe	Glu	Asn	Gly	Pro	Val	
305				310					315					320		
Pro	Asn	Gly	Trp	Leu	Val	Ile	Asp	Ala	Asp	Gly	Asp	Gly	Phe	Ser	Trp	
				325					330					335		
Gly	His	Tyr	Leu	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	
			340					345				350				
His	Cys	Ser	Leu	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	
	355					360						365				
Pro	Asp	Asn	Tyr	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	
	370				375						380					
Lys	Tyr	Trp	Val	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	
385					390					395				400		
Ala	Val	Met	Ala	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	
				405					410					415		
Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	
			420				425					430				
Arg	Thr	Ile	Asn	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	
	435					440					445					
Tyr	Asn	Cys	Thr	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	
	450				455					460						
Phe	Gly	Thr	Pro	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	
465				470					475					480		
Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	
				485				490					495			
Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	
			500				505					510				
Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	
	515					520					525					
Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	
	530				535						540					
Gln	Val	Glu	Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	
545				550												

```

Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp
      820      825      830
Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr
      835      840      845
Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu
      850      855      860
Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly
      865      870      875      880
Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp
      885      890      895
Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly
      900      905      910
Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
      915      920      925

```

(2) INFORMATION FOR SEQ ID NO:468

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

```

Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
1      5      10      15
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
      20      25      30
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
      35      40      45
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
      50      55      60
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
      65      70      75      80
Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
      85      90      95
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
      100      105      110
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
      115      120      125
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
      130      135      140
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
      145      150      155      160
Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala
      165      170      175
Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu
      180      185      190
Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr
      195      200      205
Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp
      210      215      220
Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu
      225      230      235      240
Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln
      245      250      255
Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu
      260      265      270
Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp
      275      280      285
Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr
      290      295      300
Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly
      305      310      315      320
Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr
      325      330      335

```


Leu	Asn	Ala	Tyr	Asp	Ala	Phe	Pro	Gly	His	Asn	Gly	Gly	His	Cys	Ser
		340						345					350		
Leu	Ser	Ala	Ser	Tyr	Val	Pro	Gly	Ile	Gly	Pro	Val	Thr	Pro	Asp	Asn
		355					360					365			
Tyr	Leu	Ile	Thr	Pro	Lys	Val	Glu	Gly	Ala	Lys	Arg	Val	Lys	Tyr	Trp
		370				375					380				
Val	Ser	Thr	Gln	Asp	Ala	Asn	Trp	Ala	Ala	Glu	His	Tyr	Ala	Val	Met
385					390					395					400
Ala	Ser	Thr	Thr	Gly	Thr	Ala	Val	Gly	Asp	Phe	Val	Ile	Leu	Phe	Glu
				405				410						415	
Glu	Thr	Met	Thr	Ala	Lys	Pro	Thr	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile
			420					425					430		
Asn	Leu	Pro	Glu	Gly	Thr	Lys	Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asn	Cys
		435					440					445			
Thr	Asp	Ile	Tyr	Phe	Leu	Lys	Leu	Asp	Asp	Ile	Thr	Val	Phe	Gly	Thr
		450				455					460				
Pro	Ala	Ser	Glu	Pro	Glu	Pro	Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile
465					470				475						480
Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu
				485				490						495	
Pro	Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn
			500					505					510		
Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val
		515					520					525			
Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu
		530				535					540				
Val	Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln
545					550					555					560
Ser	Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu
			565					570						575	
Tyr	Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile
			580					585					590		
Asp	Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met
		595					600					605			
Tyr	Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro
		610				615					620				
Met	Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu
625					630					635					640
Glu	Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val
			645					650						655	
Tyr	Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala
			660					665					670		
Val	Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala
		675					680					685			
Asn	Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys
		690				695					700				
Tyr	Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu
705					710					715					720
Leu	Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro
			725					730						735	
Val	Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu
			740					745					750		
Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys
		755					760					765			
Lys	Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu
		770				775					780				
Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr
785					790					795					800
Tyr	Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala
			805						810					815	
Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn
			820					825					830		
Tyr	Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys
		835					840					845			
Ile	Tyr	Pro	Asn	Pro	Ala	Ser	Tyr	Val	Val	Arg	Ile	Glu	Gly	Leu	Ser
		850				855					860				
Arg	Ser	Lys	Ser	Thr	Ile	Glu	Leu	Tyr	Asn	Ala	Leu	Gly	Ile	Cys	Ile
865					870					875					880
Leu	Arg	Glu	Glu	Thr	His	Ser	Glu	Lys	Thr	Glu	Ile	Asp	Val	Ser	Arg
			885						890					895	
Leu	Asn	Asp	Gly	Val	Tyr	Leu	Ile	Lys	Val	Val	Gly	Gly	Asn	Lys	Thr
			900					905						910	
Thr	Thr	Glu	Lys	Val	Glu	Ile	Lys	Arg	Pro						
			915					920							

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 921 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyrromonas gingivalis*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

```

Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp
1      5      10      15
Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala
20      25      30
Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser
35      40      45
Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp
50      55      60
Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro
65      70      75      80
Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile
85      90      95
Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys
100     105     110
Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His
115     120     125
Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val
130     135     140
Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp
145     150     155     160
Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp
165     170     175
Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp
180     185     190
Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp
195     200     205
Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn
210     215     220
Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln
225     230     235     240
Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln Ile
245     250     255
Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu Arg
260     265     270
Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp Glu
275     280     285
Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr Asp
290     295     300
Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly Trp
305     310     315     320
Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr Leu
325     330     335
Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser Leu
340     345     350
Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn Tyr
355     360     365
Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp Val
370     375     380
Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met Ala
385     390     395     400
Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu Glu
405     410     415
Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile Asn
420     425     430
Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys Thr
435     440     445
Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr Pro
450     455     460
Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu

```

465	Asn	Asn	Lys	Gly	Arg	Leu	Lys	Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro
				485						490					495	
Asp	Lys	Thr	Asp	Asp	Lys	Asp	Pro	Leu	Gln	Leu	Ala	Gly	Tyr	Asn	Ile	
			500					505					510			
Tyr	Ala	Asn	Gly	Ser	Leu	Leu	Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	
		515					520					525				
Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	Ser	Ser	Arg	Asp	Asp	Gln	Val	Glu	Val	
	530					535					540					
Glu	Tyr	Cys	Val	Thr	Ala	Val	Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	
545					550					555					560	
Val	Cys	Asp	Lys	Leu	Ile	Tyr	Asp	Ser	Gln	Ser	Asp	Ile	Ile	Leu	Tyr	
			565						570					575		
Glu	Gly	Phe	Glu	Ala	Gly	Ser	Ile	Pro	Glu	Gly	Trp	Leu	Leu	Ile	Asp	
		580						585						590		
Ala	Asp	Gly	Asp	Asn	Val	Asn	Trp	Asp	Tyr	Tyr	Pro	Trp	Thr	Met	Tyr	
		595					600					605				
Gly	His	Asp	Ser	Glu	Lys	Cys	Ile	Ala	Ser	Pro	Ser	Tyr	Leu	Pro	Met	
	610					615					620					
Ile	Gly	Val	Leu	Thr	Pro	Asp	Asn	Tyr	Leu	Val	Thr	Pro	Arg	Leu	Glu	
625					630						635				640	
Gly	Ala	Lys	Leu	Val	Lys	Tyr	Trp	Val	Ser	Ala	Gln	Asp	Ala	Val	Tyr	
			645						650					655		
Ser	Ala	Glu	His	Tyr	Ala	Val	Met	Val	Ser	Thr	Thr	Gly	Thr	Ala	Val	
		660					665						670			
Glu	Asp	Phe	Val	Leu	Leu	Phe	Glu	Glu	Thr	Met	Thr	Ala	Lys	Ala	Asn	
	675						680					685				
Gly	Ala	Trp	Tyr	Glu	Arg	Thr	Ile	Thr	Leu	Pro	Ala	Gly	Thr	Lys	Tyr	
	690					695					700					
Ile	Ala	Trp	Arg	His	Tyr	Asp	Cys	Thr	Asp	Met	Phe	Phe	Leu	Leu	Leu	
705				710					715						720	
Asp	Asp	Ile	Thr	Val	Tyr	Arg	Ser	Thr	Glu	Thr	Val	Pro	Glu	Pro	Val	
			725						730					735		
Thr	Asp	Phe	Val	Val	Ser	Leu	Ile	Glu	Asn	Asn	Lys	Gly	Arg	Leu	Lys	
	740							745					750			
Trp	Asn	Tyr	Pro	Asn	Gly	Tyr	Glu	Pro	Asp	Lys	Thr	Asp	Asp	Lys	Lys	
	755						760					765				
Pro	Leu	Gln	Leu	Thr	Gly	Tyr	Asn	Ile	Tyr	Ala	Asn	Gly	Ser	Leu	Leu	
	770					775					780					
Val	His	Ile	Gln	Asp	Pro	Thr	Val	Leu	Glu	Tyr	Ile	Asp	Glu	Thr	Tyr	
785					790				795						800	
Ser	Ser	Arg	Asp	Gly	Gln	Val	Glu	Met	Glu	Tyr	Cys	Val	Thr	Ala	Val	
			805						810					815		
Tyr	Asn	Asp	Asn	Ile	Glu	Ser	Gln	Ser	Val	Cys	Asp	Lys	Leu	Asn	Tyr	
			820					825					830			
Thr	Ile	Thr	Ser	Leu	Asp	Asn	Ile	Gln	Ser	Asp	Thr	Ser	Leu	Lys	Ile	
	835					840					845					
Tyr	Pro	Asn	Pro	Ala	Ser	Tyr	Val	Val	Arg	Ile	Glu	Gly	Leu	Ser	Arg	
	850					855					860					
Ser	Lys	Ser	Thr	Ile	Glu	Leu	Tyr	Asn	Ala	Leu	Gly	Ile	Cys	Ile	Leu	
865					870				875					880		
Arg	Glu	Glu	Thr	His	Ser	Glu	Lys	Thr	Glu	Ile	Asp	Val	Ser	Arg	Leu	
			885						890					895		
Asn	Asp	Gly	Val	Tyr	Leu	Ile	Lys	Val	Val	Gly	Gly	Asn	Lys	Thr	Thr	
		900						905					910			
Thr	Glu	Lys	Val	Glu	Ile	Lys	Arg	Pro								
	915						920									

(2) INFORMATION FOR SEQ ID NO:470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

[illegible]

(2) INFORMATION FOR SEQ ID NO:471

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 589 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

Met	Lys	Tyr	Gln	Leu	Tyr	Thr	Ala	Val	Ile	Met	Ala	Leu	Ser	Val	Ser
1			5						10					15	
Ser	Val	Cys	Gly	Gln	Thr	Pro	Arg	Asn	Thr	Glu	Thr	Lys	Arg	Pro	Asp
			20					25					30		
Thr	Leu	Arg	Arg	Glu	Leu	Thr	Ile	Val	Asn	Asp	Gln	Thr	Val	Glu	Met
			35				40					45			
Glu	His	Ala	Asp	Pro	Leu	Pro	Ala	Ala	Tyr	Lys	Ala	Ile	Glu	Pro	Arg
			50				55				60				
Leu	Lys	Pro	Phe	Arg	Pro	Glu	Tyr	Asn	Lys	Arg	Thr	Phe	Gly	Phe	Val
65					70					75					80
Pro	Glu	Val	Ser	Ser	Ser	Gly	Arg	Asn	Asn	Leu	Pro	Asn	Ile	Leu	Pro
				85					90					95	
Thr	Glu	Gly	His	Met	Lys	His	Arg	Gly	Tyr	Leu	Asn	Ile	Gly	Ile	Gly
			100					105					110		
His	Thr	Leu	Asn	Gln	Arg	Met	Asp	Ala	Gly	Tyr	Arg	Leu	Ile	Asp	Ala
			115					120				125			
Glu	Gln	Glu	Arg	Leu	Asn	Leu	Phe	Leu	Ser	Tyr	Arg	Gly	Met	Lys	Ser
			130				135					140			
Ala	Phe	Asn	Thr	Gly	Asp	Phe	Asp	Gly	Asp	Arg	Lys	Asp	Arg	Arg	Met
145					150					155					160
Met	Ala	Gly	Val	Asp	Tyr	Glu	Gln	Arg	Arg	Pro	Ser	Phe	Val	Leu	Ala
				165					170					175	
Thr	Gly	Leu	Tyr	Tyr	Ser	Asn	His	Tyr	Phe	Asn	Asn	Tyr	Gly	Arg	Gly
			180					185					190		
Ala	Thr	Thr	Asn	Val	Gly	Ser	Ile	Pro	Gln	Leu	Ser	Thr	Pro	Val	Thr
			195					200					205		
Pro	Gln	Met	Asp	Asn	Gly	Thr	His	Asn	Val	Arg	Val	Tyr	Leu	Gly	Ala
					215						220				
Lys	Asn	Asp	Val	Ile	Asp	Ala	Arg	Ile	Asp	Tyr	Arg	Phe	Phe	Arg	Ser
225					230					235					240
Ile	Pro	Tyr	Leu	Gly	Thr	Asp	Pro	Met	Lys	Ala	Leu	Thr	Glu	His	Thr
				245					250					255	
Pro	Glu	Leu	Asn	Val	Thr	Met	Ser	Asn	Glu	Leu	Ser	Asp	Asp	Ile	Lys
			260					265					270		
Leu	Gly	Val	Glu	Val	Arg	Thr	Gly	Gly	Leu	Phe	Phe	Ala	Lys	Asn	Ser
			275				280					285			
Glu	Met	Ile	Gln	Thr	Gly	Val	Leu	Ser	Glu	Thr	Asp	Arg	Asn	Leu	Tyr
			290				295				300				
Tyr	Val	Glu	Gly	Ala	Pro	Thr	Ile	Gly	Phe	Val	Gly	Asp	Ser	Asp	Asn
305					310					315					320
Met	Gln	Trp	Asn	Ile	Gln	Ala	Gly	Val	Gly	Ile	Ser	Ser	His	Phe	Gly
				325					330					335	
Ala	Lys	Gly	Arg	Leu	Phe	Phe	Trp	Pro	Lys	Leu	Asp	Ala	Ser	Leu	Ser
			340					345					350		
Ile	Phe	Pro	Ser	Trp	Arg	Val	Tyr	Ala	Lys	Ala	Phe	Gly	Gly	Val	Ile
			355				360					365			
Arg	Asn	Gly	Leu	Ala	Asp	Val	Met	Gln	Glu	Glu	Met	Pro	Tyr	Leu	Met
			370				375				380				
Pro	Asn	Thr	Ile	Val	Leu	Pro	Ser	Arg	Asn	Ala	Leu	Thr	Ala	Gln	Leu
385					390					395					400
Gly	Val	Lys	Gly	Asn	Ile	Ala	Asp	Val	Val	Arg	Met	Glu	Val	Tyr	Gly
				405						410				415	
Asp	Phe	Ser	Lys	Leu	Thr	Gly	Val	Pro	Phe	Tyr	Thr	Pro	Thr	Leu	Pro
			420					425					430		
Leu	Tyr	Asn	Pro	Ser	Asp	Leu	Tyr	Gln	Tyr	Asn	Val	Ser	Phe	Leu	Pro
			435				440					445			

```

Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr
450          455          460
Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys
465          470          475          480
Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile
          485          490          495
Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg
500          505          510
Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser
515          520          525
Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala
530          535          540
Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile
545          550          555          560
Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met
          565          570          575
Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
          580          585

```

(2) INFORMATION FOR SEQ ID NO:472

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

```

Met Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe
1          5          10          15
Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
20          25          30
Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
35          40          45
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
50          55          60
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
65          70          75          80
Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
85          90          95
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
100          105          110
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
115          120          125
Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
130          135          140
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
145          150          155          160
Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
165          170          175
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
180          185          190
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
195          200          205
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
210          215          220
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
225          230          235          240
Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
245          250          255
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
260          265          270
Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
275          280          285
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
290          295          300

```

```

Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
305                      310                      315                      320
Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
                      325                      330                      335
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
                      340                      345

```

(2) INFORMATION FOR SEQ ID NO:473

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

```

Met Glu Lys Cys Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met
1      5      10      15
Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe
      20      25      30
Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu
      35      40      45
Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile
50      55      60
Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly
65      70      75      80
Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser
      85      90      95
Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg
      100      105      110
Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln
115      120      125
Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp
130      135      140
Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg
145      150      155      160
Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser
      165      170      175
Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp
180      185      190
Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu
195      200      205
Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu
210      215      220
Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr
225      230      235      240
Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp
      245      250      255
Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu
260      265      270
Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln
275      280      285
Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu
290      295      300
Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser
305      310      315      320
Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly
      325      330      335
Ile Arg Leu Asp Asp Lys Ser Ile Phe
      340      345

```

(2) INFORMATION FOR SEQ ID NO:474

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

```
Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
1          5          10          15
Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
20          25          30
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
35          40          45
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
50          55          60
Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
65          70          75          80
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
85          90          95
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
100         105         110
Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
115         120         125
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
130         135         140
Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
145         150         155         160
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
165         170         175
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
180         185         190
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
195         200         205
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
210         215         220
Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
225         230         235         240
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
245         250         255
Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
260         265         270
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
275         280         285
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
290         295         300
Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
305         310         315         320
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
325         330
```

(2) INFORMATION FOR SEQ ID NO:475

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475


```

Met Cys Leu Glu Pro Ile Ile Ala Pro Ile Ser Ser Glu Leu Leu Glu
1      5      10      15
Gln Glu Leu Thr Ala Asp Arg Phe Leu Arg Met Thr Asn Lys Ala Gly
20      25      30
Asn Glu Ile Tyr Val Phe Thr Ala Glu Glu Ala Pro His Cys Met Lys
35      40      45
Glu Val Gly Arg Leu Arg Glu Ala Phe Arg His Tyr Gly Gly Gly
50      55      60
Thr Gly Lys Ala Ile Asp Ile Asp Glu Phe Asp Thr Met Pro Gly Ser
65      70      75      80
Tyr Lys Gln Leu Ile Val Trp Asp Pro Gln Asn Lys Ala Ile Leu Gly
85      90      95
Gly Tyr Arg Phe Ile Tyr Gly Arg Asp Val Ala Phe Asp Thr Asp Gly
100     105     110
Lys Pro Leu Leu Ala Thr Ala Glu Met Phe Arg Phe Ser Asp Ala Phe
115     120     125
Leu His Asp Tyr Leu Pro Tyr Thr Val Glu Leu Gly Arg Ser Phe Val
130     135     140
Ser Leu Gln Tyr Gln Ser Thr Arg Met Gly Thr Lys Ala Ile Phe Val
145     150     155     160
Leu Asp Asn Leu Trp Asp Gly Ile Gly Ala Leu Thr Val Val Asn Pro
165     170     175
Glu Ala Leu Tyr Phe Tyr Gly Lys Val Thr Met Tyr Lys Asp Tyr Asp
180     185     190
Arg Arg Ala Arg Asn Leu Ile Leu Tyr Phe Leu Arg Lys His Phe Ser
195     200     205
Asp Pro Glu Gly Leu Val Lys Pro Ile His Pro Leu Pro Ile Glu Ile
210     215     220
Ser Ala Glu Asp Glu Ala Leu Phe Ser Ser Ser Asp Phe Asp Thr Asn
225     230     235     240
Tyr Lys Thr Leu Asn Ile Glu Val Arg Lys Leu Gly Ile Asn Ile Pro
245     250     255
Pro Leu Val Ser Ala Tyr Ile Ala Leu Ser Pro Glu Met Arg Val Phe
260     265     270
Gly Thr Ala Val Asn Glu Ser Phe Gly Glu Val Glu Glu Thr Gly Ile
275     280     285
Phe Ile Ala Val Gly Lys Ile Leu Glu Glu Lys Lys Gln Arg His Ile
290     295     300
Glu Ser Phe Ile Leu Ser Arg Asn Glu Lys Lys Gly Leu Asp Ser Ser
305     310     315     320
Asn Gly Arg Ser

```

(2) INFORMATION FOR SEQ ID NO:476

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

```

Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe
1      5      10      15
Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn
20      25      30
Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg
35      40      45
Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp
50      55      60
Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr Val Arg Phe
65      70      75      80
Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro Tyr Asn Gly
85      90      95
Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg Ile Ser Val

```


Met	Lys	Lys	Leu	His	Met	Ile	Ala	Ala	Leu	Ala	Val	Leu	Pro	Phe	Cys
1				5					10					15	
Leu	Thr	Ala	Gln	Ala	Pro	Val	Ser	Asn	Ser	Glu	Ile	Asp	Ser	Leu	Ser
			20					25					30		
Asn	Val	Gln	Leu	Gln	Thr	Val	Gln	Val	Val	Ala	Thr	Arg	Ala	Thr	Ala
		35					40					45			
Lys	Thr	Pro	Val	Ala	Tyr	Thr	Asn	Val	Arg	Lys	Ala	Glu	Leu	Ser	Lys
	50					55					60				
Ser	Asn	Tyr	Gly	Arg	Asp	Ile	Pro	Tyr	Leu	Leu	Met	Leu	Thr	Pro	Ser
65					70					75					80
Val	Val	Ala	Thr	Ser	Asp	Ala	Gly	Thr	Gly	Ile	Gly	Tyr	Ser	Gly	Phe
				85					90					95	
Arg	Val	Arg	Gly	Thr	Asp	Ala	Asn	Arg	Ile	Asn	Ile	Thr	Thr	Asn	Gly
			100					105						110	
Val	Pro	Leu	Asn	Asp	Ser	Glu	Ser	Gln	Ser	Val	Phe	Trp	Val	Asn	Met
		115						120				125			
Pro	Asp	Phe	Ala	Ser	Ser	Ile	Glu	Asp	Leu	Gln	Val	Gln	Arg	Gly	Val
	130					135					140				
Gly	Thr	Ser	Thr	Asn	Gly	Ala	Gly	Ala	Phe	Gly	Ala	Ser	Val	Asn	Met
145					150					155					160
Arg	Thr	Asp	Asn	Leu	Gly	Leu	Ala	Pro	Tyr	Gly	Arg	Val	Asp	Leu	Ser
			165						170					175	
Gly	Gly	Ser	Phe	Gly	Thr	Phe	Arg	Arg	Ser	Val	Lys	Leu	Gly	Ser	Gly
			180					185						190	
Arg	Ile	Gly	Arg	His	Trp	Ala	Val	Asp	Ala	Arg	Leu	Ser	Lys	Ile	Gly
	195						200						205		
Ser	Asp	Gly	Tyr	Val	Asp	Arg	Gly	Ser	Val	Asp	Leu	Lys	Ser	Tyr	Phe
	210					215					220				
Ala	Gln	Val	Gly	Tyr	Phe	Gly	Ser	Asn	Thr	Ala	Leu	Arg	Phe	Ile	Thr
225					230					235					240
Phe	Gly	Gly	Lys	Glu	Val	Thr	Gly	Ile	Ala	Trp	Asn	Gly	Leu	Ser	Lys
			245						250					255	
Glu	Asp	Glu	Ala	Lys	Tyr	Gly	Arg	Arg	Tyr	Asn	Ser	Ala	Gly	Leu	Met
		260						265					270		
Tyr	Val	Asp	Ala	Gln	Gly	Val	Pro	His	Tyr	Tyr	His	Asn	Thr	Asp	Asn
		275						280					285		
Tyr	Glu	Gln	Arg	His	Tyr	His	Ala	Ile	Met	Thr	His	Ser	Phe	Ser	Pro
	290					295					300				
Ser	Val	Ile	Leu	Asn	Leu	Thr	Ala	His	Tyr	Thr	Ala	Gly	Tyr	Gly	Tyr
305					310					315					320
Thr	Asp	Glu	Tyr	Arg	Thr	Gly	Arg	Lys	Leu	Lys	Glu	Tyr	Ala	Leu	Gln
			325						330					335	
Pro	Tyr	Val	Glu	Asn	Ser	Val	Thr	Val	Lys	Lys	Thr	Asp	Leu	Ile	Arg
		340						345					350		
Gln	Lys	Tyr	Leu	Asp	Asn	Asp	Phe	Gly	Gly	Leu	Ile	Gly	Ser	Leu	Asn
		355					360					365			
Trp	His	Thr	Gly	Ala	Trp	Asp	Leu	Gln	Phe	Gly	Ala	Ser	Gly	Asn	Ile
	370					375						380			
Tyr	Lys	Gly	Asp	His	Phe	Gly	Arg	Ile	Thr	Tyr	Ile	Lys	Lys	Tyr	Asn
385					390					395					400
Gln	Pro	Leu	Ala	Pro	Asp	Phe	Glu	Tyr	Tyr	Arg	Asn	Arg	Ala	Asp	Lys
			405						410					415	
Arg	Glu	Gly	Ala	Ala	Phe	Ala	Lys	Ala	Asn	Trp	Gln	Ile	Thr	Pro	Glu
		420						425					430		
Leu	Asn	Met	Tyr	Ala	Asp	Leu	Gln	Tyr	Arg	Thr	Ile	Gly	Tyr	Thr	Ile
		435					440					445			
Asn	Gly	Ile	Thr	Asp	Glu	Tyr	Asp	Glu	Val	Gln	Gly	Ser	Met	Gln	His
	450					455					460				
Ile	Asp	Leu	Asp	Lys	Thr	Phe	Arg	Phe	Leu	Asn	Pro	Lys	Ala	Gly	Leu
465					470					475					480
Thr	Tyr	Ser	Phe	Asp	Asp	Ala	His	Thr	Ala	Tyr	Ala	Ser	Val	Ala	Val
			485						490					495	
Ala	His	Arg	Glu	Pro	Asn	Arg	Thr	Asn	Tyr	Thr	Glu	Ala	Gly	Ile	Gly
		500						505					510		
Gln	Tyr	Pro	Thr	Pro	Glu	Arg	Leu	Ile	Asp	Tyr	Glu	Leu	Gly	Tyr	Arg
		515					520					525			
Tyr	Ala	Ser	Pro	Leu	Leu	Ser	Ala	Gly	Val	Gly	Leu	Tyr	Tyr	Met	Gln
	530					535					540				
Tyr	Lys	Asp	Gln	Leu	Val	Leu	Asp	Gly	Arg	Leu	Ser	Asp	Val	Gly	Gln
545					550					555					560
Met	Leu	Thr	Ser	Asn	Val	Pro	Asp	Ser	Tyr	Arg	Met	Gly	Leu	Glu	Leu
			565						570					575	
Thr	Leu	Gly	Trp	Gln	Ile	Leu	Pro	Arg	Leu	Leu	Arg	Trp	Asp	Ala	Ser
		580						585					590		
Phe	Thr	Met	Ser	Arg	Asn	Lys	Ile	Asp	Arg	Tyr	Val	Gln	Tyr	Thr	Ser
		595					600					605			

```

Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu Lys Glu Glu Thr Leu
610          615          620
Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val Ile Ala Gly Ser Met
625          630          635          640
Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala Trp Thr Ser Arg Phe
645          650          655
Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg Ser Asp Arg Met Leu
660          665          670
Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly Tyr Val Leu Pro Val
675          680          685
His Phe Val Lys Arg Val Ala Leu Gly Val Gln Leu Asn Asn Leu Phe
690          695          700
Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr Asp Ala Gly Tyr Val
705          710          715          720
Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp Leu Arg Tyr Tyr Pro
725          730          735
Gln Ala Gly Phe Asn Ala Leu Gly Ser Leu Thr Ile Asp Phe
740          745          750

```

(2) INFORMATION FOR SEQ ID NO:478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

```

Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Tyr Ile Leu Ser Ser
1          5          10          15
Ile Ser Leu Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu
20          25          30
Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile
35          40          45
Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe
50          55          60
Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser
65          70          75          80
Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn
85          90          95
Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg
100          105          110
Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Phe Gly
115          120          125
Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn
130          135          140
Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly
145          150          155          160
His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu
165          170          175
Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe
180          185          190
Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser
195          200          205
Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly
210          215          220
Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala
225          230          235          240
Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu
245          250          255
Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe
260          265          270
Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu
275          280          285
Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly
290          295          300

```

```

Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys
305          310          315          320
Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala
          325          330          335
Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg
          340          345          350
Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met
          355          360          365
Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn
          370          375          380
Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn
          385          390          395          400
Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr
          405          410          415
Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser
          420          425          430
Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser
          435          440          445
Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala
          450          455          460
Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser
          465          470          475          480
Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe
          485          490

```

(2) INFORMATION FOR SEQ ID NO:479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

```

Met Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr
1          5          10          15
Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys
          20          25          30
Asp Trp Thr Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser
          35          40          45
Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu
          50          55          60
Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp
          65          70          75          80
Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys
          85          90          95
Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr
          100          105          110
Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser
          115          120          125
Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val
          130          135          140
Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile
          145          150          155          160
Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro
          165          170          175
Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu
          180          185          190
Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly
          195          200          205
Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn
          210          215          220
Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly
          225          230          235          240
Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys
          245          250          255

```

Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val
 260 265 270
 Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val
 275 280 285
 Gly Val Ala Tyr Thr Phe
 290

(2) INFORMATION FOR SEQ ID NO:480

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480

Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly
 1 5 10 15
 Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe
 20 25 30
 Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn
 35 40 45
 Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Glu Phe Ala Leu
 50 55 60
 Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg
 65 70 75 80
 Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr
 85 90 95
 Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn
 100 105 110
 Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala
 115 120 125
 Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala
 130 135 140
 Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser
 145 150 155 160
 Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His
 165 170 175
 Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg
 180 185 190
 Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
 195 200

(2) INFORMATION FOR SEQ ID NO:481

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481

Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr
 1 5 10 15
 Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe

(2) INFORMATION FOR SEQ ID NO:483

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483

```
Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val
1      5      10      15
Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro
20     25     30
Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser
35     40     45
Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp
50     55     60
Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg
65     70     75     80
Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu
85     90     95
Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr
100    105    110
Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala
115    120    125
Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr
130    135    140
Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp
145    150    155    160
Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr
165    170    175
Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr
180    185    190
Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met
195    200    205
Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe
210    215    220
Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val
225    230    235    240
Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro Ile Gly
245    250    255
Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser Gly Ile
260    265    270
Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr Leu Arg
275    280    285
Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu Ala Leu
290    295    300
Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala Gln Ser
305    310    315    320
Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala Asn Tyr
325    330    335
Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr Ser Lys
340    345    350
Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro Lys Ala
355    360    365
Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr Gly Ser
370    375    380
Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala Arg Thr
385    390    395    400
Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe Pro Gly
405    410    415
Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn Met Arg
420    425    430
Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn Met Ser
435    440    445
Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu Arg Trp
```


450		455		460
Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn Ser Ile				
465	470	475	480	
Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg Asp Trp				
	485	490	495	
Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val Pro Leu				
	500	505	510	
Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu Trp Trp				
	515	520	525	
Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys Thr Phe				
	530	535	540	
Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp Tyr Ser				
	545	550	555	560
Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys Pro Trp				
	565	570	575	
Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His Arg Phe				
	580	585	590	
Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys Arg Arg				
	595	600	605	
Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu				
	610	615	620	
His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro				
	625	630	635	640
Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu				
	645	650	655	
Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile				
	660	665	670	
Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala				
	675	680	685	
Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu				
	690	695	700	
Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu				
	705	710	715	720
Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser				
	725	730	735	
Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser				
	740	745	750	
Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly				
	755	760	765	
Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys				
	770	775	780	
Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu				
	785	790	795	800
Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg				
	805	810	815	
Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser				
	820	825	830	
Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp				
	835	840	845	
Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr				
	850	855	860	
Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser				
	865	870	875	880
Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser				
	885	890	895	
Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala				
	900	905	910	
Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser				
	915	920	925	
Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg				
	930	935	940	
Pro Ile Thr Asn Thr Trp Tyr				
945	950			

(2) INFORMATION FOR SEQ ID NO:484

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1226 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484

Met	Met	Lys	Arg	Tyr	Thr	Ile	Ile	Leu	Ala	Val	Phe	Leu	Leu	Phe	Cys
1			5					10					15		
Thr	Val	Phe	Thr	Phe	Gln	Ile	Lys	Ala	Arg	Pro	Tyr	Glu	Arg	Phe	Ala
		20					25					30			
Asp	Val	Glu	Lys	Pro	Trp	Ile	Gln	Lys	His	Ser	Met	Asp	Ser	Lys	Leu
	35					40					45				
Val	Pro	Ala	Asn	Lys	Gly	Asn	Leu	Ile	Gln	Ala	Glu	Ile	Val	Tyr	Gln
	50				55					60					
Ser	Val	Ser	Glu	His	Ser	Asp	Leu	Val	Ile	Ser	Pro	Val	Asn	Glu	Ile
65				70					75					80	
Arg	Pro	Ala	Asn	Arg	Phe	Pro	Ser	His	Arg	Lys	Ser	Phe	Phe	Ala	Glu
			85					90					95		
Asn	Leu	Arg	Ala	Ser	Pro	Pro	Val	Val	Pro	Val	Ala	Val	Asp	Lys	Tyr
		100					105					110			
Ala	Val	Pro	Val	Ala	Asn	Pro	Met	Asp	Pro	Glu	Asn	Pro	Asn	Ala	Trp
	115					120					125				
Asp	Val	Thr	Leu	Lys	Ile	Thr	Thr	Lys	Ala	Val	Thr	Val	Pro	Val	Asp
	130				135					140					
Val	Val	Met	Val	Ile	Asp	Gln	Ser	Ser	Ser	Met	Gly	Gly	Gln	Asn	Ile
145				150					155					160	
Ala	Arg	Leu	Lys	Ser	Ala	Ile	Ala	Ser	Gly	Gln	Arg	Phe	Val	Lys	Lys
		165					170						175		
Met	Leu	Pro	Lys	Gly	Thr	Ala	Thr	Glu	Gly	Val	Arg	Ile	Ala	Leu	Val
	180					185						190			
Ser	Tyr	Asp	His	Glu	Pro	His	Arg	Leu	Ser	Asp	Phe	Thr	Lys	Asp	Thr
	195					200					205				
Ala	Phe	Leu	Cys	Gln	Lys	Ile	Arg	Ala	Leu	Thr	Pro	Ile	Trp	Gly	Thr
	210				215						220				
His	Thr	Gln	Gly	Gly	Leu	Lys	Met	Ala	Arg	Asn	Ile	Met	Ala	Thr	Ser
225				230					235					240	
Thr	Ala	Val	Asp	Lys	His	Ile	Ile	Leu	Met	Ser	Asp	Gly	Leu	Ala	Thr
		245					250						255		
Glu	Gln	Tyr	Pro	Val	Lys	Asn	Val	Thr	Thr	Ala	Asp	Phe	Ile	Gly	Lys
	260					265						270			
Thr	Gly	Asn	Ala	Asn	Asp	Pro	Ile	Asp	Leu	Val	Ile	Gln	Gly	Ala	Ile
	275					280					285				
Asn	Phe	Pro	Thr	Asn	Tyr	Val	Ser	Asn	Asn	Pro	Ser	Thr	Pro	Leu	Thr
	290				295					300					
Pro	Asn	Tyr	Pro	Thr	His	Ser	Ser	Lys	Val	Gly	Arg	Arg	Asn	Leu	Pro
305				310						315				320	
Glu	Ser	Lys	Phe	Asp	Tyr	Ser	Asn	Leu	Ser	Ala	Arg	Ile	Thr	Phe	Asp
		325					330						335		
Gly	Val	Ala	Gly	Ala	Leu	Val	Tyr	Glu	Pro	Arg	Phe	Pro	His	Pro	Tyr
	340					345						350			
Tyr	Tyr	Tyr	Phe	Pro	Cys	Asn	Ala	Ala	Ile	Asn	Glu	Ala	Gln	Phe	Ala
	355					360					365				
Lys	Asn	Ser	Gly	Tyr	Thr	Ile	His	Thr	Ile	Gly	Tyr	Asp	Leu	Gly	Asp
	370				375					380					
Phe	Ala	Leu	Ala	Asn	Asn	Ser	Leu	Lys	Leu	Thr	Ala	Thr	Asp	Glu	Asn
385				390						395				400	
His	Phe	Phe	Thr	Ala	Thr	Pro	Ala	Asn	Leu	Ala	Ala	Ala	Phe	Asp	Asn
		405						410					415		
Ile	Ala	Gln	Thr	Ile	Asn	Ile	Gly	Ile	Gln	Arg	Gly	Glu	Val	Thr	Asp
	420					425						430			
Phe	Val	Ala	Pro	Gly	Phe	Ile	Val	Lys	Asn	Leu	Thr	Gln	Ser	Gly	Asp
	435					440					445				
Val	Thr	His	Leu	Leu	Asn	Val	Ser	Asn	Gly	Thr	Val	His	Tyr	Asp	Val
	450				455					460					
Ser	Thr	Lys	Lys	Leu	Thr	Trp	Thr	Thr	Gly	Thr	Ile	Leu	Ser	Ser	Ser
465				470					475					480	
Glu	Ala	Thr	Ile	Thr	Tyr	Arg	Ile	Tyr	Ala	Asp	Leu	Asp	Tyr	Ile	Gln
		485				490							495		
Asn	Asn	Asp	Ile	Pro	Val	Asn	Thr	Thr	Ser	Ala	Ile	Gly	Pro	Asp	Leu
	500					505						510			
Gly	Gly	Phe	Asp	Thr	Asn	Thr	Glu	Ala	Lys	Leu	Thr	Tyr	Thr	Asn	Ser
	515					520					525				
Asn	Gly	Glu	Pro	Asn	Gln	Gln	Leu	Ile	Phe	Pro	Arg	Pro	Thr	Val	Lys
	530				535					540					
Leu	Gly	Tyr	Gly	Val	Ile	Lys	Arg	His	Tyr	Val	Leu	Val	Asn	Lys	Asp
545				550					555					560	

Gly	Gln	Pro	Ile	Gln	Ala	Asn	Gly	Thr	Val	Val	Ser	Ser	Leu	Ser	Glu	
			565						570					575		
Ala	His	Val	Leu	Gln	Ser	Gln	Asp	Phe	Phe	Leu	Pro	Ser	Gly	Gly	Gly	
			580					585					590			
His	Ile	Val	Pro	Lys	Trp	Ile	Lys	Leu	Asp	Lys	Thr	Thr	Glu	Ala	Leu	
		595					600					605				
Gln	Tyr	Tyr	Ser	Val	Pro	Pro	Thr	Asn	Thr	Val	Ile	Thr	Thr	Ala	Asp	
	610					615					620					
Gly	Lys	Arg	Tyr	Arg	Phe	Val	Glu	Val	Pro	Gly	Ser	Thr	Pro	Asn	Pro	
	625				630					635					640	
Gly	Gln	Ile	Gly	Ile	Ser	Trp	Lys	Lys	Pro	Ala	Gly	Asn	Ala	Tyr	Phe	
			645						650					655		
Ala	Tyr	Lys	Leu	Leu	Asn	Tyr	Trp	Met	Gly	Gly	Thr	Thr	Asp	Gln	Gln	
		660						665					670			
Ser	Glu	Trp	Asp	Val	Thr	Ser	Asn	Trp	Thr	Gly	Ala	Gln	Val	Pro	Leu	
		675					680					685				
Thr	Gly	Glu	Asp	Val	Glu	Phe	Ala	Thr	Thr	Glu	Asn	Phe	Gly	Ser	Pro	
	690					695					700					
Ala	Val	Ala	Asp	Leu	His	Val	Pro	Thr	Thr	Asn	Pro	Lys	Ile	Ile	Gly	
	705				710					715					720	
Asn	Leu	Ile	Asn	Asn	Ser	Asp	Lys	Asp	Leu	Val	Val	Thr	Thr	Ser	Ser	
			725						730					735		
Gln	Leu	Thr	Ile	Asn	Gly	Val	Val	Glu	Asp	Asn	Asn	Pro	Asn	Val	Gly	
		740						745					750			
Thr	Ile	Val	Val	Lys	Ser	Ser	Lys	Asp	Asn	Pro	Thr	Gly	Thr	Leu	Leu	
		755					760					765				
Phe	Ala	Asn	Pro	Gly	Tyr	Asn	Gln	Asn	Val	Gly	Gly	Thr	Val	Glu	Phe	
	770					775					780					
Tyr	Asn	Gln	Gly	Tyr	Asp	Cys	Ala	Asp	Cys	Gly	Met	Tyr	Arg	Arg	Ser	
	785				790					795					800	
Trp	Gln	Tyr	Phe	Gly	Ile	Pro	Val	Asn	Glu	Ser	Gly	Phe	Pro	Ile	Asn	
			805						810					815		
Asp	Val	Gly	Gly	Asn	Glu	Thr	Val	Asn	Gln	Trp	Val	Glu	Pro	Phe	Asn	
		820						825					830			
Gly	Asp	Lys	Trp	Arg	Pro	Ala	Pro	Tyr	Ala	Pro	Asp	Thr	Glu	Leu	Gln	
		835					840					845				
Lys	Phe	Lys	Gly	Tyr	Gln	Ile	Thr	Asn	Asp	Val	Gln	Ala	Gln	Pro	Thr	
	850					855					860					
Gly	Val	Tyr	Ser	Phe	Lys	Gly	Met	Ile	Cys	Val	Cys	Asp	Ala	Phe	Leu	
	865				870					875					880	
Asn	Leu	Thr	Arg	Thr	Ser	Gly	Val	Asn	Tyr	Ser	Gly	Ala	Asn	Leu	Ile	
			885						890					895		
Gly	Asn	Ser	Tyr	Thr	Gly	Ala	Ile	Asp	Ile	Lys	Gln	Gly	Ile	Val	Phe	
		900						905					910			
Pro	Pro	Glu	Val	Glu	Gln	Thr	Val	Tyr	Leu	Phe	Asn	Thr	Gly	Thr	Arg	
		915					920					925				
Asp	Gln	Trp	Arg	Lys	Leu	Asn	Gly	Ser	Thr	Val	Ser	Gly	Tyr	Arg	Ala	
	930					935					940					
Gly	Gln	Tyr	Leu	Ser	Val	Pro	Lys	Asn	Thr	Ala	Gly	Gln	Asp	Asn	Leu	
	945				950					955					960	
Pro	Asp	Arg	Ile	Pro	Ser	Met	His	Ser	Phe	Leu	Val	Lys	Met	Gln	Asn	
			965						970					975		
Gly	Ala	Ser	Cys	Thr	Leu	Unk	Ile	Leu	Tyr	Asp	Lys	Leu	Leu	Lys	Asn	
		980					985						990			
Thr	Thr	Val	Asn	Asn	Gly	Asn	Gly	Thr	Gln	Ile	Thr	Trp	Arg	Ser	Gly	
		995					1000					1005				
Asn	Ser	Gly	Ser	Ala	Asn	Met	Pro	Ser	Leu	Val	Met	Asp	Val	Leu	Gly	
	1010					1015					1020					
Asn	Glu	Ser	Ala	Asp	Arg	Leu	Trp	Ile	Phe	Thr	Asp	Gly	Gly	Leu	Ser	
	1025				1030					1035					1040	
Phe	Gly	Phe	Asp	Asn	Gly	Trp	Asp	Gly	Arg	Lys	Leu	Thr	Glu	Lys	Gly	
			1045						1050					1055		
Leu	Ser	Gln	Leu	Tyr	Ala	Met	Ser	Asp	Ile	Gly	Asn	Asp	Lys	Phe	Gln	
		1060						1065					1070			
Val	Ala	Gly	Val	Pro	Glu	Leu	Asn	Asn	Leu	Leu	Ile	Gly	Phe	Asp	Ala	
		1075					1080					1085				
Asp	Lys	Asp	Gly	Gln	Tyr	Thr	Leu	Glu	Phe	Ala	Leu	Ser	Asp	His	Phe	
	1090					1095					1100					
Ala	Lys	Gly	Ala	Val	Tyr	Leu	His	Asp	Leu	Gln	Ser	Gly	Ala	Lys	His	
	1105				1110					1115					1120	
Arg	Ile	Thr	Asn	Ser	Thr	Ser	Tyr	Ser	Phe	Asp	Ala	Lys	Arg	Gly	Asp	
			1125						1130					1135		
Ser	Gly	Ala	Arg	Phe	Arg	Leu	Ser	Tyr	Gly	Cys	Asp	Glu	Asn	Val	Asp	
		1140						1145					1150			
Asp	Ser	His	Val	Val	Ser	Thr	Asn	Gly	Arg	Glu	Ile	Ile	Leu	Asn		
	1155						1160				1165					
Gln	Asp	Ala	Leu	Asp	Cys	Thr	Val	Thr	Leu	Phe	Thr	Ile	Glu	Gly	Lys	

1170 1175 1180
 Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys
 1185 1190 1195 1200
 Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr
 1205 1210 1215
 Asn Asp Val His Lys Val Leu Val Glu Tyr
 1220 1225

(2) INFORMATION FOR SEQ ID NO:485

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485

Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys Thr
 1 5 10 15
 Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp
 20 25 30
 Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu Val
 35 40 45
 Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser
 50 55 60
 Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile Arg
 65 70 75 80
 Pro Ala Asn Arg Phe Pro Ser His Arg Lys Ser Phe Phe Ala Glu Asn
 85 90 95
 Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr Ala
 100 105 110
 Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp Asp
 115 120 125
 Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp Val
 130 135 140
 Val Met Val Ile Asp Gln Ser Ser Ser Met Gly Gly Gln Asn Ile Ala
 145 150 155 160
 Arg Leu Lys Ser Ala Ile Ala Ser Gly Gln Arg Phe Val Lys Lys Met
 165 170 175
 Leu Pro Lys Gly Thr Ala Thr Glu Gly Val Arg Ile Ala Leu Val Ser
 180 185 190
 Tyr Asp His Glu Pro His Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala
 195 200 205
 Phe Leu Cys Gln Lys Ile Arg Ala Leu Thr Pro Ile Trp Gly Thr His
 210 215 220
 Thr Gln Gly Gly Leu Lys Met Ala Arg Asn Ile Met Ala Thr Ser Thr
 225 230 235 240
 Ala Val Asp Lys His Ile Ile Leu Met Ser Asp Gly Leu Ala Thr Glu
 245 250 255
 Gln Tyr Pro Val Lys Asn Val Thr Thr Ala Asp Phe Ile Gly Lys Thr
 260 265 270
 Gly Asn Ala Asn Asp Pro Ile Asp Leu Val Ile Gln Gly Ala Ile Asn
 275 280 285
 Phe Pro Thr Asn Tyr Val Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro
 290 295 300
 Asn Tyr Pro Thr His Ser Ser Lys Val Gly Arg Asn Leu Pro Glu
 305 310 315 320
 Ser Lys Phe Asp Tyr Ser Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly
 325 330 335
 Val Ala Gly Ala Leu Val Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr
 340 345 350
 Tyr Tyr Phe Pro Cys Asn Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys
 355 360 365
 Asn Ser Gly Tyr Thr Ile His Thr Ile Gly Tyr Asp Leu Gly Asp Phe
 370 375 380
 Ala Leu Ala Asn Asn Ser Leu Lys Leu Thr Ala Thr Asp Glu Asn His

385		390		395		400
Phe Phe Thr Ala Thr Pro Ala Asn Leu Ala Ala Phe Asp Asn Ile						
	405			410		415
Ala Gln Thr Ile Asn Ile Gly Ile Gln Arg Gly Glu Val Thr Asp Phe						
	420		425		430	
Val Ala Pro Gly Phe Ile Val Lys Asn Leu Thr Gln Ser Gly Asp Val		440		445		
Thr His Leu Leu Asn Val Ser Asn Gly Thr Val His Tyr Asp Val Ser		455		460		
	450					
Thr Lys Lys Leu Thr Trp Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu		470		475		480
Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn						
	485		490			495
Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly						
	500		505		510	
Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn						
	515		520		525	
Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu						
	530		535		540	
Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly						
	545		550		555	560
Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala						
	565		570			575
His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His						
	580		585			590
Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln						
	595		600		605	
Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly						
	610		615		620	
Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly						
	625		630		635	640
Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala						
	645		650			655
Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser						
	660		665		670	
Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr						
	675		680		685	
Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala						
	690		695		700	
Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn						
	705		710		715	720
Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Thr Thr Ser Ser Gln						
	725		730			735
Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr						
	740		745			750
Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe						
	755		760		765	
Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr						
	770		775		780	
Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp						
	785		790		795	800
Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn Asp						
	805		810			815
Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn Gly						
	820		825			830
Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys						
	835		840		845	
Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr Gly						
	850		855		860	
Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn						
	865		870		875	880
Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly						
	885		890			895
Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro						
	900		905			910
Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp						
	915		920			925
Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly						
	930		935		940	
Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro						
	945		950		955	960
Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly						
	965		970			975
Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr						
	980		985			990
Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn						
	995		1000		1005	

```

Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn
1010          1015          1020
Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe
1025          1030          1035          1040
Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu
          1045          1050          1055
Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val
          1060          1065          1070
Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp
          1075          1080          1085
Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala
          1090          1095          1100
Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg
1105          1110          1115          1120
Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser
          1125          1130          1135
Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp
          1140          1145          1150
Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln
          1155          1160          1165
Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu
          1170          1175          1180
Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val
1185          1190          1195          1200
Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn
          1205          1210          1215
Asp Val His Lys Val Leu Val Glu Tyr
          1220          1225

```

(2) INFORMATION FOR SEQ ID NO:486

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486

```

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe
1      5      10      15
Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly
20     25     30
Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His
35     40     45
Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg
50     55     60
Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val
65     70     75     80
Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu
85     90     95
Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu
100    105    110
Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg
115    120    125
Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln
130    135    140
Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val
145    150    155    160
Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe Glu
165    170    175
Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser
180    185    190
Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala
195    200    205
Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp
210    215    220

```

```

Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr
225                230                235                240
Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu
                245                250                255
Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly Asp
                260                265                270
Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe
                275                280                285
Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly
                290                295                300
Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly
305                310                315                320
Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr
                325                330                335
Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn
                340                345                350
Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr
                355                360                365
Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp
370                375                380
Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe
385                390                395                400
Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu
                405                410                415
Leu Trp Phe Lys Ala Arg Tyr Ser Phe
                420                425

```

(2) INFORMATION FOR SEQ ID NO:487

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487

```

Met Ser Ser Cys Glu Val Ala Tyr Phe Ser Leu Lys Pro Ile Asp Leu
1      5      10      15
Gln Asn Ile Arg Glu Arg Asn His Ser Ser Asp Ile Ala Leu Ser Asn
20     25     30
Leu Leu Asp Asn Ser Asn Gln Leu Leu Ala Thr Ile Leu Ile Gly Asn
35     40     45
Asn Val Ile Asn Val Ala Ile Val Ile Leu Ser Asn Tyr Ala Ile Glu
50     55     60
Gln Thr Phe Val Phe Ser Ser Pro Ile Ile Gly Phe Leu Ile Gln Thr
65     70     75     80
Ile Leu Leu Thr Thr Val Leu Leu Leu Phe Gly Glu Ile Leu Pro Lys
85     90     95
Val Tyr Ala Arg Lys Asn Pro Leu Gln Tyr Ser Arg Phe Ser Ala Ala
100    105    110
Ala Met Ser Val Ile Tyr Lys Ile Leu Ser Pro Phe Ser Lys Leu Leu
115    120    125
Val Lys Ser Thr Gly Ile Val Thr Arg Gly Ile Ser Lys Lys Lys Tyr
130    135    140
Asp Met Ser Val Asp Glu Leu Ser Lys Ala Val Ala Leu Thr Thr Thr
145    150    155    160
Glu Gly Glu Pro Glu Glu Lys Glu Met Ile Asn Glu Ile Ile Lys Phe
165    170    175
Tyr Asn Lys Thr Ala Cys Glu Ile Met Val Pro Arg Ile Asp Ile Val
180    185    190
Asp Val Asp Leu Ser Trp Pro Phe Arg Lys Met Leu Asp Phe Val Val
195    200    205
Ser Ser Gly Tyr Ser Arg Leu Pro Val Ser Glu Gly Ser Glu Asp Asn
210    215    220
Ile Lys Gly Val Ile Tyr Ile Lys Asp Leu Ile Pro His Met Asp Lys
225    230    235    240

```

Gly Asp Glu Phe Asp Trp His Pro Leu Ile Arg Lys Ala Tyr Phe Val
 245 250 255
 Pro Glu Asn Lys Arg Ile Asp Asp Leu Leu Glu Glu Phe Arg Ala Asn
 260 265 270
 Lys Val His Val Ser Ile Val Val Asp Glu Phe Gly Gly Thr Cys Gly
 275 280 285
 Leu Ile Thr Met Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Thr
 290 295 300
 Asp Glu Tyr Asp Glu Glu Glu Leu Pro Phe Lys Val Leu Gly Asp Gly
 305 310 315 320
 Ser Tyr Leu Phe Glu Gly Lys Thr Ser Leu Ser Asp Val Arg His Tyr
 325 330 335
 Leu Asp Leu Pro Glu Asn Ala Phe Gly Glu Leu Gly Asp Glu Val Asp
 340 345 350
 Thr Leu Ser Gly Leu Phe Leu Glu Ile Lys Gln Glu Leu Pro His Val
 355 360 365
 Gly Asp Thr Ala Val Tyr Glu Pro Phe Arg Phe Gln Val Thr Gln Met
 370 375 380
 Asp Lys Arg Arg Ile Ile Glu Ile Lys Ile Phe Pro Phe Glu Arg Thr
 385 390 395 400
 Trp Glu Val Glu

(2) INFORMATION FOR SEQ ID NO:488

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488

Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro
 1 5 10 15
 Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp
 20 25 30
 Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys
 35 40 45
 Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn
 50 55 60
 Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu
 65 70 75 80
 Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His
 85 90 95
 Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr
 100 105 110
 Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser
 115 120 125
 Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu
 130 135 140
 Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln
 145 150 155 160
 Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile
 165 170 175
 Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp
 180 185 190
 Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe
 195 200 205
 Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr
 210 215 220
 Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala
 225 230 235 240
 Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile
 245 250 255
 Asp Ile Ser Phe
 260

(2) INFORMATION FOR SEQ ID NO:489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489

```
Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu
1      5      10      15
Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr
20      25      30
Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser
35      40      45
Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr
50      55      60
Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr
65      70      75      80
His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile
85      90      95
Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu
100     105     110
Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg
115     120     125
Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp
130     135     140
Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val
145     150     155     160
Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser
165     170     175
Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser
180     185     190
Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys
195     200     205
Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly
210     215     220
Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu
225     230     235     240
Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala
245     250     255
Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr
260     265     270
Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe
275     280     285
Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly
290     295     300
Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu
305     310     315     320
Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp
325     330     335
Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser
340     345     350
Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala
355     360     365
Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro
370     375     380
Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn
385     390     395     400
Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala
405     410     415
Asn Thr Ile Gln Tyr Ala Gly Gln His Ser Lys Ser Asp Ala Gly Met
420     425     430
Asp Glu His Thr Ala Gln Val Asp Tyr Thr Arg Pro Leu Gly Gln Ala
435     440     445
```

His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser
 450 455 460
 Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro
 465 470 475 480
 Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp
 485 490 495
 Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln
 500 505 510
 Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala
 515 520 525
 Leu Phe Pro Glu Asn Ala Ala Asp Phe Ser His Asn Ser Phe Asp
 530 535 540
 Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln
 545 550 555 560
 Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln
 565 570 575
 Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Tyr Gln Val Gln Tyr Gly
 580 585 590
 Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr
 595 600 605
 Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp
 610 615 620
 Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn
 625 630 635 640
 Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser
 645 650 655
 Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg
 660 665 670
 Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala
 675 680 685
 Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu
 690 695 700
 Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr
 705 710 715 720
 Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe
 725 730 735
 Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val
 740 745 750
 Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser
 755 760 765
 Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile
 770 775 780
 Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn
 785 790 795 800
 Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys
 805 810 815
 Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gln Gly Asn Pro Thr
 820 825 830
 Gly Asn

(2) INFORMATION FOR SEQ ID NO:490

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490

Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala
 1 5 10 15
 Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu
 20 25 30
 Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala
 35 40 45

```

Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr
50          55          60
Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro
65          70          75          80
Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr Leu Asn Tyr
85          90          95
Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser Asp Leu Pro
100         105         110
Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile Leu Pro Tyr
115         120         125
Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu Met Leu Gly
130         135         140
Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro Ile Tyr Asn
145         150         155         160
Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val Gln Phe Arg
165         170         175
Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn Trp Met Ser
180         185         190
Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val Phe Gly Leu
195         200         205
Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp Arg Leu Glu
210         215         220
Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu Tyr Asn Trp
225         230         235         240
Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala Val Gly Leu
245         250         255
Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln Ile Trp Gly
260         265         270
Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr Phe Pro Tyr
275         280         285
Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp Leu Glu His
290         295         300
Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr Val Ser Pro
305         310         315         320
Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys Gln Pro Leu
325         330         335
Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp Tyr Ser Trp
340         345         350
Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg Val Trp Phe
355         360         365
Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met
370         375         380
Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His
385         390         395

```

(2) INFORMATION FOR SEQ ID NO:491

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491

```

Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met
1          5          10          15
Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro
20         25         30
Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu
35         40         45
Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp
50         55         60
Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
65         70         75         80
Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg
85         90         95

```

```

Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn
100 105 110
Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser
115 120 125
Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp
130 135 140
Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met
145 150 155 160
Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu
165 170 175
Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala
180 185 190
Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro
195 200 205
Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu
210 215 220
His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn
225 230 235 240
Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile
245 250 255
Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys
260 265 270
Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val
275 280 285
Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln
290 295 300
Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala
305 310 315 320
Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly
325 330 335
Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr
340 345 350
Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr
355 360 365
Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
370 375 380

```

(2) INFORMATION FOR SEQ ID NO:492

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492

```

Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
1 5 10 15
Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
20 25 30
Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
35 40 45
Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
50 55 60
Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
65 70 75 80
Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
85 90 95
Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
100 105 110
Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe
115 120 125
Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His
130 135 140
Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys
145 150 155 160

```

Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His
165 170 175
Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr Asp Leu Thr Ser Cys
180 185 190
Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe
195 200 205
Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu
210 215 220

(2) INFORMATION FOR SEQ ID NO:493

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493

Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile
1 5 10 15
Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn
20 25 30
Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg
35 40 45
Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr
50 55 60
Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala
65 70 75 80
Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp
85 90 95
Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu
100 105 110
Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu
115 120 125
Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn
130 135 140
Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe
145 150 155 160
Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His
165 170 175
Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala
180 185 190
Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp
195 200 205
Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp
210 215 220
Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr
225 230 235 240
Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu
245 250 255
Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn
260 265 270
Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser
275 280 285
Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu
290 295 300
Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser
305 310 315 320
Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro
325 330 335
Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met
340 345 350
Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser
355 360 365
Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp
370 375 380

Gly Leu Arg Asn Leu Phe His
385 390

(2) INFORMATION FOR SEQ ID NO:494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494

Met	Lys	Thr	Thr	Val	Gln	Gln	Ile	Ile	Leu	Cys	Leu	Ala	Leu	Met	Met
1				5					10					15	
Ser	Gly	Val	Leu	Gly	Gly	Asn	Ala	Gln	Ser	Phe	Trp	Glu	Glu	Ile	Ala
			20					25					30		
Pro	Pro	Phe	Ile	Ser	Asn	Glu	Pro	Asn	Val	Lys	Tyr	Ile	Ile	Pro	Asn
		35				40					45				
Met	Gly	Ile	Asp	Ser	Lys	Gly	Thr	Ile	Tyr	Val	Thr	Val	Thr	Lys	Arg
	50					55				60					
Ile	Gln	Gln	Gly	Ala	Asn	Tyr	Thr	Ser	Glu	Gln	Leu	Gly	Met	Tyr	Tyr
65					70					75				80	
Arg	Pro	Leu	Gly	Asp	Asn	Glu	Gln	Trp	Trp	Lys	His	Asp	Pro	Tyr	Phe
			85					90					95		
Asp	Asp	Lys	Ile	Val	Ala	Asp	Ile	Gln	Thr	Asp	Ala	Tyr	Gly	Arg	Val
		100					105					110			
Tyr	Val	Cys	Thr	Thr	Ser	Ser	Arg	Asp	Gln	Glu	Tyr	Gln	Leu	Tyr	Ile
	115						120				125				
Asn	Glu	Gln	Asn	Glu	Trp	Arg	Cys	Ile	Phe	Lys	Thr	Ser	Val	Ser	Thr
	130					135				140					
Tyr	Glu	His	Gly	Met	Ala	Val	Phe	Arg	Ser	Ser	Thr	Gly	Val	Thr	Tyr
145				150					155					160	
Ile	Gly	Thr	Arg	His	His	Ile	Phe	Ala	Ser	Gly	Val	Asn	Asp	Phe	Glu
			165					170					175		
Phe	Asn	Thr	Ile	Tyr	Glu	Asp	Ser	Thr	Pro	Met	Ser	Cys	Arg	Phe	Ala
	180						185					190			
Glu	Ala	Thr	Asn	Ser	Gly	Thr	Ile	Tyr	Leu	Ala	Leu	Met	His	Glu	Thr
	195						200				205				
Thr	Met	Ser	Thr	Thr	Ile	Leu	Thr	Tyr	Gln	Asn	Gly	Glu	Phe	Val	Asp
	210				215						220				
Ile	Ser	Glu	Ser	Glu	Leu	Ser	Asn	Ser	Ile	Ile	Ala	Ser	Met	Cys	Ser
225				230						235				240	
Asn	Lys	Glu	Gly	Asp	Ile	Ile	Ala	Leu	Val	Thr	Ser	Tyr	Thr	Gly	Phe
		245						250					255		
Met	Ser	Gly	Thr	Leu	Ala	Ile	Arg	Lys	Ala	Asp	Glu	Gly	Lys	Trp	Gln
		260					265						270		
Leu	Val	Gly	Gly	Asp	Ile	Gln	Asn	Ala	Ile	Val	Gln	Asn	Ile	Cys	Met
	275						280					285			
Met	Asp	Asp	Asn	Lys	Ile	Ala	Cys	Glu	Val	Phe	Gly	Thr	Pro	Asn	Gly
	290				295						300				
Val	Asp	Gly	Arg	Thr	Arg	Val	Cys	Val	Ser	Asp	Ala	Ser	Val	Phe	Asp
305				310						315				320	
Phe	Glu	Trp	Tyr	Glu	Asp	Glu	Ile	Tyr	Gly	Gly	Leu	Ile	Phe	Asp	Thr
		325							330				335		
Phe	Phe	Tyr	Ser	Pro	Trp	Asp	Lys	Leu	Leu	Tyr	Ala	Lys	Phe	Gly	Gly
		340					345						350		
Ile	Met	Leu	Arg	Ser	Lys	Glu	Ser	Phe	Ile	Thr	Ser	Phe	Ile	Ser	Pro
	355					360						365			
Thr	Val	Val	Gln	Gly	Val	Asp	Val	Tyr	Thr	Leu	Ala	Gly	Lys	Ile	Arg
	370				375						380				
Ile	Glu	Ser	Glu	Thr	Pro	Val	Ser	Glu	Val	Leu	Leu	Phe	Asp	Leu	Ala
385				390						395				400	
Gly	Arg	Met	Val	Leu	Arg	Gln	Thr	Ile	Asp	Asn	Lys	Ile	Tyr	Ser	Asp
		405							410				415		
Ile	Asp	Thr	Asn	Gly	Leu	Lys	Arg	Ser	Gly	Ile	Tyr	Val	Val	Ser	Val
	420						425						430		

Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val
 435 440 445

(2) INFORMATION FOR SEQ ID NO:495

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495

```

Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly
1      5      10      15
Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys
20      25      30
Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu
35      40      45
Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe
50      55      60
Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp
65      70      75      80
Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn
85      90      95
Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu
100     105     110
Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp
115     120     125
Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu
130     135     140
Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe
145     150     155     160
Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln
165     170     175
Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp
180     185     190
Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln
195     200     205
Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser
210     215     220
Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser
225     230     235     240
Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro
245     250     255
Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val
260     265     270
Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile
275     280     285
Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr
290     295     300
Gly Asp Lys Lys
305

```

(2) INFORMATION FOR SEQ ID NO:496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496

Met Lys Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu
1 5 10 15
Thr Gly Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr
20 25 30
Ala Phe Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser
35 40 45
Ala Tyr Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Ser Ile
50 55 60
Thr Arg Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu
65 70 75 80
Asn Leu Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg
85 90 95
Trp Met Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn
100 105 110
Pro Ala Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala
115 120 125
Ala Ala Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met
130 135 140
Asp Asn Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly
145 150 155 160
Gly Ile Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu
165 170 175
Tyr Thr Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser
180 185 190
Glu Thr Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe
195 200 205
Gly Ile Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe
210 215 220
Leu Leu Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly
225 230 235 240
Lys Phe Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg
245 250 255
Asn Phe Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser
260 265 270
Ser Leu Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile
275 280 285
Gly Phe Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn
290 295 300
Thr Gly Arg Arg Thr Ser Leu Tyr Tyr His Asp
305 310 315

(2) INFORMATION FOR SEQ ID NO:497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497

Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Val Arg
1 5 10 15
Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala
20 25 30
Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr
35 40 45
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala
50 55 60
Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser


```

65          70          75          80
Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly Ile His
      85          90          95
Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg Ser Ala
      100         105         110
Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile Arg Ser
      115         120         125
Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys Ser Ser
      130         135         140
Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys Val Phe
145         150         155         160
Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly Leu Arg
      165         170         175
Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp Ala Ile
      180         185         190
Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr Arg Thr
      195         200         205
Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln Ile Gly
210         215         220
Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala Asn Val
225         230         235         240
Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr Asp Leu
      245         250         255
Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala Val Gly
      260         265         270
Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
      275         280         285

```

(2) INFORMATION FOR SEQ ID NO:498

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498

```

Met Glu Asn Leu Lys Asn Ile Gln Pro Arg Glu Asp Phe Asn Trp Glu
1          5          10          15
Glu Phe Glu Ala Gly Gly Val His Ala Ala Val Ser Arg Gln Glu Gln
      20          25          30
Glu Ala Ala Tyr Asp Lys Thr Leu Asn Thr Ile Lys Glu Lys Glu Val
      35          40          45
Val Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn
      50          55          60
Val Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr
65          70          75          80
Asn Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn
      85          90          95
Gln Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg
      100         105         110
Ala Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu
      115         120         125
Ile Val Lys Gly Tyr Val Lys Cys Arg Thr Lys Gly Met Ile Val
      130         135         140
Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Val
145         150         155         160
Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr Met Glu Phe
      165         170         175
Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val Val Ser His
      180         185         190
Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys Glu Ile Ile
      195         200         205
Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val Lys Asn Ile
210         215         220
Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp Gly Leu Ile

```

```

225          230          235          240
His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro Glu Glu Ile
          245          250          255
Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp Phe Asp Glu
          260          265          270
Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met Pro His Pro
          275          280          285
Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys Val Lys Gly
          290          295          300
Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu Ile Ala Gln
305          310          315          320
Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp Thr Gln His
          325          330          335
Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu Val Glu Ala
          340          345          350
Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser Leu Gly Leu
          355          360          365
Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr Arg Phe Pro
          370          375          380
Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr Asn Phe Gly
385          390          395          400
Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile His Ile Ser
          405          410          415
Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu Phe Thr Glu
          420          425          430
Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp Lys Glu Asn
          435          440          445
Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn Pro Trp Asp
          450          455          460
Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu Gly Thr Val
465          470          475          480
Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro Tyr Gly Val
          485          490          495
Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp Gly Ser Gln
          500          505          510
Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu Phe Asn Lys
          515          520          525
Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe Glu Asp Glu
          530          535          540
Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys Ala Glu Ala
545          550          555          560
Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn Pro Ala Gln
          565          570          575
Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu Ala Ala Leu
          580          585          590
Lys Glu Lys Leu Ser Glu Asn
          595

```

(2) INFORMATION FOR SEQ ID NO:499

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499

```

Met Gly Arg Val Thr Ala Ile Asn Lys Arg Glu Val Val Ile Asn Val
1          5          10          15
Gly Tyr Lys Ser Glu Gly Val Val Pro Ala Thr Glu Phe Arg Tyr Asn
          20          25          30
Pro Glu Leu Lys Val Gly Asp Glu Val Glu Val Tyr Ile Glu Asn Gln
          35          40          45
Glu Asp Lys Lys Gly Gln Leu Val Leu Ser His Arg Lys Gly Arg Ala
          50          55          60
Ala Arg Ser Trp Glu Arg Val Asn Glu Ala Leu Glu Lys Asp Glu Ile

```

65				70				75				80			
Val	Lys	Gly	Tyr	Val	Lys	Cys	Arg	Thr	Lys	Gly	Gly	Met	Ile	Val	Asp
				85					90					95	
Val	Phe	Gly	Ile	Glu	Ala	Phe	Leu	Pro	Gly	Ser	Gln	Ile	Asp	Val	Arg
			100					105					110		
Pro	Ile	Arg	Asp	Tyr	Asp	Ala	Phe	Val	Glu	Lys	Thr	Met	Glu	Phe	Lys
		115					120					125			
Ile	Val	Lys	Ile	Asn	Gln	Glu	Tyr	Lys	Asn	Val	Val	Val	Ser	His	Lys
		130				135					140				
Val	Leu	Ile	Glu	Ala	Glu	Leu	Glu	Gln	Gln	Lys	Lys	Glu	Ile	Ile	Gly
145					150					155					160
Lys	Leu	Glu	Lys	Gly	Gln	Val	Leu	Glu	Gly	Ile	Val	Lys	Asn	Ile	Thr
			165					170						175	
Ser	Tyr	Gly	Val	Phe	Ile	Asp	Leu	Gly	Gly	Val	Asp	Gly	Leu	Ile	His
			180					185					190		
Ile	Thr	Asp	Leu	Ser	Trp	Gly	Arg	Val	Ala	His	Pro	Glu	Glu	Ile	Val
		195				200						205			
Gln	Leu	Asp	Gln	Lys	Ile	Asn	Val	Val	Ile	Leu	Asp	Phe	Asp	Glu	Asp
		210				215					220				
Arg	Lys	Arg	Ile	Ala	Leu	Gly	Leu	Lys	Gln	Leu	Met	Pro	His	Pro	Trp
225				230						235					240
Asp	Ala	Leu	Asp	Ser	Glu	Leu	Lys	Val	Gly	Asp	Lys	Val	Lys	Gly	Lys
			245					250						255	
Val	Val	Val	Met	Ala	Asp	Tyr	Gly	Ala	Phe	Val	Glu	Ile	Ala	Gln	Gly
			260					265					270		
Val	Glu	Gly	Leu	Ile	His	Val	Ser	Glu	Met	Ser	Trp	Thr	Gln	His	Leu
		275				280						285			
Arg	Ser	Ala	Gln	Asp	Phe	Leu	His	Val	Gly	Asp	Glu	Val	Glu	Ala	Val
		290				295				300					
Ile	Leu	Thr	Leu	Asp	Arg	Glu	Glu	Arg	Lys	Met	Ser	Leu	Gly	Leu	Lys
305				310						315					320
Gln	Leu	Lys	Pro	Asp	Pro	Trp	Ala	Asp	Ile	Glu	Thr	Arg	Phe	Pro	Val
			325					330						335	
Gly	Ser	Arg	His	His	Ala	Arg	Val	Arg	Asn	Phe	Thr	Asn	Phe	Gly	Val
		340					345					350			
Phe	Val	Glu	Ile	Glu	Glu	Gly	Val	Asp	Gly	Leu	Ile	His	Ile	Ser	Asp
		355				360						365			
Leu	Ser	Trp	Thr	Lys	Lys	Ile	Lys	His	Pro	Ser	Glu	Phe	Thr	Glu	Val
		370				375					380				
Gly	Ala	Asp	Ile	Glu	Val	Gln	Val	Ile	Glu	Ile	Asp	Lys	Glu	Asn	Arg
385				390						395					400
Arg	Leu	Ser	Leu	Gly	His	Lys	Gln	Leu	Glu	Glu	Asn	Pro	Trp	Asp	Val
			405					410						415	
Phe	Glu	Thr	Val	Phe	Thr	Val	Gly	Ser	Ile	His	Glu	Gly	Thr	Val	Ile
		420					425						430		
Glu	Val	Met	Asp	Lys	Gly	Ala	Val	Val	Ser	Leu	Pro	Tyr	Gly	Val	Glu
		435				440					445				
Gly	Phe	Ala	Thr	Pro	Lys	His	Met	Val	Lys	Glu	Asp	Gly	Ser	Gln	Ala
		450				455				460					
Val	Leu	Glu	Glu	Lys	Leu	Pro	Phe	Lys	Val	Ile	Glu	Phe	Asn	Lys	Asp
465				470						475					480
Ala	Lys	Arg	Ile	Ile	Val	Ser	His	Ser	Arg	Val	Phe	Glu	Asp	Glu	Gln
			485					490						495	
Lys	Met	Ala	Gln	Arg	Glu	Ala	Asn	Ala	Glu	Arg	Lys	Ala	Glu	Ala	Lys
		500					505						510		
Ala	Ala	Gln	Lys	Glu	Ala	Ala	Ala	Glu	Ala	Ala	Asn	Pro	Ala	Gln	Ala
		515				520					525				
Val	Glu	Lys	Ala	Thr	Leu	Gly	Asp	Leu	Gly	Glu	Leu	Ala	Ala	Leu	Lys
		530				535					540				
Glu	Lys	Leu	Ser	Glu	Asn										
545				550											

(2) INFORMATION FOR SEQ ID NO:500

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500

```
Met Ile Val Asp Val Phe Gly Ile Glu Ala Phe Leu Pro Gly Ser Gln
1      5      10      15
Ile Asp Val Arg Pro Ile Arg Asp Tyr Asp Ala Phe Val Glu Lys Thr
      20      25      30
Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val
      35      40      45
Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys
      50      55      60
Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val
65      70      75      80
Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp
      85      90      95
Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro
      100      105      110
Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp
      115      120      125
Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met
      130      135      140
Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys
145      150      155      160
Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu
      165      170      175
Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp
      180      185      190
Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu
      195      200      205
Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser
      210      215      220
Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr
225      230      235      240
Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr
      245      250      255
Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile
      260      265      270
His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu
      275      280      285
Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp
      290      295      300
Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn
305      310      315      320
Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu
      325      330      335
Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro
      340      345      350
Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp
      355      360      365
Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu
      370      375      380
Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe
385      390      395      400
Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys
      405      410      415
Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn
      420      425      430
Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu
      435      440      445
Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn
450      455
```

(2) INFORMATION FOR SEQ ID NO:501

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501

```
Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val
1      5      10      15
Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys
      20      25      30
Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val
      35      40      45
Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp
      50      55      60
Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro
      65      70      75      80
Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp
      85      90      95
Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met
      100     105     110
Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys
      115     120     125
Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu
      130     135     140
Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp
      145     150     155     160
Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu
      165     170     175
Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser
      180     185     190
Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr
      195     200     205
Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr
      210     215     220
Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile
      225     230     235     240
His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu
      245     250     255
Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp
      260     265     270
Lys Glu Asn Arg Arg Leu Ser Leu Gly His Lys Gln Leu Glu Glu Asn
      275     280     285
Pro Trp Asp Val Phe Glu Thr Val Phe Thr Val Gly Ser Ile His Glu
      290     295     300
Gly Thr Val Ile Glu Val Met Asp Lys Gly Ala Val Val Ser Leu Pro
      305     310     315     320
Tyr Gly Val Glu Gly Phe Ala Thr Pro Lys His Met Val Lys Glu Asp
      325     330     335
Gly Ser Gln Ala Val Leu Glu Glu Lys Leu Pro Phe Lys Val Ile Glu
      340     345     350
Phe Asn Lys Asp Ala Lys Arg Ile Ile Val Ser His Ser Arg Val Phe
      355     360     365
Glu Asp Glu Gln Lys Met Ala Gln Arg Glu Ala Asn Ala Glu Arg Lys
      370     375     380
Ala Glu Ala Lys Ala Ala Gln Lys Glu Ala Ala Ala Glu Ala Ala Asn
      385     390     395     400
Pro Ala Gln Ala Val Glu Lys Ala Thr Leu Gly Asp Leu Gly Glu Leu
      405     410     415
Ala Ala Leu Lys Glu Lys Leu Ser Glu Asn
      420     425
```

(2) INFORMATION FOR SEQ ID NO:502

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502

```
Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys
1      5      10      15
Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile
20      25      30
Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn
35      40      45
Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp
50      55      60
Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu
65      70      75      80
Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly
85      90      95
Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala
100     105     110
Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr
115     120     125
Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile
130     135     140
Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn
145     150     155     160
Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly
165     170     175
Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln
180     185     190
Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn
195     200     205
Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met
210     215     220
Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn
225     230     235     240
```

(2) INFORMATION FOR SEQ ID NO:503

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503

```
Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp Tyr Ala
1      5      10      15
Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala Gln Asn
20      25      30
Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly Arg Leu
35      40      45
Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu Gly Val
50      55      60
Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala Ser Tyr
65      70      75      80
Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala Ser Thr
85      90      95
Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg Lys Met
100     105     110
Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys Ser Ile
115     120     125
Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr Gln Phe
130     135     140
Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr Arg Lys
145     150     155     160
Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile Gly Ala
```

```

      165      170      175
Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser Leu Phe
      180      185      190
Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu Ala Pro
      195      200      205
Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala Lys Phe
      210      215      220
Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg Ser Leu
      225      230      235      240
Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser Glu Leu
      245      250      255
Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu Ser Glu
      260      265      270
Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro His Thr
      275      280      285
Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Leu Gly
      290      295      300
Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser
      305      310      315      320
Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile
      325      330      335
Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg
      340      345      350
Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly
      355      360      365
Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly
      370      375      380
Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr
      385      390      395      400
Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys
      405      410      415
Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys
      420      425      430
Leu Asn

```

(2) INFORMATION FOR SEQ ID NO:504

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504

```

Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu Ala Ser Leu
1      5      10      15
Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala Gly Arg Val
      20      25      30
Leu Asp Glu Gly Asn Pro Met Ile Gln Ala Asn Val Gln Leu Val
      35      40      45
Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr Asn Glu Lys
      50      55      60
Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr Ile Leu Arg
      65      70      75      80
Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile Ser Leu Arg
      85      90      95
Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn Glu Asp Ala
      100      105      110
Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala Glu Val Val
      115      120      125
Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr Thr Val Ala
      130      135      140
Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro Gly Ala Glu
      145      150      155      160
Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp Ile Ser Lys

```

[illegible]


```

Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn
785              790              795              800
Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp
              805              810              815
Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp
              820              825              830
Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys
              835              840              845
Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser
              850              855              860
Ser Ile Ser Arg Ser Ala Ile Asn Ile Glu Glu Ser Met Ser
865              870              875              880
Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn
              885              890              895
Ala Phe Ser Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met
              900              905              910
Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser
              915              920              925

```

(2) INFORMATION FOR SEQ ID NO:505

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505

```

Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val
1              5              10              15
Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu
              20              25              30
Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val
              35              40              45
Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr
              50              55              60
Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly
65              70              75              80
Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser
              85              90              95
Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe
              100              105              110
Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val
              115              120              125
Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp
130              135              140
Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe
145              150              155              160
Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr
              165              170              175
Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly
              180              185              190
Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe
195              200              205
Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp
210              215              220
Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr
225              230              235              240
His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala
              245              250              255
Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly
              260              265              270
Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser
275              280              285
Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu
290              295              300

```

```

Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn
305          310          315          320
Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Asn Arg Pro Val
          325          330          335
Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile
          340          345          350
Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro
          355          360          365
Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser
          370          375          380
Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
385          390          395          400

```

(2) INFORMATION FOR SEQ ID NO:506

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506

```

Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Gly Ala Val Leu Leu
1          5          10          15
Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp
          20          25          30
Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp
          35          40          45
Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val
          50          55          60
Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser
65          70          75          80
Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg
          85          90          95
Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys
          100          105          110
Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp
          115          120          125
Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser
130          135          140
Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr
145          150          155          160
Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn
          165          170          175
Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr
          180          185          190
Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn
          195          200          205
Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser
210          215          220
Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His
225          230          235          240
Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr
          245          250          255
Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys
          260          265          270
Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys
          275          280          285
Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn
290          295          300
Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu
305          310          315          320
Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln
          325          330          335
Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser
          340          345          350

```

Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg
 355 360 365
 Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly
 370 375 380
 Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
 385 390 395

(2) INFORMATION FOR SEQ ID NO:507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507

Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser
 1 5 10 15
 Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg
 20 25 30
 Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro
 35 40 45
 Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met
 50 55 60
 Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser
 65 70 75 80
 Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg
 85 90 95
 Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Gly
 100 105 110
 Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu
 115 120 125
 Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe
 130 135 140
 Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly
 145 150 155 160
 Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile
 165 170 175
 Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn
 180 185 190
 Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu
 195 200 205
 Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly
 210 215 220
 Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly
 225 230 235 240
 Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile
 245 250 255
 Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala
 260 265 270
 Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile
 275 280 285
 Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys
 290 295 300
 Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe
 305 310 315 320
 Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met
 325 330 335
 Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro
 340 345 350
 Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg
 355 360 365
 Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly
 370 375 380
 Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu
 385 390 395 400

Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser
 405 410 415
 Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile
 420 425 430
 Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn
 435 440 445
 Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro
 450 455 460
 Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu
 465 470 475 480
 Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys
 485 490 495
 Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu
 500 505 510
 Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr
 515 520 525
 Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His
 530 535 540
 Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser
 545 550 555 560
 Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser
 565 570 575
 Tyr Ser Thr Asn Leu
 580

(2) INFORMATION FOR SEQ ID NO:508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508

Met Arg Ser Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly
 1 5 10 15
 Ser Glu Arg Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg
 20 25 30
 Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp
 35 40 45
 His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp
 50 55 60
 Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr
 65 70 75 80
 His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg
 85 90 95
 Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser
 100 105 110
 Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala
 115 120 125
 Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val
 130 135 140
 Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys
 145 150 155 160
 Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val
 165 170 175
 Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr
 180 185 190
 His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg
 195 200 205
 Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe
 210 215 220
 Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
 225 230 235

(2) INFORMATION FOR SEQ ID NO:509

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509

```

Met Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
1      5      10      15
Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe
      20      25      30
Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr
      35      40      45
Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg
      50      55      60
Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu
      65      70      75      80
His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro
      85      90      95
Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile
      100     105     110
Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His
      115     120     125
Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp
      130     135     140
Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln
      145     150     155     160
Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu
      165     170     175
Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile
      180     185     190
Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly
      195     200     205
Leu Asn His
      210

```

(2) INFORMATION FOR SEQ ID NO:510

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 781 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510

```

Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu
1      5      10      15
Cys Leu Phe Val Gly Arg Pro Leu Phe Ala Gln Ser Tyr Val Asp Tyr
      20      25      30
Val Asp Pro Leu Ile Gly Thr Leu Ser Ser Phe Glu Leu Ser Ala Gly
      35      40      45
Asn Thr Tyr Pro Val Ile Gly Leu Pro Trp Gly Met Asn Ser Trp Thr
      50      55      60
Pro Met Thr Gly Val Pro Gly Asp Gly Trp Gln Tyr Thr Tyr Ser Ala

```

65	70	75	80
His Lys Ile Arg Gly Phe Lys Gln Thr His Gln Pro Ser Pro Trp Ile			
	85	90	95
Asn Asp Tyr Gly Gln Phe Ser Leu Leu Pro Leu Thr Ala Pro Gln Lys			
	100	105	110
Pro Ser Ser Asn Asp Ser Ile Ala Leu Thr Lys Trp Cys Lys Gln Leu			
	115	120	125
Phe Ser Asp Glu Gln Thr Ser Trp Phe Ser His Lys Ala Glu Thr Ala			
	130	135	140
Thr Pro Tyr Tyr Tyr Ser Val Tyr Leu Ala Asp Tyr Asp Thr Arg Val			
	145	150	155
Glu Met Ala Pro Thr Glu Arg Ala Ala Ile Phe Arg Ile Arg Tyr Ser			
	165	170	175
Gly Asn Thr Glu Ser Gly Ser Gly Arg Trp Leu Arg Leu Asp Ala Phe			
	180	185	190
Thr Gly Gly Ser Glu Ile Ser Ile Val Asp Pro His Thr Val Val Gly			
	195	200	205
Ile Ser Arg Lys Asn Ser Gly Gly Val Pro Ala Asn Phe Ala Cys Tyr			
	210	215	220
Phe Ile Leu Gln Ser Asp Thr Pro Met Ala Asp Val Leu Leu Glu Thr			
	225	230	235
Asp Thr Gly Lys Ser Asp Glu Gly Thr Arg Ala Trp Ala Ala Cys Arg			
	245	250	255
Phe Asp Ser Gln Glu Val Thr Val Arg Val Ala Ser Ser Phe Ile Ser			
	260	265	270
Val Glu Gln Ala Glu Arg Asn Leu Ala Glu Val Lys Gly Gln Ser Phe			
	275	280	285
Asp Arg Ile Arg Leu Ala Gly Arg Glu Ala Trp Asn Lys Val Leu Gly			
	290	295	300
Arg Ile His Val Glu Gly Thr Lys Asp Glu Arg Thr Thr Phe Tyr			
	305	310	315
Ser Ala Leu Tyr Arg Cys Leu Leu Phe Pro Arg Arg Phe Tyr Glu Glu			
	325	330	335
Asp Ala Ser Gly Asn Phe Val His Tyr Ser Pro Tyr Asn Gly Glu Val			
	340	345	350
Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg			
	355	360	365
Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys			
	370	375	380
Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro			
	385	390	395
Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser			
	405	410	415
Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp			
	420	425	430
Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His			
	435	440	445
Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser			
	450	455	460
Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg			
	465	470	475
Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg			
	485	490	495
Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser			
	500	505	510
Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly			
	515	520	525
Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp			
	530	535	540
Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val			
	545	550	555
Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro			
	565	570	575
Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp			
	580	585	590
Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile			
	595	600	605
Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met			
	610	615	620
Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg			
	625	630	635
Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr			
	645	650	655
Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser			
	660	665	670
Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu			
	675	680	685

Gly	Ser	Pro	Ile	Phe	Ser	Lys	Val	Ile	Leu	Ser	Phe	Pro	Asp	Gly	His
690						695					700				
Lys	Thr	Val	Leu	His	Ala	Pro	Ala	Asn	Ser	Ala	Asp	Thr	Pro	Tyr	Ile
705					710					715					720
Arg	Ser	Ile	Ser	Val	Glu	Gly	Lys	Glu	Trp	Ser	Cys	Asn	Tyr	Leu	Thr
				725					730						735
His	Glu	Gln	Leu	Arg	Ser	Ser	Ala	Ser	Ile	Gln	Trp	Met	Met	Asp	Thr
			740						745					750	
Lys	Pro	Asn	Tyr	Asn	Arg	Gly	Met	Lys	Glu	Ser	Asp	Arg	Pro	Tyr	Ser
		755					760					765			
Phe	Ser	Thr	Glu	Gln	Gln	Arg	Arg	Ala	Asn	His	Ser	Asn			
770						775						780			

(2) INFORMATION FOR SEQ ID NO:511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511

Met	Met	Lys	Ser	Met	Arg	Ser	Val	Leu	Leu	Leu	Leu	Phe	Pro	Leu	Ser
1				5					10					15	
Leu	Ile	Thr	Ala	Leu	Gly	Cys	Ser	Asn	Asn	Lys	Ala	Ala	Glu	Ser	Lys
			20					25					30		
Ser	Val	Ser	Phe	Asp	Ser	Ala	Tyr	Leu	Glu	Arg	Tyr	Ile	Pro	Leu	Arg
		35				40					45				
Ala	Asp	Ile	Asp	Thr	Pro	Ser	Leu	His	Val	Met	Ile	Ser	Tyr	Val	Tyr
	50					55				60					
Pro	Ser	Gly	Asp	Asp	Met	Leu	Thr	Glu	Ile	Phe	Asn	Gly	Leu	Leu	Phe
65					70					75				80	
Gly	Asp	Ser	Leu	Met	Asp	Ser	Ser	Ser	Pro	Glu	Asn	Ala	Met	Glu	Gly
			85					90						95	
Tyr	Ala	Gln	Met	Leu	Gly	Glu	Asp	Tyr	Arg	Ser	Asn	Asn	Ala	Glu	Ala
		100					105						110		
Asn	Leu	Gln	Gly	Leu	Pro	Ser	Asp	Leu	Leu	Asp	Tyr	Ile	Tyr	Lys	Gln
		115					120					125			
Glu	Asn	Thr	Ile	Ala	Tyr	Cys	Asp	Thr	Gly	Leu	Ile	Ser	Thr	Arg	Ile
	130					135				140					
Asn	Thr	Tyr	Thr	Tyr	Glu	Gly	Gly	Ala	His	Thr	Glu	Asn	Thr	Val	Arg
145				150						155				160	
Phe	Ala	Asn	Ile	Leu	Arg	Thr	Thr	Gly	Lys	Val	Leu	Glu	Glu	Arg	Asp
			165					170						175	
Ile	Phe	Lys	Ile	Asp	Tyr	Ala	Glu	Arg	Leu	Ser	Ala	Leu	Ile	Ile	Gly
		180						185					190		
Gln	Leu	Val	His	Asp	Phe	Gly	Lys	Thr	Thr	Pro	Ala	Glu	Leu	Asp	Ala
	195						200					205			
Ile	Gly	Phe	Phe	Asn	Ala	Glu	Glu	Ile	Gln	Pro	Asn	Gly	Asn	Phe	Met
	210					215					220				
Ile	Asp	Asp	Lys	Gly	Leu	Thr	Tyr	Cys	Phe	Asn	Glu	Tyr	Gln	Ile	Ala
225				230						235				240	
Ala	Tyr	Ala	Arg	Gly	Ala	Val	Tyr	Val	Arg	Leu	Gly	Tyr	Asp	Val	Leu
			245					250						255	
Ala	Pro	Leu	Leu	Arg	Asp	Asp	Ser	Pro	Leu	Lys	Arg	Tyr	Leu	Pro	
		260					265						270		

(2) INFORMATION FOR SEQ ID NO:512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512

```
Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
1      5      10      15
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
      20      25      30
Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
      35      40      45
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
      50      55      60
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
      65      70      75      80
Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
      85      90      95
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
      100      105      110
Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
      115      120      125
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
      130      135      140
Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
      145      150      155      160
Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
      165      170      175
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
      180      185      190
Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
      195      200      205
Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
      210      215      220
Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
      225      230      235      240
Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
      245      250      255
Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
      260      265      270
```

(2) INFORMATION FOR SEQ ID NO:513

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513

```
Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu Ile Thr Ala
1      5      10      15
Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser Val Ser Phe
      20      25      30
Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala Asp Ile Asp
      35      40      45
Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro Ser Gly Asp
      50      55      60
Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly Asp Ser Leu
      65      70      75      80
Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr Ala Gln Met
```


	85		90		95
Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn Leu Gln Gly	100		105		110
Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu Asn Thr Ile	115		120		125
Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn Thr Tyr Thr	130		135		140
Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe Ala Asn Ile	145		150		155
Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile Phe Lys Ile	165		170		175
Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln Leu Val His	180		185		190
Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile Gly Phe Phe	195		200		205
Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile Asp Asp Lys	210		215		220
Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala Tyr Ala Arg	225		230		235
Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala Pro Leu Leu	245		250		255
Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro	260		265		

(2) INFORMATION FOR SEQ ID NO:514

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514

Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe	1	5	10	15
Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile	20	25	30	
Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly	35	40	45	
Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His	50	55	60	
Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg	65	70	75	80
Arg Ala His Trp Glu Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn	85	90	95	
Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp	100	105	110	
Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser	115	120	125	
Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr	130	135	140	
Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His	145	150	155	160
Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu	165	170	175	
Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys	180	185	190	
Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg	195	200	205	
Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr	210	215	220	
Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro	225	230	235	240
Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu	245	250	255	
Trp Thr Asn				

(2) INFORMATION FOR SEQ ID NO:515

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515

```
Met Gly Lys Tyr Lys Arg Ala Lys Tyr Arg Tyr Trp Leu Phe Pro Phe
1      5      10      15
Cys Ser Asp Tyr Tyr Thr Phe Glu Gly Val Thr Phe Leu Cys Ala Ser
      20      25      30
Asp Asp Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys
      35      40      45
Ala Tyr Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser
      50      55      60
Trp Ser Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val
      65      70      75      80
Glu Leu Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile
      85      90      95
Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser
      100     105     110
Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu
      115     120     125
Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser
      130     135     140
Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
      145     150     155     160
Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
      165     170     175
Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu
      180     185     190
Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu
      195     200     205
Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu
      210     215     220
Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser
      225     230     235     240
Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala
      245     250     255
Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu
      260     265     270
Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser
      275     280     285
Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu
      290     295     300
Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser
      305     310     315     320
Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
      325     330     335
Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
      340     345     350
Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu
      355     360     365
Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu
      370     375     380
Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu
      385     390     395     400
Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp
      405     410     415
Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr
      420     425     430
Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp
```

435	440	445
Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn Asp Ile Gln		
450	455	460
Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu Gln Thr Leu		
465	470	475
Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser Ser Gly Leu		480
	485	490
Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys Ala Leu Leu		495
	500	505
Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu Tyr His Pro		510
	515	520
Phe Cys Lys Val Met Leu Leu Gly Asn His Ser Ser Gly Lys Thr Thr		525
	530	535
Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys Asn Thr His		540
545	550	555
Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile Phe Tyr Asp		560
	565	570
Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala Phe Phe Thr		575
	580	585
Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys Asp Arg Asn		590
	595	600
Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn Phe Asn Arg		605
610	615	620
Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg Cys Met Ser		625
625	630	635
Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr Thr Asp Asp		640
	645	650
Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala Lys Gln Gln		655
	660	665
Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu Ile Tyr Val		670
675	680	685
Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu Asn Tyr Leu		690
	695	700
Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys Ser Ile Gln		705
	710	715
Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro Thr Ile Ala		720
	725	730
Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu Ala Ala Gln		735
	740	745
Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile Glu Tyr Leu		750
	755	760
Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val Leu Tyr Tyr		765
770	775	780
Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp Pro Ala Ala		785
	790	795
Phe Val Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp Asn Ile Asn		800
	805	810
Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu His Asn Leu		815
	820	825
Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly Asn Met Ile		830
	835	840
Leu Gln Leu Leu Leu Glu Glu Ile Val Tyr Glu Asp Lys Asp Cys		845
850	855	860
Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp Glu Ala Tyr		865
865	870	875
Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val Leu Lys Phe		880
	885	890
Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile Ala Tyr Tyr		895
	900	905
Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp Gln Val Ile		910
	915	920
Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu Gln Glu Glu		925
930	935	940
Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr Gln Ile Trp		945
	950	955
Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe Ile Lys Glu		960
	965	970
Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu Ala Thr Ile		975
	980	985
Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro Pro Arg Glu		990
	995	1000
Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr Ile Arg Glu		1005
	1010	1015
Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala		1020
1025	1030	1035
Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr		1040
	1045	1050
		1055

Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu
 1060 1065 1070
 Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg
 1075 1080 1085
 Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln
 1090 1095 1100
 Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys
 1105 1110 1115 1120
 Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr
 1125 1130 1135
 Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg
 1140 1145 1150
 Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg
 1155 1160 1165
 Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg
 1170 1175 1180
 Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe
 1185 1190 1195 1200
 Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln
 1205 1210 1215
 Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser
 1220 1225 1230
 Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg
 1235 1240 1245
 Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr
 1250 1255 1260
 Asp Glu
 1265

(2) INFORMATION FOR SEQ ID NO:516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516

Met Thr Thr Lys Lys Pro Gln Ala Ile Leu Asp Leu Glu Lys Ala Tyr
 1 5 10 15
 Asn Ile Glu Ile Pro Asp Leu Ser Ser Gln Glu Gly Ile Ser Trp Ser
 20 25 30
 Val Asn Arg Tyr Phe Lys Gln Asp Ser Ser Gly Ala Val Val Glu Leu
 35 40 45
 Cys Leu Arg Glu Cys Gln Ile Glu Ser Met Thr Trp Leu Ile Asp Phe
 50 55 60
 Pro Ala Leu Lys Lys Leu Asp Leu Ser Tyr Asn Gln Ile Ser Lys Leu
 65 70 75 80
 Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser
 85 90 95
 Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser Leu Thr
 100 105 110
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu
 115 120 125
 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Ser
 130 135 140
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu
 145 150 155 160
 Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser
 165 170 175
 Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly
 180 185 190
 Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln
 195 200 205
 Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu
 210 215 220

Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu
 225 230 235 240
 Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Ser Lys Leu
 245 250 255
 Glu Gly Leu Glu Arg Leu Ser Ser Leu Thr Lys Leu Arg Leu Arg Ser
 260 265 270
 Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr
 275 280 285
 Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu
 290 295 300
 Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln Ile Arg
 305 310 315 320
 Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys Leu Arg Leu
 325 330 335
 Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Ser Leu Thr Ser
 340 345 350
 Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile Ser Lys Leu Glu Gly
 355 360 365
 Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr Leu Leu Asp Asn Gln
 370 375 380
 Ile Arg Lys Leu Glu Gly Leu Asp Gly Leu Ala Ser Leu Thr Arg Leu
 385 390 395 400
 Ser Leu Arg Arg Asn Gln Ile Ser Lys Leu Glu Gly Leu Asp Arg Leu
 405 410 415
 Lys Val Leu Arg Lys Leu Asp Val Ser Gly Asn Asp Ile Gln Ser Ile
 420 425 430
 Asp Asp Ile Lys Leu Leu Ala Pro Ile Leu Glu Gln Thr Leu Glu Lys
 435 440 445
 Leu Arg Ile His Asp Asn Pro Phe Val Ala Ser Ser Gly Leu Ile Leu
 450 455 460
 Ser Pro Tyr Asp Asn His Leu Pro Glu Ile Lys Ala Leu Leu Glu Lys
 465 470 475 480
 Glu Lys Glu Lys Gln Lys Lys Thr Ser Val Glu Tyr His Pro Phe Cys
 485 490 495
 Lys Val Met Leu Leu Gly Asn His Ser Ser Gly Lys Thr Thr Phe Leu
 500 505 510
 Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr Gln Lys Asn Thr His Val Leu
 515 520 525
 Ser Ile His Arg Ser Asn Asn Pro Asn Ala Ile Phe Tyr Asp Phe Gly
 530 535 540
 Gly Gln Asp Tyr Tyr His Gly Ile Tyr Gln Ala Phe Phe Thr Thr Gln
 545 550 555 560
 Ser Leu Tyr Leu Leu Phe Trp Asp Ala Lys Lys Asp Arg Asn Phe Val
 565 570 575
 Ser Val Asp Asp Lys Glu Tyr Gln Thr Leu Asn Phe Asn Arg Pro Tyr
 580 585 590
 Trp Leu Gly Gln Ile Ala Tyr Ala Cys Asn Arg Cys Met Ser Val Gly
 595 600 605
 Gly Asn Pro Asp Gly Lys Asp Thr Pro Gln Thr Thr Asp Asp Thr Ile
 610 615 620
 Ile Ile Gln Thr His Ala Asp Glu Thr Gly Ala Lys Gln Gln Thr Leu
 625 630 635 640
 Gly Cys Ala Ala Glu Asn Gly Val Leu Glu Glu Ile Tyr Val Ser Leu
 645 650 655
 Glu Pro Lys Ala Asn Ser Ala Val His Ala Leu Asn Tyr Leu Asn Glu
 660 665 670
 Arg Val Arg Glu Val Val Ala Ser Arg Ser Lys Ser Ile Gln Ile Thr
 675 680 685
 Glu Lys Asp Lys Gly Leu Tyr Glu Ala Leu Pro Thr Thr Ile Ala Gly Asp
 690 695 700
 Asn Lys His Ile Pro Ile Ser Leu Glu Ala Leu Ala Ala Gln Leu Asn
 705 710 715 720
 Lys Gly Arg Ala Glu Asn Asp Leu Tyr Thr Ile Glu Tyr Leu Gln Thr
 725 730 735
 Glu Leu Asn Gln Leu Ser Leu Arg Gly Glu Val Leu Tyr Tyr Arg Glu
 740 745 750
 Asn Glu Lys Leu Asn Asn Tyr Val Trp Leu Asp Pro Ala Ala Phe Val
 755 760 765
 Gln Met Ile His Gly Glu Ile Leu Gln Lys Asp Asn Ile Asn Arg Gly
 770 775 780
 Thr Val Pro Lys Asp Ile Phe Glu Cys Lys Leu His Asn Leu Ser Ser
 785 790 795 800
 Gly Ser Ile Phe Glu Glu Asp Gly Gln Asn Gly Asn Met Ile Leu Gln
 805 810 815
 Leu Leu Leu Glu Glu Leu Ile Val Tyr Glu Asp Lys Asp Cys Tyr Val
 820 825 830
 Ile Pro Gly Tyr Leu Pro Leu His Ser Asp Asp Glu Ala Tyr Lys Trp

835	840	845
Leu Thr Leu Gly Phe Glu Arg Pro Asn Phe Val Leu Lys Phe Glu Arg		
850	855	860
Phe Ile Pro Phe Gly Leu Ile Asn Gln Ile Ile Ala Tyr Tyr Gly Arg		
865	870	875
Glu Glu Gly Ala Leu Lys Arg Tyr Trp Arg Asp Gln Val Ile Phe Thr		880
	885	890
Ala Gly Arg Glu Met Asp Arg Gln Thr Leu Glu Gln Glu Glu Lys		895
	900	905
Glu Gly Leu Pro Lys Thr Asn Ala Glu Asp Tyr Gln Ile Trp Ile Lys		910
	915	920
Leu Asp Phe Thr Asp Leu Ala Ile Ser Val Phe Ile Lys Glu Gln Arg		925
	930	935
Lys Thr Ser Ala Lys Asp Met Gln Arg Lys Glu Ala Thr Ile Leu Ser		940
945	950	955
Asp Met Leu Asp Met Tyr Trp Asn Asn Ile Pro Pro Arg Glu Gln Ile		960
	965	970
Gly Asp Lys Asp Thr Glu Gln Thr Arg Ser Thr Ile Arg Glu Thr Asn		975
	980	985
Arg Lys Lys Arg Pro Ile Gln Asp Leu Tyr Leu Ser Cys Ala Gln Ala		990
	995	1000
Asp Lys Asp Leu Thr Glu Ser His Tyr Ile His Leu Gly Thr Leu Asp		1005
	1010	1015
Asp Glu Ser Lys Thr Thr Ala Arg Ile Ala Ala Tyr Pro Leu Lys Asn		1020
1025	1030	1035
Gly Val Ile Asp Lys Glu Arg Val Arg Glu Val Ser Thr Arg Pro Tyr		1040
	1045	1050
Lys His Leu Ser Val Asn Lys Asn Leu Ala Thr Ala Lys Gln Ile Phe		1055
	1060	1065
Ile Ser Tyr Ser Lys Glu Asp Gln Thr Glu Leu Glu Thr Cys Leu Gln		1070
	1075	1080
Phe Phe Lys Pro Leu Glu Lys Asn Gly Gln Ile Glu Ile Tyr Tyr Asp		1085
	1090	1095
Lys Leu Thr Lys Phe Glu Thr Pro Ile His Pro Glu Ile Arg Lys Arg		1100
1105	1110	1115
Ile Val Glu Ala Asp Cys Ile Ile Ala Leu Ile Ser Gln Arg Tyr Leu		1120
	1125	1130
Ala Thr Asp Tyr Ile Leu Asp His Glu Leu Pro Val Phe Arg Glu Tyr		1135
	1140	1145
Asn Lys Thr Ile Val Pro Ile Leu Ile Lys Pro Cys Thr Phe Glu Asp		1150
	1155	1160
Asp Glu Phe Leu Arg Glu Lys Tyr Phe Ala Gln Lys Ala Gln Ile Ile		1165
	1170	1175
Asn Leu Gly Lys Glu Gly Lys Thr Ile Lys Ala Tyr Asp Ser Ile Thr		1180
1185	1190	1195
Ala Ser Ala His Arg Asp Glu Asn Trp Val Ala Val Val Arg Glu Phe		1200
	1205	1210
Lys Glu Lys Ile Leu Arg Ile Thr Lys Gln Glu Val Asn Thr Asp Glu		1215
	1220	1225
		1230

(2) INFORMATION FOR SEQ ID NO:517

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517

Met Thr Trp Leu Ile Asp Phe Pro Ala Leu Lys Lys Leu Asp Leu Ser		
1	5	10
Tyr Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu		15
	20	25
Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Arg Lys Leu Glu Gly Leu		30
	35	40
Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile		45

50	55	60
Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr		
65	70	75
Leu Leu Asp Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr		80
	85	90
Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys Leu Glu		95
	100	105
Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn		110
	115	120
Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Thr Lys		125
	130	135
Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg		140
145	150	155
Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser Gly Asn Gln Ile Arg Lys		160
	165	170
Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Thr Leu Glu Leu Ser		175
	180	185
Gly Asn Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Ser Ser Leu		190
	195	200
Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu Gly Leu		205
	210	215
Glu Arg Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn Gln Ile		220
225	230	235
Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu Leu Tyr		240
	245	250
Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Glu Arg Leu Thr		255
	260	265
Ser Leu Thr Lys Leu Arg Leu Arg Ser Asn Gln Ile Ser Lys Leu Glu		270
	275	280
Gly Leu Asp Ser Leu Thr Ser Leu Thr Lys Leu Ser Leu Ser Asp Asn		285
	290	295
Gln Ile Ser Lys Leu Glu Gly Leu Glu Arg Leu Thr Ser Leu Ala Glu		300
305	310	315
Leu Tyr Leu Leu Asp Asn Gln Ile Arg Lys Leu Glu Gly Leu Asp Gly		320
	325	330
Leu Ala Ser Leu Thr Arg Leu Ser Leu Arg Arg Asn Gln Ile Ser Lys		335
	340	345
Leu Glu Gly Leu Asp Arg Leu Lys Val Leu Arg Lys Leu Asp Val Ser		350
	355	360
Gly Asn Asp Ile Gln Ser Ile Asp Asp Ile Lys Leu Leu Ala Pro Ile		365
	370	375
Leu Glu Gln Thr Leu Glu Lys Leu Arg Ile His Asp Asn Pro Phe Val		380
385	390	395
Ala Ser Ser Gly Leu Ile Leu Ser Pro Tyr Asp Asn His Leu Pro Glu		400
	405	410
Ile Lys Ala Leu Leu Glu Lys Glu Lys Glu Lys Gln Lys Lys Thr Ser		415
	420	425
Val Glu Tyr His Pro Phe Cys Lys Val Met Leu Leu Gly Asn His Ser		430
	435	440
Ser Gly Lys Thr Thr Phe Leu Ser Gln Tyr Asp Thr Asn Tyr Thr Tyr		445
	450	455
Gln Lys Asn Thr His Val Leu Ser Ile His Arg Ser Asn Asn Pro Asn		460
465	470	475
Ala Ile Phe Tyr Asp Phe Gly Gly Gln Asp Tyr Tyr His Gly Ile Tyr		480
	485	490
Gln Ala Phe Phe Thr Thr Gln Ser Leu Tyr Leu Leu Phe Trp Asp Ala		495
	500	505
Lys Lys Asp Arg Asn Phe Val Ser Val Asp Asp Lys Glu Tyr Gln Thr		510
	515	520
Leu Asn Phe Asn Arg Pro Tyr Trp Leu Gly Gln Ile Ala Tyr Ala Cys		525
	530	535
Asn Arg Cys Met Ser Val Gly Gly Asn Pro Asp Gly Lys Asp Thr Pro		540
545	550	555
Gln Thr Thr Asp Asp Thr Ile Ile Ile Gln Thr His Ala Asp Glu Thr		560
	565	570
Gly Ala Lys Gln Gln Thr Leu Gly Cys Ala Ala Glu Asn Gly Val Leu		575
	580	585
Glu Glu Ile Tyr Val Ser Leu Glu Pro Lys Ala Asn Ser Ala Val His		590
	595	600
Ala Leu Asn Tyr Leu Asn Glu Arg Val Arg Glu Val Val Ala Ser Arg		605
	610	615
Ser Lys Ser Ile Gln Ile Thr Glu Lys Asp Lys Gly Leu Tyr Glu Ala		620
625	630	635
Leu Pro Thr Ile Ala Gly Asp Asn Lys His Ile Pro Ile Ser Leu Glu		640
	645	650
Ala Leu Ala Ala Gln Leu Asn Lys Gly Arg Ala Glu Asn Asp Leu Tyr		655
	660	665
		670

Thr Ile Glu Tyr Leu Gln Thr Glu Leu Asn Gln Leu Ser Leu Arg Gly
 675 680 685
 Glu Val Leu Tyr Tyr Arg Glu Asn Glu Lys Leu Asn Asn Tyr Val Trp
 690 695 700
 Leu Asp Pro Ala Ala Phe Val Gln Met Ile His Gly Glu Ile Leu Gln
 705 710 715 720
 Lys Asp Asn Ile Asn Arg Gly Thr Val Pro Lys Asp Ile Phe Glu Cys
 725 730 735
 Lys Leu His Asn Leu Ser Ser Gly Ser Ile Phe Glu Glu Asp Gly Gln
 740 745 750
 Asn Gly Asn Met Ile Leu Gln Leu Leu Glu Glu Leu Ile Val Tyr
 755 760 765
 Glu Asp Lys Asp Cys Tyr Val Ile Pro Gly Tyr Leu Pro Leu His Ser
 770 775 780
 Asp Asp Glu Ala Tyr Lys Trp Leu Thr Leu Gly Phe Glu Arg Pro Asn
 785 790 795 800
 Phe Val Leu Lys Phe Glu Arg Phe Ile Pro Phe Gly Leu Ile Asn Gln
 805 810 815
 Ile Ile Ala Tyr Tyr Gly Arg Glu Glu Gly Ala Leu Lys Arg Tyr Trp
 820 825 830
 Arg Asp Gln Val Ile Phe Thr Ala Gly Arg Glu Met Asp Arg Gln Thr
 835 840 845
 Leu Glu Gln Glu Glu Glu Lys Glu Gly Leu Pro Lys Thr Asn Ala Glu
 850 855 860
 Asp Tyr Gln Ile Trp Ile Lys Leu Asp Phe Thr Asp Leu Ala Ile Ser
 865 870 875 880
 Val Phe Ile Lys Glu Gln Arg Lys Thr Ser Ala Lys Asp Met Gln Arg
 885 890 895
 Lys Glu Ala Thr Ile Leu Ser Asp Met Leu Asp Met Tyr Trp Asn Asn
 900 905 910
 Ile Pro Pro Arg Glu Gln Ile Gly Asp Lys Asp Thr Glu Gln Thr Arg
 915 920 925
 Ser Thr Ile Arg Glu Thr Asn Arg Lys Lys Arg Pro Ile Gln Asp Leu
 930 935 940
 Tyr Leu Ser Cys Ala Gln Ala Asp Lys Asp Leu Thr Glu Ser His Tyr
 945 950 955 960
 Ile His Leu Gly Thr Leu Asp Asp Glu Ser Lys Thr Thr Ala Arg Ile
 965 970 975
 Ala Ala Tyr Pro Leu Lys Asn Gly Val Ile Asp Lys Glu Arg Val Arg
 980 985 990
 Glu Val Ser Thr Arg Pro Tyr Lys His Leu Ser Val Asn Lys Asn Leu
 995 1000 1005
 Ala Thr Ala Lys Gln Ile Phe Ile Ser Tyr Ser Lys Glu Asp Gln Thr
 1010 1015 1020
 Glu Leu Glu Thr Cys Leu Gln Phe Phe Lys Pro Leu Glu Lys Asn Gly
 1025 1030 1035 1040
 Gln Ile Glu Ile Tyr Tyr Asp Lys Leu Thr Lys Phe Glu Thr Pro Ile
 1045 1050 1055
 His Pro Glu Ile Arg Lys Arg Ile Val Glu Ala Asp Cys Ile Ile Ala
 1060 1065 1070
 Leu Ile Ser Gln Arg Tyr Leu Ala Thr Asp Tyr Ile Leu Asp His Glu
 1075 1080 1085
 Leu Pro Val Phe Arg Glu Tyr Asn Lys Thr Ile Val Pro Ile Leu Ile
 1090 1095 1100
 Lys Pro Cys Thr Phe Glu Asp Asp Glu Phe Leu Arg Glu Lys Tyr Phe
 1105 1110 1115 1120
 Ala Gln Lys Ala Gln Ile Ile Asn Leu Gly Lys Glu Gly Lys Thr Ile
 1125 1130 1135
 Lys Ala Tyr Asp Ser Ile Thr Ala Ser Ala His Arg Asp Glu Asn Trp
 1140 1145 1150
 Val Ala Val Val Arg Glu Phe Lys Glu Lys Ile Leu Arg Ile Thr Lys
 1155 1160 1165
 Gln Glu Val Asn Thr Asp Glu
 1170 1175

(2) INFORMATION FOR SEQ ID NO:518

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518

```
Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser
1      5      10      15
Ser Phe Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr
      20      25      30
Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro
      35      40      45
Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro
      50      55      60
Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile
65      70      75      80
Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp
      85      90      95
Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe
      100     105     110
Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg
      115     120     125
Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro
      130     135     140
Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile
      145     150     155     160
Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr
      165     170     175
Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe
      180     185     190
Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr
      195     200     205
Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr
      210     215     220
Val Ser Gln Gln Lys
225
```

(2) INFORMATION FOR SEQ ID NO:519

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519

```
Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser
1      5      10      15
Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe
      20      25      30
Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val
      35      40      45
Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe
      50      55      60
Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala
65      70      75      80
Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys
      85      90      95
Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp
      100     105     110
Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile
      115     120     125
Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys
      130     135     140
```

```

Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg
145          150          155          160
Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe
          165          170          175
Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu
          180          185          190
Leu Asn Thr Asn Val Lys Ile Val Val Gly Asp Val Ser Gln Lys Tyr Ala
          195          200          205
Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val
          210          215          220
Ser Gln Gln Lys
225

```

(2) INFORMATION FOR SEQ ID NO:520

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520

```

Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
1          5          10          15
Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
          20          25          30
Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
          35          40          45
Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
          50          55          60
Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
          65          70          75          80
Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
          85          90          95
Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
          100          105          110
Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser
          115          120          125
Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu
          130          135          140
Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile
          145          150          155          160
Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro
          165          170          175
Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile
          180          185          190
Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn
          195          200          205
Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val
          210          215          220
Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp
          225          230          235          240
Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser
          245          250          255
Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln
          260          265          270
Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro
          275          280          285
Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu
          290          295          300
Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr
          305          310          315          320
Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr
          325          330          335
Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu
          340          345          350

```

```

Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys
355 360 365
Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly
370 375 380
Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn
385 390 395 400
Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala
405 410 415
Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys
420 425 430
Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp
435 440 445
Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu
450 455 460
Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile
465 470 475 480
Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln
485 490 495
Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu
500 505 510
Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser
515 520 525
Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu
530 535 540

```

(2) INFORMATION FOR SEQ ID NO:521

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521

```

Met Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile
1 5 10 15
Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu
20 25 30
Thr Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr
35 40 45
Asn Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe
50 55 60
Asn Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp
65 70 75 80
Trp Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser
85 90 95
His Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu
100 105 110
Leu Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly
115 120 125
Ser Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val
130 135 140
Leu Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr
145 150 155 160
Ala Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu
165 170 175
Asn Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe
180 185 190
Leu Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys
195 200 205
Tyr Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser
210 215 220
Arg Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr
225 230 235 240
Val Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp
245 250 255

```

Gly Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser
 260 265 270
 Phe Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser
 275 280 285
 Phe Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu
 290 295 300
 Glu Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala
 305 310 315 320
 Ile Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val
 325 330 335
 Glu Val Glu Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala
 340 345 350
 Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly
 355 360 365
 Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp
 370 375 380
 Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro
 385 390 395 400
 Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr
 405 410 415
 Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu
 420 425 430
 Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val
 435 440 445
 Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr
 450 455 460
 Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His
 465 470 475 480
 Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro
 485 490 495
 Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr
 500 505 510
 Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys
 515 520 525
 Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr
 530 535 540
 Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser
 545 550 555 560
 Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn
 565 570 575
 Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro
 580 585 590
 His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe
 595 600 605
 Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
 610 615 620
 Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
 625 630 635 640
 Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
 645 650 655
 Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
 660 665 670
 Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
 675 680 685
 Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
 690 695 700
 Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
 705 710 715 720
 Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
 725 730 735
 Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
 740 745 750
 His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
 755 760 765
 Arg Pro Arg
 770

(2) INFORMATION FOR SEQ ID NO:522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522

```
Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu
1      5      10      15
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn
20     25     30
Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys
35     40     45
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu
50     55     60
Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp
65     70     75     80
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val
85     90     95
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg
100    105    110
Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys
115    120    125
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly
130    135    140
Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala
145    150    155    160
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn
165    170    175
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu
180    185    190
Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn
195    200    205
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile
210    215    220
Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser
225    230    235    240
Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr
245    250    255
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe
260    265    270
Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe Pro Ile Ala Asp Val Leu
275    280    285
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly
290    295    300
Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala Glu Gly Ser Thr Ala Glu
305    310    315    320
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu
325    330    335
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly
340    345    350
Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn
355    360    365
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly
370    375    380
Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp
385    390    395    400
Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe
405    410    415
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile
420    425    430
Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp
435    440    445
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile
450    455    460
Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro
465    470    475    480
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn
485    490    495
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg
500    505    510
Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser
515    520    525
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala
```

530	535	540
Ala Ile Gly His Lys Thr	Ile Tyr Ala Met	Ala Val Asp His Asn Gly
545	550	555
Ser Val Trp Met Gly Ser	Asp Ile Gly Ile	Phe Gly Val Tyr Asn Ala
565	570	575
Ala Gly Val Leu Ser Ser	Thr Ser Thr Pro	Ile Ala Val Arg Pro Val
580	585	590
Gly Gly Glu Glu Pro Asn	Leu Tyr Tyr Val	Leu Asp Lys Val Thr Val
595	600	605
Thr Asp Ile Val Val Asp	Lys Leu Asn His Lys	Trp Val Ala Thr Gln
610	615	620
Gly Thr Gly Leu Tyr Leu	Leu Ser Glu Asp	Cys Ser Lys Ile Leu Ala
625	630	635
Gln Phe Thr Val Glu Asn	Ser Pro Leu Leu	Ser Asn Asn Ile Leu Ser
645	650	655
Leu Ala Leu Asn Asp Asp	Asn Gly Leu Leu	Tyr Ile Gly Thr Ala Asp
660	665	670
Gly Leu Met Thr Phe Gln	Thr Gly Thr Gly	Ser Gly Ser Ala Ser Glu
675	680	685
Leu Asp Gly Val Tyr Val	Tyr Pro Asn Pro	Leu Arg Pro Glu Tyr Pro
690	695	700
Asp Gly Val Thr Ile Ala	Gly Leu Gln Ala	Gly Cys Ser Val Lys Ile
705	710	715
Thr Asp Thr Thr Gly Arg	Leu Leu Tyr Gln	Thr Glu Ser Val Thr Thr
725	730	735
Glu Val Lys Trp Asn Ala	Arg Gly Ala Asp	Gly Asn Arg Val Ala Ser
740	745	750
Gly Val Tyr Ala Val Ala	Val Tyr Asp Pro	Val Ser Lys Lys Ser Lys
755	760	765
Leu Ile Arg Phe Ala Val	Ile Arg	
770	775	

(2) INFORMATION FOR SEQ ID NO:523

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523

Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala	1	5	10	15
Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp	20	25	30	
Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala	35	40	45	
Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe	50	55	60	
Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu	65	70	75	80
Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro	85	90	95	
Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val	100	105	110	
Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn	115	120	125	
Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala	130	135	140	
Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala	145	150	155	160
Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr	165	170	175	
Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala	180	185	190	
Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser				

195					200					205					
Ser	Gly	Glu	Leu	Gly	Thr	Val	Phe	Ser	Tyr	Ile	Ala	Lys	Ala	Arg	Ser
210						215					220				
Ala	Gly	Gly	Gly	Arg	Glu	Met	Ser	Leu	Ser	Ala	Asn	Gly	Ile	Leu	Ile
225					230					235					240
Phe	Ser	Asp	Pro	Phe	Ser	Met	Thr	Ser	Asn	Glu	Val	Ser	Asn	Ser	Tyr
				245					250					255	
Leu	Ala	Gly	Lys	Lys	Arg	Arg	Leu	Tyr	His	Ser	Thr	Pro	Met	Asn	Ser
			260					265					270		
Leu	Val	Asn	Glu	Leu	Arg	Leu	Asp	Ala	Asn	Tyr	Ser	Met	Thr	Gly	Asp
		275					280					285			
Ala	Val	Asn	Leu	Asp	Phe	Ile	Glu	Val	Ala	Thr	Gln	Asn	Asp	Leu	Arg
290						295					300				
Tyr	Asp	Gly	Ala	Pro	Met	His	Ile	Arg	Arg	Phe	Ser	Asn	Leu	Pro	Val
305					310					315					320
Leu	Gly	Gly	Glu	Ser	Cys	Arg	Phe	Val	Ile	Ser	Glu	Val	Pro	Glu	Ser
				325					330					335	
Leu	Val	Val	Leu	Gln	Ala	Asn	Ser	Ser	Leu	Thr	Ala	Ser	Leu	Val	Pro
			340					345					350		
Val	Lys	Thr	Val	Gly	Asp	Lys	Thr	Ile	Glu	Phe	Val	Ala	Pro	Pro	Lys
			355				360					365			
Gly	Gln	Asp	Arg	Arg	Thr	Ile	Asn	Thr	Phe	Tyr	Ala	Val	Asp	Leu	Ser
370						375					380				
Gln	Ala	Ser	Ala	Pro	Glu	Ile	Leu	Gly	Ala	Val	Pro	Asn	Gln	Asn	Leu
385					390					395					400
His	Gly	Glu	Glu	Ile	Pro	Asp	Leu	Ile	Ile	Val	Ser	Thr	Gln	Ala	Leu
				405					410					415	
Leu	Leu	Glu	Ala	Asp	Arg	Leu	Ala	Thr	Tyr	Arg	Arg	Glu	Lys	Asn	Gly
			420					425					430		
Leu	Lys	Val	Leu	Val	Val	Leu	Gln	Glu	Gln	Val	Phe	Asn	Glu	Phe	Ser
		435					440					445			
Gly	Gly	Thr	Pro	Asp	Ala	Thr	Ala	Tyr	Arg	Leu	Phe	Ala	Lys	Met	Phe
450						455					460				
Tyr	Asp	Arg	Trp	Lys	Ala	Asn	Ala	Pro	Val	Gly	Glu	Thr	Phe	Pro	Met
465					470					475				480	
Gln	Met	Leu	Leu	Phe	Gly	Asp	Gly	Ala	His	Asp	Asn	Arg	Lys	Val	Ser
				485					490					495	
Val	Ala	Trp	Gln	Lys	Pro	Tyr	Leu	Gln	Gln	Thr	Glu	Phe	Leu	Leu	Thr
			500					505					510		
Phe	Gln	Ala	Val	Asn	Ser	Thr	Asn	Val	Asn	Ser	Tyr	Val	Thr	Asp	Asp
			515					520				525			
Tyr	Phe	Gly	Leu	Leu	Asp	Asp	Gln	Pro	Ala	Ser	Val	Asn	Ile	Gly	Trp
530						535					540				
Arg	Asn	Tyr	Asn	Met	Ala	Val	Gly	Arg	Phe	Pro	Val	Arg	Thr	Pro	Ala
545					550					555					560
Glu	Ala	Arg	Ile	Ala	Val	Asp	Lys	Thr	Ile	Arg	Tyr	Glu	Glu	Asp	Arg
				565					570					575	
Glu	Ser	Gly	Ala	Trp	Arg	Ile	Arg	Ala	Cys	Phe	Ala	Ala	Asp	Asn	Gly
			580					585					590		
Asp	Lys	His	Ala	Thr	Glu	Thr	Ser	Arg	Leu	Ile	Asp	Thr	Val	Lys	Arg
		595					600					605			
Tyr	Ala	Pro	Ala	Ile	Met	Pro	Val	Arg	Ala	Phe	Gln	Asp	Val	Tyr	Pro
610						615					620				
His	Val	Ile	Glu	Asn	Gly	Leu	His	Ser	Ile	Pro	Gly	Ala	Lys	Lys	Lys
625					630					635					640
Met	Leu	Glu	Thr	Leu	Gln	Ser	Gly	Ile	Ile	Leu	Leu	Asn	Tyr	Ala	Gly
				645					650					655	
His	Gly	Gly	Pro	Ala	Gly	Trp	Ser	Asp	Glu	His	Leu	Leu	Thr	Leu	Asn
			660					665					670		
Asp	Ile	His	Lys	Phe	Asn	Tyr	Lys	His	Met	Pro	Ile	Trp	Ile	Thr	Ala
			675					680				685			
Thr	Cys	Asp	Phe	Ala	Asn	Tyr	Asp	Ser	Gln	Thr	Thr	Ser	Ala	Gly	Glu
690						695					700				
Glu	Val	Phe	Leu	His	Glu	Lys	Ser	Gly	Thr	Pro	Ile	Met	Phe	Ser	Thr
705					710					715					720
Thr	Arg	Val	Val	Tyr	Asn	Thr	Gln	Asn	Glu	Lys	Ile	Asn	Gly	Phe	Met
				725					730					735	
Leu	Arg	Arg	Met	Phe	Glu	Lys	Ala	Lys	Asp	Gly	Arg	Tyr	Arg	Thr	Met
			740					745					750		
Gly	Glu	Ile	Ile	Arg	Ser	Ala	Lys	Gln	Gly	Met	Leu	Ser	Thr	Val	Phe
			755				760				765				
Pro	Asp	Ser	Ile	Asn	Gln	Leu	Ser	Phe	Phe	Leu	Met	Gly	Asp	Pro	Ser
770						775					780				
Val	Arg	Met	Asn	Leu	Pro	Thr	His	Lys	Val	Gln	Leu	Thr	Ala	Ile	Asn
785					790					795					800
Gly	Gln	Asp	Pro	Glu	Gly	Gln	Tyr	Gly	Thr	Ile	Met	Leu	Lys	Ser	Leu
			805						810					815	

Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu Lys Gly Thr Phe
 820 825 830
 Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val Phe Asp Gly Arg
 835 840 845
 Lys Lys Met Thr Ala Leu Glu Glu Gly Asn Asp Leu Ser Leu Val
 850 855 860
 Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile Ala Glu Val Lys
 865 870 875 880
 Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys Asp Val Asn Tyr
 885 890 895
 Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr Asn Glu Ser Thr
 900 905 910
 Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg Val Gln Pro Gly
 915 920 925
 Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro Glu Ile Ile Ser
 930 935 940
 Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp Glu Val Asn Pro
 945 950 955 960
 Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn Gly Ile Asn Ile
 965 970 975
 Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys Ile Asp Gly Arg
 980 985 990
 Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr Ser Ser Ala Thr
 995 1000 1005
 Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro Ala Leu Ala Glu
 1010 1015 1020
 Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile Phe Asn Asn Ala
 1025 1030 1035 1040
 Val His His Asp Phe Ser Phe Arg Val Val Asp Gly Ile Ala Pro Asp
 1045 1050 1055
 Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg Glu Ser Ala Thr
 1060 1065 1070
 Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu Asn Val Ala Val
 1075 1080 1085
 Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser Leu Pro Val Lys
 1090 1095 1100
 Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile Lys Trp Asp Leu
 1105 1110 1115 1120
 Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe Tyr Leu Tyr Arg
 1125 1130 1135
 Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser Met Ala Lys Lys
 1140 1145 1150
 Met Ile Val Val Gly Gln
 1155

(2) INFORMATION FOR SEQ ID NO:524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524

Met Lys Lys Leu Phe Pro Leu Leu Leu Ile Leu Ser Ile Leu Val
 1 5 10 15
 Gly Cys Gly Lys Lys Glu Lys His Ser Val Thr Glu Ile Ala Arg Glu
 20 25 30
 Lys Lys Arg Ile Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp
 35 40 45
 Ser Val Lys Lys Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val
 50 55 60
 Gly Gln Met Leu Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met
 65 70 75 80
 Ser Gln Tyr Thr Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala
 85 90 95

Ala Leu Asn Leu Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His
 100 105 110
 Leu Gly Thr Asp Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp
 115 120 125
 Tyr His Tyr Lys Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln
 130 135 140
 Asn Arg Pro Ala Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly
 145 150 155 160
 Asn Ile Asn Leu Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe
 165 170 175
 Leu Lys Ala Leu Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln
 180 185 190
 Ala Ile Asn Tyr Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu
 195 200 205
 Tyr Asp Lys Ala Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn
 210 215 220
 Met Ala Glu Asn Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly
 225 230 235 240
 Glu Val Asp Glu Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr
 245 250 255
 Ala Thr Ala Tyr Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp
 260 265 270
 Leu Asn Ser Cys Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn
 275 280 285
 Glu Arg Leu Tyr Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys
 290 295 300
 Glu Ile Asn Ser Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr
 305 310 315 320
 Glu Asn Leu Glu Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe
 325 330 335
 Cys Leu Ser Lys Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val
 340 345 350
 Ser Ser Ile Gln Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln
 355 360 365
 Lys Glu Leu Glu Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys
 370 375 380
 Ser Lys Phe Ile Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile
 385 390 395 400
 Leu Leu Ile Ser Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His
 405 410 415
 Asn Lys Leu Ile Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr
 420 425 430
 Gly Ile Thr His Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu
 435 440 445
 Asn Glu Lys Met Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr
 450 455 460
 Glu Leu His Lys Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu
 465 470 475 480
 Val Asn Gln Leu Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr
 485 490 495
 Pro Glu Trp Arg Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile
 500 505 510
 Asp Ser Phe Ala Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu
 515 520 525
 Gln Pro Glu Ser Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu
 530 535 540
 Gln Lys Ile Ile Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu
 545 550 555 560
 Ala Gly Gly Arg Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys
 565 570 575
 Asn Leu Ile Ile Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr
 580 585 590
 Asp Gln Ala His Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr
 595 600 605
 Glu Lys His Gly Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val
 610 615 620
 Glu Asn Leu Arg Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly
 625 630 635 640
 Ser Ala Phe Thr Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala
 645 650 655
 Glu Ile Leu Pro Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val
 660 665 670
 His Ile Ala Pro Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu
 675 680 685
 Asn His Arg Phe Glu Asp Glu Arg Pro Thr Ile Leu Val Glu Asp
 690 695 700
 Asn Lys Asp Ile Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr

705					710					715					720	
Asn	Val	Leu	Ser	Ala	Ala	Asn	Gly	Lys	Glu	Gly	Ile	Ala	Leu	Ala	Thr	
				725					730					735		
Glu	His	Ile	Pro	Asp	Ile	Ile	Ile	Thr	Asp	Ile	Met	Met	Pro	Ile	Met	
				740					745					750		
Asp	Gly	Ile	Glu	Met	Thr	Ile	Arg	Met	Lys	Gln	Ser	Pro	Leu	Leu	Cys	
				755					760					765		
His	Ile	Pro	Ile	Val	Ala	Leu	Thr	Ala	Lys	Ser	Thr	Glu	Gln	Asp	Arg	
				770					775					780		
Leu	Glu	Gly	Ile	Lys	Ser	Gly	Val	Val	Ser	Tyr	Leu	Cys	Lys	Pro	Phe	
				785					790					795		
Ser	Pro	Glu	Glu	Leu	Leu	Met	Arg	Ile	Glu	Gln	Leu	Leu	Lys	Asp	Arg	
				805					810					815		
Glu	Leu	Leu	Lys	Lys	Phe	Tyr	Met	Gln	Lys	Leu	Met	Leu	Asp	Arg	Lys	
				820					825					830		
Pro	Glu	Glu	Glu	Pro	Gln	Pro	Ile	Asp	Asp	Ser	Ser	Met	Gln	Phe	Leu	
				835					840					845		
Leu	Ala	Ala	Lys	Asp	Ala	Val	Ser	Gly	Gly	Ile	Lys	Gln	Asn	Pro	Asp	
				850					855					860		
Phe	Ser	Ala	Gln	Asp	Leu	Ala	Glu	Lys	Met	Cys	Met	Ser	Pro	Ser	Gln	
				865					870					875		
Leu	Asn	Arg	Lys	Leu	Thr	Ser	Val	Val	Gly	Cys	Ser	Thr	Ile	Gly	Tyr	
				885					890					895		
Ile	Gln	Gln	Ile	Lys	Ile	Lys	Leu	Ala	Cys	Lys	Leu	Leu	Ala	Asp	Glu	
				900					905					910		
Ser	Lys	Asn	Ile	Ser	Asp	Ile	Ser	Ile	Glu	Ala	Gly	Phe	Ser	Asp	Pro	
				915					920					925		
Ala	Tyr	Phe	Ser	Arg	Thr	Phe	Lys	Arg	Tyr	Met	Asn	Cys	Ser	Pro	Ser	
				930					935					940		
Gln	Tyr	Arg	Gln	Lys	Leu	Leu	Ala	Met	Pro	Gly	Ser	Asp	Lys	Glu	Thr	
				945					950					955		
Val																

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525

180	185	190
Val Gln Ser His Ile Ala Tyr	Thr Glu Asn Ser Ser Leu Ser Gln Ala	
195	200	205
Gln Val Asn Gln Lys Met Lys Asp Tyr Leu Gly Ile Thr His His Asp		
210	215	220
Val Val Gln Asp Pro Asn Gly Glu Tyr Ile Asn His Val Asp Cys Trp		
225	230	235
Gly Lys Tyr Leu Ala Pro Asn Lys Ile Leu Ile Arg Lys Val Pro Asp		
245	250	255
Asn His Pro Gln His Gln Ala Leu Glu Asp Met Ala Ala Tyr Phe Ala		
260	265	270
Ala Gln Thr Cys Ala Trp Gly Thr Lys Tyr Glu Val Tyr Arg Ala Leu		
275	280	285
Ala Thr Asn Glu Gln Pro Tyr Thr Asn Ser Leu Ile Leu Asn Asn Arg		
290	295	300
Val Phe Val Pro Val Asn Gly Pro Ala Ser Val Asp Asn Asp Ala Leu		
305	310	315
Asn Val Tyr Lys Thr Ala Met Pro Gly Tyr Glu Ile Ile Gly Val Lys		
325	330	335
Gly Ala Ser Gly Thr Pro Trp Leu Gly Thr Asp Ala Leu His Cys Arg		
340	345	350
Thr His Glu Val Ala Asp Lys Gly Tyr Leu Tyr Ile Lys His Tyr Pro		
355	360	365
Ile Leu Gly Glu Gln Ala Gly Pro Asp Tyr Lys Ile Glu Ala Asp Val		
370	375	380
Val Ser Cys Ala Asn Ala Thr Ile Ser Pro Val Gln Cys Tyr Tyr Arg		
385	390	395
Ile Asn Gly Ser Gly Ser Phe Lys Ala Ala Asp Met Thr Met Glu Ser		
405	410	415
Thr Gly His Tyr Thr Tyr Ser Phe Thr Gly Leu Asn Lys Asn Asp Lys		
420	425	430
Val Glu Tyr Tyr Ile Ser Ala Ala Asp Asn Ser Gly Arg Lys Glu Thr		
435	440	445
Tyr Pro Phe Ile Gly Glu Pro Asp Pro Phe Lys Phe Thr Cys Met Asn		
450	455	460
Glu Thr Asn Thr Cys Thr Val Thr Gly Ala Ala Lys Ala Leu Arg Ala		
465	470	475
Trp Phe Asn Ala Gly Arg Ser Glu Leu Ala Val Ser Val Ser Leu Asn		
485	490	495
Ile Ala Gly Thr Tyr Arg Ile Lys Leu Tyr Asn Thr Ala Gly Glu Glu		
500	505	510
Val Ala Ala Met Thr Lys Glu Leu Val Ala Gly Thr Ser Val Phe Ser		
515	520	525
Met Asp Val Tyr Ser Gln Ala Pro Gly Thr Tyr Val Leu Val Val Glu		
530	535	540
Gly Asn Gly Ile Arg Glu Thr Met Lys Ile Leu Lys		
545	550	555

(2) INFORMATION FOR SEQ ID NO:526

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526

Met Lys Leu Ser Ser Lys Lys Ile Leu Ala Ile Ile Ala Leu Leu Thr	
1	5 10 15
Met Gly His Ala Val Gln Ala Gln Phe Val Pro Ala Pro Thr Thr Gly	
	20 25 30
Ile Arg Met Ser Val Thr Thr Thr Lys Ala Val Gly Glu Lys Ile Glu	
	35 40 45
Leu Leu Val His Ser Ile Glu Lys Lys Gly Ile Trp Ile Asp Leu Asn	
	50 55 60
Gly Asp Ala Thr Tyr Gln Gln Gly Glu Glu Ile Thr Val Phe Asp Glu	

65		70		75		80
Ala Tyr His Glu Tyr Thr Ile Gly Thr Gln Thr Leu Thr Ile Tyr Gly						
	85			90		95
Asn Thr Thr Arg Leu Gly Cys Arg Ser Thr Gly Ala Thr Ala Val Asp						
	100		105		110	
Val Thr Lys Asn Pro Asn Leu Thr Tyr Leu Ala Cys Pro Lys Asn Asn						
	115		120		125	
Leu Lys Ser Leu Asp Leu Thr Gln Asn Pro Lys Leu Leu Arg Val Trp						
	130		135		140	
Cys Asp Ser Asn Glu Ile Glu Ser Leu Asp Leu Ser Gly Asn Pro Ala						
145		150		155		160
Leu Ile Ile Leu Gly Cys Asp Arg Asn Lys Leu Thr Glu Leu Lys Thr						
	165		170		175	
Asp Asn Asn Pro Lys Leu Ala Ser Leu Trp Cys Ser Asp Asn Asn Leu						
	180		185		190	
Thr Glu Leu Glu Leu Ser Ala Asn Pro Arg Leu Asn Asp Leu Trp Cys						
	195		200		205	
Phe Gly Asn Arg Ile Thr Lys Leu Asp Leu Ser Ala Asn Pro Leu Leu						
210		215		220		
Val Thr Leu Trp Cys Ser Asp Asn Glu Leu Ser Thr Leu Asp Leu Ser						
225		230		235		240
Lys Asn Ser Asp Val Ala Tyr Leu Trp Cys Ser Ser Asn Lys Leu Thr						
	245		250		255	
Ser Leu Asn Leu Ser Gly Val Lys Gly Leu Ser Val Leu Val Cys His						
	260		265		270	
Ser Asn Gln Ile Ala Gly Glu Glu Met Thr Lys Val Val Asn Ala Leu						
	275		280		285	
Pro Thr Leu Ser Pro Gly Ala Gly Ala Gln Ser Lys Phe Val Val Val						
	290		295		300	
Asp Leu Lys Asp Thr Asp Glu Lys Asn Ile Cys Thr Val Lys Asp Val						
305		310		315		320
Glu Lys Ala Lys Ser Lys Asn Trp Arg Val Phe Asp Phe Asn Gly Asp						
	325		330		335	
Ser Asp Asn Met Leu Pro Tyr Glu Gly Ser Pro Thr Ser Asn Leu Ala						
	340		345		350	
Val Asp Ala Pro Thr Val Arg Ile Tyr Pro Asn Pro Val Gly Arg Tyr						
	355		360		365	
Ala Leu Val Glu Ile Pro Glu Ser Leu Leu Gly Gln Glu Ala Ala Leu						
	370		375		380	
Tyr Asp Met Asn Gly Val Lys Val Tyr Ser Phe Ala Val Glu Ser Leu						
385		390		395		400
Arg Gln Asn Ile Asp Leu Thr His Leu Pro Asp Gly Thr Tyr Phe Phe						
	405		410		415	
Arg Leu Asp Asn Tyr Thr Thr Lys Leu Ile Lys Gln						
	420		425			

(2) INFORMATION FOR SEQ ID NO:527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527

Met Arg Lys Thr Ile Ile Phe Cys Leu Leu Leu Ala Leu Phe Gly Cys						
1		5		10		15
Ser Trp Ala Gln Glu Arg Val Asp Glu Lys Val Phe Ser Ala Gly Thr						
	20		25		30	
Ser Ile Phe Arg Gly Ile Leu Glu Lys Val Lys Ala Pro Leu Met Tyr						
	35		40		45	
Gly Asp Arg Glu Val Trp Gly Met Ala Arg Ala Ser Glu Asp Phe Phe						
	50		55		60	
Phe Ile Leu Pro Val Thr Asp Asp Leu Thr Pro Val Leu Phe Tyr Asn						
65		70		75		80
Arg Leu Thr Asn Glu Pro Cys Phe Val Ser Asp Gln Gly Ile Thr Glu						

210	215	220
Val Val Gln Gln Gly	Lys Ala Trp Gln Val	Leu Lys Arg Glu Glu Tyr
225	230	235
Thr Tyr Glu Asp Asn	Cys Ile Gln Tyr Leu	Ala Ile Asn Gly Thr
245	250	255
Asp Thr Lys Val Tyr	Lys Arg Asp Ile Glu Ser	Asp Lys Ser Ile Ser
260	265	270
Ala Asn Val Ile Asp	Ile Pro Ser Met Pro Glu	Gln Thr Trp Pro Asn
275	280	285
Met Tyr Gly Phe Asn	Ala Lys Arg Leu Lys Glu	Thr Tyr Ser Ser Tyr
290	295	300
Glu Gly Asp Val Ala	Thr Pro Ile Phe Asp Tyr	Ile Tyr Thr Tyr Lys
305	310	315
Ala Leu Thr Ser Met	Ala Thr Pro Ser Thr Glu	Ala Gln Val Ala Val
325	330	335
Tyr Leu Asn Pro Ser	Thr Asp Arg Leu Val Ile	Leu Ala Asn Gly Ile
340	345	350
Thr His Leu Ser Met	Tyr Asp Leu Gln Gly Lys	Leu Ile Arg Asp Cys
355	360	365
Ala Leu Ser Gly Asp	Lys Val Glu Met Gly Val	Gly Ser Leu Thr Lys
370	375	380
Gly Thr Tyr Leu Leu	Lys Val Asn Thr Asp Gln	Gly Ala Phe Val Arg
385	390	395
Lys Val Val Ile Arg		400
405		

(2) INFORMATION FOR SEQ ID NO:529

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...2037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529

GTAATGGACT	ACAAACTCAC	TTCTCGATTC	AAGCCCACGG	GCGACCAGCC	GGAAGCCATT	60
CGCCAACCTG	TACAGGGCAT	CAACGAAGGG	ATGCCGGCTC	AGACGCTGCT	CGGCGTAACG	120
GGTTCGGGCA	AAACTTTTAC	GGTGGCTAAC	GTGGTGGCGG	CGGTCAATCG	TCCGACCCCT	180
GTCCTGAGTC	ACAACAAGAC	CTTGGCAGCA	CAGCTATACG	GAGAGTTCAA	AGCCTTCTTC	240
CCCGAGAATG	CGGTGGAGTA	TTTCGTCAGC	TACTACGACT	ACTATCAGCC	CGAGGCCTAC	300
CTCCCCGTCA	CAGACACCTA	TATCGAAAAG	GACATGGCCA	TCAACGCGGA	GATCGAAAAA	360
TGCGCATTTG	GGGCCACGGC	TTGCTCCTG	TCAGGGCGGA	AAGATGTGCT	TGTGGTCAGC	420
TCCGTATCCT	GTCTCTACGG	TATGGCCAAT	CCTGAAGCTT	TTTCCGAAAA	GGTGATCAGC	480
CTGCACACGG	GACAAAGGGC	AGACAGGGAT	CATTTTATCC	GCCTGCTGGT	AGAGAGCTAC	540
TACACGAACA	ATAAAGTAGA	GTTTCGAGAG	GGCAACTTCC	GTGTCAAAGG	CGACAGCGTG	600
GACATATTCC	CCGCCGTAGA	AGGTTATGAC	GGCGTGGCAT	ACAGGGTGGA	GTTTTGGGAT	660
GGAGAGGTCT	AGCGGCTGAG	TACCTTCGAT	CCGCGAACGG	GACGGGAATA	CGGCCTGCTG	720
TCGGAGCTGA	AGATATATCC	GGCCAATCTC	TTCTGTGACG	CTAAGGAGCA	GGTGGATCGG	780
GCAGTAGGGA	AAATCGATGT	GGATCTGGGC	GCACAGGTCT	ATTTTCTGAA	AGAAATCGGC	840
AAACCATATG	AAGCCAAACG	CTTGATATGAG	CGGGTCACGT	ATGACTTGGA	AATGATCCGT	900
GAGTTGGGTT	ATTGTTCCGG	TATAGAGAAC	TATTCGCGCT	ACTTCGACGG	CCGTGACGCG	960
GGCGAACGTC	CTTTCTGTCT	GTTGGATTAT	TTCCCGGAGG	ATTTCTGTGT	GGTCATAGAC	1020
GAAAGCCATG	TAACGATACC	GCAGATACGT	GCCATGTACG	GAGGCGATCG	TTGCGCGAAG	1080
GAGAATCTGG	TCGAATACGG	ATTCCGCCTG	CCTGCCGCTC	TCGACAATCG	GCCGCTTCGC	1140
TTGACGAGT	TCGAAGCTCT	CACCCCCCGG	ACCCTTTATA	TCAGTGCCAC	GCCTGCCGAC	1200
TATGAGCTGA	ACAGAAGCGA	AGGCGTGATC	GTCGAGCAGC	TGATCCGTCC	GACCGGACTG	1260
CTGGATCCCA	TCATCGACGT	CAAGCCGACG	GCAAACCAAG	TGGACGATCT	GATGGAGGAG	1320
ATAGACGCTG	GCATCGAAAA	GAAAGAGCGC	GTACTGGTAA	CGACCTTGAC	CAAACGTATG	1380
GCAGAGGAGC	TTAGCGAATA	CCTGCTACGC	CACGGTATCA	GCACCGGCTA	CATACACAGC	1440
GATGTGGACA	CGCTGGAGCG	TGTGCGTATC	ATGGAAGACC	TGCGCAAGGG	GGTCTACGAT	1500
GCACTCATCG	GGGTGAATCT	GCTCCGCGAA	GGATTGGACT	TGCCGGAAGT	TTGCTTGTG	1560
GCTATTCTGG	ATGCGGATAA	GGAAGGATTG	CTGCGCTCGC	ATCGTTCGCT	CACGCAGACT	1620
GCAGGACGTG	CCGCCCGGCA	CATTTCATGG	CGTGTCTACT	TCTACGCGGA	CAAGATCACC	1680

GACAGTATGC	AGCTCACCAT	GGACGAGACT	GCACGCCGAC	GCGCAAAGCA	ACTGGCCTAC	1740
AACGAAGCGC	ACGGGATCAC	CCCCCAACAG	ATAGTGAAGA	ACAGTGCTGC	CATTTGGGGA	1800
GAAGGCGATG	TGTCGGCCTT	GCAATCCGAT	ACAGAATCCG	GTGCGTACAT	AGAAGAGAGC	1860
AGCATGGTGG	CTGCCGATCC	TTTGCCCGAC	TATCTGAGCA	AACCCAAGCT	GGAAGCACTC	1920
ATTGCTTCGA	CCAAGAAGCA	AATGTGGCA	GCAGCCAAAG	AGCTGGACTT	TCTGGAAGCG	1980
GCACGACTTC	GGGACGAAGC	CGCACGATTG	GAAAAGAAAC	TGGAGCAACT	CACAGCC	2037

(2) INFORMATION FOR SEQ ID NO:530

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2034 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Porphyromonas gingivalis
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...2034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530

ATGGACTACA	AACTCACTTC	TCGATTCAAG	CCACGGGCG	ACCAGCCGGA	AGCCATTTCG	60
CAACTCGTAC	AGGGCATCAA	CGAAGGGGATG	CCGGCTCAGA	CGCTGCTCGG	CGTAACGGGT	120
TCGGGCAAAA	CTTTTACCGT	GGCTAACGTG	GTGGCGGCGG	TCAATCGTCC	GACCCTTGTC	180
CTGAGTCACA	ACAAGACCTT	GGCAGCACAG	CTATACGGAG	AGTTCAAAGC	CTTCTTCCCC	240
GAGAAATGCG	TGGAGTATTT	CGTCAGCTAC	TACGACTACT	ATCAGCCCGA	GGCCTACCTC	300
CCCGTCACAG	ACACCTATAT	CGAAAAGGAC	ATGGCCATCA	ACGCGGAGAT	CGAAAACTG	360
CGATTGAGGG	CCACGGCTTC	GCTCCTGTCA	GGGCGGAAAG	ATGTGCTTGT	GGTCAGCTCC	420
GTATCCTGTC	TCTACGGTAT	GGCCAATCCT	GAAGCTTTTT	CCGAAAAGGT	GATCAGCCTG	480
CACACGGGAC	AAAGGGCAGA	CAGGGATCAT	TTTATCCGCC	TGCTGGTAGA	GAGCTACTAC	540
ACGAACAATA	AAGTAGAGTT	CGAGAGCGGC	AACCTCCGTG	TCAAAGGCGA	CAGCGTGGAC	600
ATATTTCCCG	CCGTAGAAGG	TTATGACGGC	GTGGCATA	GGGTGGAGTT	TTGGGATGGA	660
GAGGTCGAGC	GGCTGAGTAC	CTTCGATCCG	CGAACGGGAC	GGAATACGG	CCTGCTGTGC	720
GAGCTGAAGA	TATATCCGGC	CAATCTCTTC	GTGACGACTA	AGGAGCAGGT	GGATCGGGCA	780
GTAGGGAAAA	TCGATGTGGA	TCTGGGCGCA	CAGGTCGATT	TTCTGAAAGA	AATCGGCAAA	840
CCATATGAAG	CCAAACGCTT	GTATGAGCGG	GTCACGTATG	ACTTGGAAT	GATCCGTGAG	900
TTGGGTTATT	GTTCCGGTAT	AGAGAATAT	TCGCGTACT	TCGACGGCCG	TGACGCGGGC	960
GAACGTCCTT	TCTGTCTGTT	GGATTATTTC	CCGGAGGATT	TCCTGTTGGT	CATAGACGAA	1020
AGCCATGTAA	CGATACCGCA	GATACGTGCC	ATGTACGGAG	GCGATCGTTC	GCGCAAGGAG	1080
AATCTGGTCG	AATACGATT	CCGCCTGCCT	GCCGCTCTCG	ACAATCGGCC	GCTTCGCTTC	1140
GACGAGTTTC	AAGCTCTCAC	CCCCCGGACC	CTTTATATCA	GTGCCACGCC	TGCCGACTAT	1200
GAGCTGAACA	GAAGCGAAGG	CGTGATCGTC	GAGCAGCTGA	TCCGTCCGAC	CGGACTGCTG	1260
GATCCCATCA	TCGACGTCAA	GCCGACGGCA	AACCAAGTGG	ACGATCTGAT	GGAGGAGATA	1320
GCACGCTGCA	TCGAAAAGAA	AGAGCGCGTA	CTGGTAACGA	CCCTGACCAA	ACGTATGGCA	1380
GAGGAGCTTA	GCGAATACCT	GCTACGCCAC	GGTATCAGCA	CCGGCTACAT	ACACAGCGAT	1440
GTGGACACGC	TGAGGCTGTG	GCGTATCATG	GAAGACCTGC	GCAAGGGGGT	CTACGATGCA	1500
CTCATCGGGG	TGAATCTGCT	CCGCGAAGGA	TTGGACTTGC	CGGAAGTTTC	GCTTGTGGCT	1560
ATTCTGGATG	CGGATAAGGA	AGGATTCTCTG	CGCTCGCATC	GTTCTGCTCAC	GCAGACTGCA	1620
GGACGTGCCG	CCCGGCACAT	TCATGGGCGT	GTCATCTTCT	ACGCGGACAA	GATCACCAGC	1680
AGTATGCAGC	TCACCATGGA	CGAGACTGCA	CGCCGACGCG	CAAAGCAACT	GGCCTACAAC	1740
GAAGCGCACG	GCATCACCCC	CCAACAGATA	GTGAAGAACA	GTGCTGCCAT	TTGGGGAGAA	1800
GGCGATGTGT	CGGCCTTGCA	ATCCGATACA	GAATCCGGTG	CGTACATAGA	AGAGAGCAGC	1860
ATGGTGGCTG	CCGATCCTTT	GGCCGACTAT	CTGAGCAAAC	CCAAGCTGGA	AGCACTCATT	1920
GCTTCGACCA	AGAAGCAAAT	GCTGGCAGCA	GCCAAAGAGC	TGGACTTTCT	GGAAGCGGCA	1980
CGACTTCGGG	ACGAAGCCGC	ACGATTGGAA	AAGAACTGG	AGCAACTCAC	AGCC	2034

(2) INFORMATION FOR SEQ ID NO:531

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 679 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531

```
Val Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln
1      5      10      15
Pro Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro
      20      25      30
Ala Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val
      35      40      45
Ala Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His
      50      55      60
Asn Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe
      65      70      75      80
Pro Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln
      85      90      95
Pro Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met
      100     105     110
Ala Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser
      115     120     125
Leu Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Val Ser Cys
      130     135     140
Leu Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser
      145     150     155     160
Leu His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu
      165     170     175
Val Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn
      180     185     190
Phe Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly
      195     200     205
Tyr Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu
      210     215     220
Arg Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu
      225     230     235     240
Ser Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu
      245     250     255
Gln Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln
      260     265     270
Val Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu
      275     280     285
Tyr Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr
      290     295     300
Cys Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala
      305     310     315     320
Gly Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu
      325     330     335
Leu Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met
      340     345     350
Tyr Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe
      355     360     365
Arg Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe
      370     375     380
Glu Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp
      385     390     395     400
Tyr Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg
      405     410     415
Pro Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn
      420     425     430
Gln Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys
      435     440     445
Glu Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu
      450     455     460
Ser Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser
      465     470     475     480
Asp Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys
      485     490     495
Gly Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu
      500     505     510
Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu
      515     520     525
Gly Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala
```



```

      530              535              540
Ala Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr
545              550              555              560
Asp Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys
      565              570              575
Gln Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val
      580              585              590
Lys Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln
      595              600              605
Ser Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala
      610              615              620
Ala Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu
      625              630              635              640
Ile Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp
      645              650              655
Phe Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys
      660              665              670
Lys Leu Glu Gln Leu Thr Ala
      675

```

(2) INFORMATION FOR SEQ ID NO:532

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532

```

Met Asp Tyr Lys Leu Thr Ser Arg Phe Lys Pro Thr Gly Asp Gln Pro
1              5              10              15
Glu Ala Ile Arg Gln Leu Val Gln Gly Ile Asn Glu Gly Met Pro Ala
      20              25              30
Gln Thr Leu Leu Gly Val Thr Gly Ser Gly Lys Thr Phe Thr Val Ala
      35              40              45
Asn Val Val Ala Ala Val Asn Arg Pro Thr Leu Val Leu Ser His Asn
      50              55              60
Lys Thr Leu Ala Ala Gln Leu Tyr Gly Glu Phe Lys Ala Phe Phe Pro
      65              70              75              80
Glu Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro
      85              90              95
Glu Ala Tyr Leu Pro Val Thr Asp Thr Tyr Ile Glu Lys Asp Met Ala
      100             105             110
Ile Asn Ala Glu Ile Glu Lys Leu Arg Leu Arg Ala Thr Ala Ser Leu
      115             120             125
Leu Ser Gly Arg Lys Asp Val Leu Val Val Ser Ser Val Ser Cys Leu
      130             135             140
Tyr Gly Met Ala Asn Pro Glu Ala Phe Ser Glu Lys Val Ile Ser Leu
      145             150             155             160
His Thr Gly Gln Arg Ala Asp Arg Asp His Phe Ile Arg Leu Leu Val
      165             170             175
Glu Ser Tyr Tyr Thr Asn Asn Lys Val Glu Phe Glu Ser Gly Asn Phe
      180             185             190
Arg Val Lys Gly Asp Ser Val Asp Ile Phe Pro Ala Val Glu Gly Tyr
      195             200             205
Asp Gly Val Ala Tyr Arg Val Glu Phe Trp Asp Gly Glu Val Glu Arg
      210             215             220
Leu Ser Thr Phe Asp Pro Arg Thr Gly Arg Glu Tyr Gly Leu Leu Ser
      225             230             235             240
Glu Leu Lys Ile Tyr Pro Ala Asn Leu Phe Val Thr Thr Lys Glu Gln
      245             250             255
Val Asp Arg Ala Val Gly Lys Ile Asp Val Asp Leu Gly Ala Gln Val
      260             265             270
Asp Phe Leu Lys Glu Ile Gly Lys Pro Tyr Glu Ala Lys Arg Leu Tyr
      275             280             285
Glu Arg Val Thr Tyr Asp Leu Glu Met Ile Arg Glu Leu Gly Tyr Cys

```

290		295		300
Ser Gly Ile Glu Asn Tyr Ser Arg Tyr Phe Asp Gly Arg Asp Ala Gly				
305	310		315	320
Glu Arg Pro Phe Cys Leu Leu Asp Tyr Phe Pro Glu Asp Phe Leu Leu				
	325		330	335
Val Ile Asp Glu Ser His Val Thr Ile Pro Gln Ile Arg Ala Met Tyr				
	340		345	350
Gly Gly Asp Arg Ser Arg Lys Glu Asn Leu Val Glu Tyr Gly Phe Arg				
	355		360	365
Leu Pro Ala Ala Leu Asp Asn Arg Pro Leu Arg Phe Asp Glu Phe Glu				
	370		375	380
Ala Leu Thr Pro Arg Thr Leu Tyr Ile Ser Ala Thr Pro Ala Asp Tyr				
385	390		395	400
Glu Leu Asn Arg Ser Glu Gly Val Ile Val Glu Gln Leu Ile Arg Pro				
	405		410	415
Thr Gly Leu Leu Asp Pro Ile Ile Asp Val Lys Pro Thr Ala Asn Gln				
	420		425	430
Val Asp Asp Leu Met Glu Glu Ile Ala Arg Cys Ile Glu Lys Lys Glu				
	435		440	445
Arg Val Leu Val Thr Thr Leu Thr Lys Arg Met Ala Glu Glu Leu Ser				
	450		455	460
Glu Tyr Leu Leu Arg His Gly Ile Ser Thr Gly Tyr Ile His Ser Asp				
465	470		475	480
Val Asp Thr Leu Glu Arg Val Arg Ile Met Glu Asp Leu Arg Lys Gly				
	485		490	495
Val Tyr Asp Ala Leu Ile Gly Val Asn Leu Leu Arg Glu Gly Leu Asp				
	500		505	510
Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu Gly				
	515		520	525
Phe Leu Arg Ser His Arg Ser Leu Thr Gln Thr Ala Gly Arg Ala Ala				
	530		535	540
Arg His Ile His Gly Arg Val Ile Phe Tyr Ala Asp Lys Ile Thr Asp				
545	550		555	560
Ser Met Gln Leu Thr Met Asp Glu Thr Ala Arg Arg Arg Ala Lys Gln				
	565		570	575
Leu Ala Tyr Asn Glu Ala His Gly Ile Thr Pro Gln Gln Ile Val Lys				
	580		585	590
Asn Ser Ala Ala Ile Trp Gly Glu Gly Asp Val Ser Ala Leu Gln Ser				
	595		600	605
Asp Thr Glu Ser Gly Ala Tyr Ile Glu Glu Ser Ser Met Val Ala Ala				
	610		615	620
Asp Pro Leu Ala Asp Tyr Leu Ser Lys Pro Lys Leu Glu Ala Leu Ile				
625	630		635	640
Ala Ser Thr Lys Lys Gln Met Leu Ala Ala Ala Lys Glu Leu Asp Phe				
	645		650	655
Leu Glu Ala Ala Arg Leu Arg Asp Glu Ala Ala Arg Leu Glu Lys Lys				
	660		665	670
Leu Glu Gln Leu Thr Ala				
675				

BSI
cont